(19) World Intellectual Property Organization International Bureau





(43) International Publication Date 10 April 2003 (10.04.2003)

PCT

(10) International Publication Number **WO 03/029432 A2**

(51) International Patent Classification	17: C12N	(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
(21) International Application Number	r: PCT/US02/31662	CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC
(22) International Filing Date: 3 Octo	ber 2002 (03.10.2002)	LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG.
(25) Filing Language:	English	SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ VN, YU, ZA, ZM, ZW.
(26) Publication Language:	English	
(30) Priority Data:	01 (03.10.2001) US	(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW). Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM)

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28 November 2001 (28.11.2001)

20 September 2002 (20.09.2002)

28 January 2002 (28.01.2002)

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60/334,277

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Published:

without international search report and to be republished upon receipt of that report

GW, ML, MR, NE, SN, TD, TG).

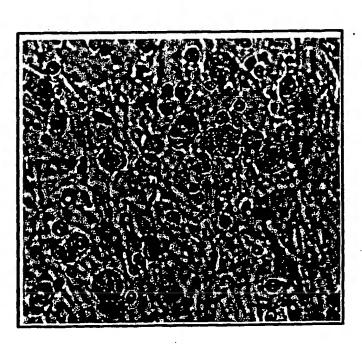
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,

ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK,

TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN MESENCHYMAL PROGENITOR CELL



(57) Abstract: Pluri-differentiated human mesenchymal progenitor cells (MPCs) are isolated. A method isolates and purifies human mesenchymal progenitor cells from Dexter-type cultures for characterization of and uses, particularly therapeutic uses for such cells. Specifically, isolated MPCs can be used for diagnostic purposes, to enhance the engraftment of hematopoietic progenitor cells, enhance bone marrow transplantation, or aid in the treatment or prevention of graft versus host disease.

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HUMAN MESENCHYMAL PROGENITOR CELL FIELD OF THE INVENTION

The present invention generally relates to pluri-differentiated mesenchymal progenitor cells and therapeutic uses for the same. More specifically, the isolated mesenchymal progenitor cells are isolated from hematopoietic cells and macrophages in Dexter-type cultures cells.

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BACKGROUND OF THE INVENTION

Bone marrow, the site of blood cell production and home to various leukemia and lymphoma cells, comprises a complex cellular population including hematopoietic progenitor or stem cells and the stromal cells that support them. Hematopoietic stem cells have the capacity for self-regeneration and for generating all blood cell lineages while stromal stem cells have the capacity for self-renewal and for producing the hematopoietic microenvironment.

Two bone-marrow culture systems introduced in the mid-1970's have evolved as favored media for the *in vitro* analysis of mesengenesis and hematopoiesis. The Friedenstein culture system was introduced in 1976 as a media for the analysis and study of mesengenesis. (Friedenstein, et al, in *Exp Hematol* 4,267-74 (1976). In order to obtain mesenchymal stem cells (MSCs) for expansion in the culture medium, it is necessary to first isolate rare pluripotant mesenchymal stem cells from other cells in the bone marrow. In the Friedenstein culture system, isolating the nonhematopoietic cells is achieved by utilizing their tendency to adhere to plastic. Once isolated, a monolayer of homogeneous, undifferentiated stromal cells is then grown in the culture medium, in the <u>absence</u> of hematopoietic cells. The stromal cells from this system have the potential to differentiate into discrete mesenchymal tissues, namely bone, cartilage, adipose tissue and muscle depending on specific growth supplements. These MSCs have been the target of extensive investigation including exploration of their potential clinical utility in repair or replacement of genetically damaged mesenchymal tissues.

In 1977, Dexter, et al. developed another bone marrow culture system for the study of hematopoiesis. (Dexter et al. *J Cell Physiol 91*, 335-44 (1977). The Dexter culture does not require isolation of the mesenchymal cells before culturing. Thus, the monolayer of stromal cells is grown in the <u>presence</u> of hematopoietic cells. Greenberger later modified the Dexter system by the addition of hydrocortisone to

the culture medium, making it more reproducible (Greenberger, *Nature 275*, 752-4 (1978).

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Based on the Dexter system's ability to support sustained growth and preservation of hematopoietic progenitor cells, it has become the standard *in vitro* model for the study of hematopoiesis. Although the Dexter-type stromal cells and the MSCs in Friedenstein-type cultures express similar cytokine/growth factor profiles, the Dexter cultures have been found to be more efficient at maintaining preservation of hematopoietic progenitor cells. Over the last 23 years, questions have remained as to whether the cells from the Dexter cultures retained the potential to differentiate, like the MSCs in the Friedenstein culture, or whether they have differentiated into another and discrete phenotype due to their interaction with the hematopoietic cells (Prockop, *Science* v276 n5309, p71(4)(April 1997)). It has been widely believed that the stromal cells of the Dexter cultures are a heterogeneous mixture of adipocytes, osteoblasts, fibroblasts, muscle cells, and vascular endothelial cells.

The *in vitro* analysis and study of hematopoiesis in Friedenstein and Dexter culture systems has been of great importance in both veterinary and human medicine. A number of diseases and immune disorders, as well as malignancies, appear to be related to disruptions within the hematopoietic system.

Allogeneic bone marrow transplantation is the preferred treatment for a variety of malignant and genetic diseases of the blood and blood-forming cells. The success rate of allogeneic bone marrow transplantation is, in large part, dependent on the ability to closely match the major histocompatibility complex of the donor cells with that of the recipient cells to minimize the antigenic differences between the donor and the recipient, thereby reducing the frequency of host-versus-graft responses and graft-versus-host disease (GvHD). Unfortunately, only about 20% of all potential candidates for bone marrow transplantation have a suitable family member match.

Bone marrow transplantation can be offered to those patients who lack an appropriate sibling donor by using bone marrow from antigenically matched, genetically unrelated donors (identified through a national registry), or by using bone marrow from a genetically related sibling or parent whose transplantation antigens differ by one to three of six human leukocyte antigens from those of the patient. Unfortunately, the likelihood of fatal GvHD and/or graft rejection increases from 20%

for matched sibling donors to 50% in the cases of matched, unrelated donors and un-matched donors from the patient's family.

The potential benefits of bone marrow transplantation have stimulated research on the cause and prevention of GvHD. The removal of T cells from the bone marrow obtained from matched unrelated or unmatched sibling donors results in a decreased incidence of graft versus host reactions, but an increased incidence of rejection of the allogeneic bone marrow graft by the patient.

Current therapy for GvHD is imperfect, and the disease can be disfiguring and/or lethal. Thus, risk of GvHD restricts the use of bone marrow transplantation to patients with otherwise fatal diseases, such as severe immunodeficiency disorders, severe aplastic anemia, and malignancies.

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The potential to enhance engraftment of bone marrow or stem cells from antigenically mis-matched donors to patients without graft rejection or GvHD would greatly extend the availability of bone marrow transplantation to those patients without an antigenically matched sibling donor.

Thus, it would be useful to develop methods of improving and/or enhance bone marrow transplantation by enhancing the engraftment of bone marrow or hematopoietic progenitor cells and/or decreasing the occurrence of graft rejection or GvHD in allogenic transplants.

Studies of hematopoiesis and mesengenesis and the urgent need for improved methods of treatment in the field of bone marrow transplants have led to the isolation of MSCs from bone marrow stroma. These MSCs are the same pluripotential cells that result from expansion in Friedenstein type cultures. Several patents describe the isolation and therapeutic uses of these MSCs.

U.S. Patent No. 5,486,359, to Caplan, et al., discloses isolated human MSCs, and a method for their isolation, purification, and culturing. Caplan, et al. also describes methods for characterizing and using the purified mesenchymal stem cells for research, diagnostic, and therapeutic purposes. The invention in `359, to Caplan, et al., describes pluri-potential cells that remain pluri-potential, even after cultural expansion. Caplan, et al. also teaches that it is necessary to first isolate the pluri-potent MSCs from other cells in the bone marrow and then, in some applications, uses culture medium to expand the population of the isolated MSCs. The Caplan et al. patent fails to disclose the use of Dexter-type cultures, pluri-

differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

U.S. Patent No. 5,733,542, to Haynesworth, et al., discloses methods and preparations for enhancing bone marrow engraftment in an individual by administering culturally expanded MSC preparations and a bone marrow graft. U.S. Patent 6,010,696, to Caplan, et al., discloses methods and preparations for enhancing hematopoietic progenitor cell engraftment in an individual by administering culturally expanded MSC preparations and hematopoietic progenitor cells. The cells utilized in the Haynesworth, et al. patent and the `696 patent to Caplan, et al. are the pluri-potential cells described in U.S. Patent 5,486,359. Neither patent discloses the use of Dexter-type cultures, pluri-differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

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Mesenchymal stem cells that are isolated from bone marrow are further described by Prockop, in *Science* v276 n5309, p71 (4)(1997) and Pittenger, et al. in *Science* v284 i5411, p143 (1). These articles also describe pluri-potential but undifferentiated MSCs and fail to teach or disclose a pluri-differentiated mesenchymal cell or the isolation of mesenchymal cells from Dexter- type cultures.

While the cells disclosed in the prior art may provide some benefit, the isolated MSCs in the prior art have not solved the problems associated with engraftment of hematopoietic progenitor cells or bone marrow. Consequently, there exists a need in the art for methods of improving engraftment of hematopoietic progenitor cells and bone marrow in mammals in need of such treatment. There also exists a need in the art for treating and preventing the occurrence of GvHD in mammals that receive allogeneic bone marrow transplants.

SUMMARY OF THE INVENTION

According to the present invention there is provided isolated pluridifferentiated mesenchymal progenitor cells, a method of isolation, diagnostic uses, and therapeutic uses relating to enhancing the engraftment of human bone marrow or hematopoietic progenitor cells and treating GvHD.

The present invention provides an isolated mesenchymal progenitor cell that is pluri-differentiated.

Accordingly, the present invention also provides a method for purifying pluri-differentiated mesenchymal progenitor cells including the steps of: providing a

cell culture preparation by the Dexter method, treating the cells to obtain a cell suspension, removing macrophages, fractionating the cells, and collecting the fraction of pluri-differentiated mesenchymal progenitor cells.

The present invention also provides a method for enhancing bone marrow engraftment in a mammal in need thereof which includes administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

The present invention provides a method for enhancing engraftment of hematopoietic progenitor cells in a mammal in need thereof which includes the step of administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) hematopoietic progenitor cells, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the hematopoietic progenitor cells in the mammal.

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Another embodiment of the present invention provides a method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

Yet another embodiment of the present invention provides a method for diagnosing a disease state by: a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; c) identifying gene sets that are unique to a given state; and d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to the gene sets.

Additionally, the present invention provides a method for identifying therapeutic targets for treatment of hematopoietic function by: a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest; b)

identifying gene groups that are up-regulated, down regulated, and common to each disease state; and c) identifying gene sets that are unique to a given state.

The present invention also includes therapeutic compositions including isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein the pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance bone marrow engraftment in a mammal in need thereof; enhance hematopoietic progenitor cell engraftment in a mammal in need thereof; or treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.

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BRIEF DESCRIPTION OF THE FIGURES

Other advantages of the present invention can be readily appreciated as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings. The following is a brief description of the drawings which are presented only for the purposes of further illustrating the invention and not for the purposes of limiting same. Referring to the drawing figures, like reference numerals designate identical or corresponding elements throughout the several figures.

Figure 1 is a photograph showing the phase contrast photomicrograph view of a Dexter-type stromal cell monolayer reflecting on cellular complexity.

Figure 2 is a photograph showing the percoll gradient centrifugation technique of the present invention that purifies the MPCs (2) in large quantities to greater than 95% purity.

Figure 3 is a photograph showing the Wright-Giemsa staining of Dexter-type stromal cell cultures depicting three morphologically identifiable cell populations, macrophages (5), hematopoietic cells (3), and the mesenchymal progenitor cells (4) of the present invention.

Figures 4A-H show a series of photomicrographs showing the morphologic and phenotypic characteristics of the MPCs of the present invention, as uncovered by staining for representative mesenchymal cell lineage markers. The methods applied are shown in parentheses. (Figure 4A) Wright-Giemsa (Harleco stain using HMS Series Programmable Slide Stainer, Carl Zeiss, Inc.). (Figure 4B) Immunostain using anti-CD68 antibody (Immunotech, Clone PG-M1; Vector,

Vectastain Elite ABC Kit). (Figure 4C) Immunostain using anti-CD45 antibody (Dako, Clone PD7/26 & 2B11; ABC Kit). (Figure 4D) Periodic acid-Schiff (Sigma). (Figure 4E) Nile Red (Sigma), counterstained with DAPI (Vector). (Figure 4F) Alkaline phosphatase (Sigma Kit No. 85), counterstained with Nuclear Fast Red (Baker). (Figure 4G) Immunostain using antibody to fibronectin (Immunotech, Clone 120.5; ABC Kit). (Figure 4H) Immunostain using anti-muscle actin antibody (Ventana, clone HUC 1-1; Ventana system using a section of formalin-fixed, paraffin-embedded cell block, instead of a cytospin). Appropriate positive controls and isotype-matched negative controls were employed to ascertain antibody staining-specificity. All parts of figure as shown, except 4E and 4H, have clearly identifiable built-in cell controls. The morphological features of the cells are listed in row 1 of Table 1.

Figure 5 is a photograph which shows a transmission electron micrograph of an MPC of the present invention bearing microvilli, irregular nucleus, and pools of glycogen (6) in the ectoplasm (x 4,600).

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Figure 6A-M are photographs which show Northern blot analysis of bone marrow stromal cell RNAs for expression of genes specific for multiple mesenchymal cell lineages. Figures 6A-M represent different gene probes used for hybridization. The following outlines the sources of the gene probes employed and the approximate sizes of the major transcripts observed (shown in parentheses): Figure 6A) CD68 (Clone ID 3176179, Genome Systems, Inc (GSI); 2-3 kb); Figure 6B) Cathepsin B (Clone ID 2806166, GSI; 2-3 kb); Figure 6C) GAPDH probe (generated using PCR primers from R&D Systems, Inc; ~2 kb) hybridized to same blot as A and B; Figure 6 D) Adipsin (probe generated using PCR primers as described, Ref 20; 0.5-1 kb); Figure 6E) Osteoblast-specific cadherin-11 (Clone ID 434771, GSI; ~3 kb); Figure 6F) Chondroitin sulfate proteoglycan 2 (Clone ID 1623237, GSI; >10 kb); Figure 6G) Collagen type I alpha 1 (Clone ID 782235, GSI; >10 kb); Figure 6H) Decorin (Clone ID 3820761, GSI; 2-3 kb); Figure 6I) GAPDH probe hybridized to same blot as D-H; Figure 6J) Fibronectin (Clone ID 3553729, GSI; >10 kb); Figure 6K) Caldesmon (Clone ID 1319608, GSI; ~4 kb); Figure 6L) Transgelin (Clone ID 4049957, GSI; ~1.5 kb); and Figure 6M) GAPDH probe hybridized to same blot as J-L.

Figure 7 is a photograph which shows RT-PCR analysis for expression of representative hematopoietic growth factors (G-CSF and SCF) and extracellular

matrix receptors (ICAM-1, VCAM-1, and ALCAM) by the MPCs of the present invention.

Figure 8 is a graph comparing of the ability to support *in vitro* hematopoiesis by the purified MPCs (heavy fraction represented by gray) of the present invention vs. unfractionated bone marrow stromal cells (represented by black).

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Figures **9A** and Figure **9B** are graphs showing flow cytometric evidence of human hematopoietic cell engraftment in a SCID mouse cotransplanted with the MPCs of the present invention. Figure **9A** shows CD45+/CD34+ progenitors in the marrow. Figure **9B** shows CD45/CD34- mature hematopoietic cells circulating in the blood.

Figures 10A-H are photographs which show engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Figures 12A-C are photographs which show Southern blotting data. Figure 12A shows that hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) results in a 2.7 Kb band (7)

(arrow; autoradiogram exposed for only 45 minutes). Figure 12B shows EcoR1 digest of thymic genomic DNA from SCID mice. Figure 12C shows EcoR1 digest of lymph node genomic DNA from SCID mice. Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention vs. unpurified bone marrow stromal cells. In the line graphs provided the line with diamonds represents MPCs and bone marrow mononuclear cells, squares represents bone marrow mononuclear cells only, triangles represents unfractionated bone marrow stromal cells, the Xs represent MPCs only, and the circles represent the control. In the bar graphs, the gray bars represent mice that survived and the black bars represent mice with engraftment. Figures 14A-C are photographs which demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died.

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Figure 15 shows photomicrographs of single-cell MPCs that were isolated by laser capture microdissection (LCM) and subsequently targeted for microarray analysis.

Figure 16 shows a Venn diagram displaying the stromal-cell gene-list. Stromal cell genes are operationally defined as being active in at least 9 out of 10 single cell MPCs AND 4 out of 5 collective MPC samples AND 7 out of 8 collective USC samples, i.e., 20 of 23 samples tested. This criterion was very stringent and automatically excluded the outliers, independently of filtering for genes with weak expressions on the basis of control strength (referred to as C or CS). The stromal cell gene list of 2755 includes 13 AFFX microarray-assay positive controls.

Figure 17 shows a two-dimensional hierarchical clustering of 2755 stromal cell genes based on the expression profiles of 23 samples. The gene tree is displayed on top and the experiment or sample tree is shown on left. Accordingly, each column represents a particular gene on the chip and each row represents a separate stromal cell sample.

Figure 18 shows composite gene-expression plots of 2755 stromal cell genes comparing collective purified stromal cell samples (cMPC), collective

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unpurified stromal cell samples (cUSC) and single-cell stromal cell samples (sMPC). Individual samples are represented on X-axis. Normalized intensity of gene expression is shown on Y-axis in log scale.

Figures 19 A & B show gene-expression plots of diverse mesenchymal lineage-associated genes and housekeeping genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note the differing log scales, particularly the wide range of log scale for ACTB. Representative lineage markers are shown as follows. Osteoblast markers: osteoblast-specific factor 2 (probe ID 1451_s-at), osteoblast cadherin 11 (ID 2087_s_at) and collagen 1 alpha 2 (ID 32306_g_at). Muscle markers: caldesmon (ID 41738 at), transgelin-2 (ID 36678_at) and smooth muscle myosin heavy chain (ID 32838_at). Fibroblast markers: fibronectin (ID 31719_at) and prolyl 4-hydroxylase (ID 37037_at). Adipocyte markers: adipsin (ID 40282_at) and adipocyte-specific ECM protein (ID 39673_i_at). Housekeeping genes: GAPD (ID 35905_s_at) and ACTB (ID 32318_s_at). Samples 1-5, respectively, represent MPC A, MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1. SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

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Figure 20 shows gene-expression plots of representative precursor Blymphocyte-associated genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note that the CD markers that are traditionally associated with hematopoietic cells, CD45 (probe ID 40518_at), CD19 (ID 1116_at) and CD34 (ID (538_at), are expressed by sMPCs. CD45, when present, is more abundantly detected in single MPCs than in collective MPCs, and is particularly noticeable by wide range of log scale for CD45. The other pre-B cell associated markers that are expressed by sMPCs are CD10 (ID 1389_at), HLA-Dr (ID 33261_at) and CD79A (ID 34391_at). Samples 1-5, respectively, represent MPC A. MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1, SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

Figure 21 shows the master stromal cell table.

DETAILED DESCRIPTION OF THE INVENTION

Generally, the present invention provides isolated and purified mesenchymal progenitor cells that are pluri-differentiated. Also provided by the present invention is a therapeutic composition including an effective amount of isolated and purified pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier.

The terms "enhance" or "improve" as used herein are intended to indicate that the there is a more beneficial end result. In other words, the product provides a more effective result.

The term "pluri-differentiated" as used herein refers to cells that are a single cell type co-expressing genes specific for multiple lineages. The term "pluri-potential" as used herein refers to cells that are undifferentiated and have the potential to be differentiated into discrete mesenchymal tissues.

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Dexter-type cultures contain stromal cells that co-express multiple message lineage markers. These pluri-differentiated cells are referred to by the inventor as mesenchymal progenitor cells (MPCs). Disclosed herein is a process for isolating and purifying MPCs from Dexter-type cultures. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis.

The present invention also provides various methods for using MPCs to enhance bone marrow transplantation, enhance hematopoietic progenitor cell engraftment, for diagnostic purposes, or for the treatment of GvHD.

The exact cell types in Dexter cultures have been identified. No evidence was found for the existence of discrete cellular populations, such as adipocytes, osteoblasts, fibroblasts, smooth muscle cells and endothelial cells, notwithstanding the abundance of literature and wide spread belief (*See*, J.L. Liesveld *et al.*, *Blood* 73, 1794 (1989); A.K. Sullivan, D. Claxton, G. Shematek *et al.*, *Lab Invest* 60, 667 (1989); K. Dorshlind, *Ann Rev Immunol* 8, 126 (1990); S. Perkins, R.A. Fleischman, *Blood* 75, 620 (1990); I.A. Denkers, R.H. Beelen, G.J. Ossenkoppele *et al.*, *Ann Hematol* 64, 210 (1992); P.E. Penn, D.Z. Jiang, R.G. Fei *et al.*, *Blood* 81, 1205 (1993); E. de Wynter *et al.*, *J Cell Sci* 106, 761 (1993); A. Ferrajoli *et al.*, *Stem Cells (Dayt)* 12, 638 (1994); B.R. Clark, A. Keating, *Ann NY Acad Sci* 770, 70 (1995); B.S. Wilkins, D.B. Jones, *Br J Haematol* 90, 757 (1995); S. Gronthos, P.J. Simmons, *J Hematother* 5, 15 (1996); D. Soligo *et al.*, Abstract

#3926, Blood 94, Supplement 1 (Part 2 of 2), p. 168b, Forty 1st Annual Meeting of the American Society of Hematology, New Orleans, LA, December 3-7, 1999, M-A. Dorheim et al., J Cell Physiol 154, 317 (1993), M.K. Majumdar, M.A. Thiede, J.D. Mosca et al., J Cell Physiol. 176, 57 (1998), D.J. Prockop, Science 276, 71 (1997). R.S. Taichman, S.G. Emerson, J Exp Med 179, 1677 (1994); R.S. Taichman, M.J. Reilly, S.G. Emerson, Blood 87, 518 (1996); C.M. Verfaillie, in HEMATOLOGY: Basic Principles and Practice, R. Hoffman, et al., Eds. (Churchill Livingstone, New York, 2000), pp. 140-142.), A.J. Henderson, A. Johnson, K. Dorshkind, J Immunol 145, 423 (1990); M.W. Long, J.L. Williams, K.G. Mann, J Clin Invest 86, 1387 (1990); P.J. Simmons, S. Gronthos, A. Zannettino et al., Prog Clin Biol Res 389, 271 1994); B.A. Roecklein, B. Torok-Storb, Blood 85, 997 (1995); J. Wineman, K. Moore, 1. Lemischka et al., Blood 87, 4082 (1996); K.A. Kelly, J.M. Gimble, Endocrinology 139, 2622 (1998); K.C. Hicok et al., J Bone Miner Res 13, 205 (1998); S.R. Park, R.O. Oreffo, J.T. Triffitt, Bone 24, 549 (1999); J.E. Dennis et al., J Bone Miner Res 14, 700 (1999); and B. Torok-Storb et al., Ann NY Acad Sci 872, 164 (1999)). Instead, the inventor determined that there are only three types of cells in Dextertype cultures, namely, macrophages (~35%), hematopoietic cells (~5%), and a type applicant calls "nonhematopoietic cells" (~60%)(Figure 3, Figure 4A, and Table 1).

Bone marrow mesenchymal cells, the nonhematopoietic cells in Dexter type cultures, possess distinctive features that have previously gone unrecognized. There is both direct visual (Figures 4A-E and Figure 5) and molecular biological (Figure 6) evidence to support the existence of this unique cell type. These findings challenge the prevailing belief that stromal cells derived from Dexter cultures comprise multiple singly-differentiated mesenchymal cell types. Because Dexter cultures represent a primary cell culture system, and not a cell line, these studies indicate that cells in these primary cultures themselves are pluri-differentiated, which has been previously unsuspected. The nonhematopoietic cells of the present invention (MPCs) simultaneously express marker genes specific for multiple mesenchymal cell lineages, including adipocytes, osteoblasts, fibroblasts and smooth muscle cells. As shown in the present disclosure, MPCs can also differentiate into B cells and therefore be useful in affecting the functionality of the immune system.

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The MPCs in Dexter type cultures were characterized using a variety of techniques. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains. Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers.

Only rarely have investigators in this field taken the approach of preparing a cell suspension and staining cells on cytospins as was done to characterize the cells of the present invention (Simmons, et al., Nature 328, p429-32 (1987)) and no other group has used this method to address the issue of pluridifferentiation by bone marrow stromal cells. Almost all of the published studies in the field, with a rare exception (Simmons, et al., Nature, 328, p429-32 (1987)), conducted cytochemical and immunocytochemical staining on layers of stromal cells grown to confluence on coverslips. In this situation, the stromal cultures appear very complex especially in the areas of hematopoietic activity, so-called "cobblestones" with macrophages and hematopoietic cells enmeshed in them. Macrophages and nonhematopoietic cells spread themselves and assume varied shapes when they adhere to and grow on plastic or glass. This spreading further contributes to the The complexity precludes a clear perceived heterogeneity and complexity. morphological visualization of the nonhematopoietic cells and consequently interferes with the determination of what percent of what cell type is positive for any given marker.

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In terms of lineage markers, up to 100% of the nonhematopoietic cells or MPCs of the present invention expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the MPCs were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31.

In addition, the Dexter type stromal cells had not previously been subjected to Periodic Acid-Schiff (PAS) staining, which revealed a strong and uniform positivity by almost 100% of the MPCs studied. This indicates the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed

by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

The MPCs also exhibited cytoplasm compartmentalization into endoplasm and ectoplasm. This morphologic finding sheds light on their internal architecture because of correlation of restricted localization of glycogen and smooth muscle actin to ectoplasm; and the restricted localization of acid phosphatase, alkaline phosphotase, Nile Red, Oil Red O, fibronectin, and prolyl-4-hydrolase to endoplasm.

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Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting of unfractionated cells and purified MPCs to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

Taken together, the morphologic, cytochemical, and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter cultures co-express markers specific for at least four different mesenchymal cell lineages. Using a variety of techniques, applicant has demonstrated that the MPCs co-express multilineage mesenchymal cell phenotypes, and in this respect the multi-or pluri-differentiated MPCs are distinct from the pluri-potential, but undifferentiated, MSCs of Friedenstein cultures (Prockop, Science 276, 71-74 (1997).

The nonhematopoietic cells of the present invention were purified from the macrophages, the dominant "contaminating" cell type, using a Percoll gradient method developed by applicant. MPCs were purified by the following process: cells from a Dexter-type culture were treated to obtain a cell suspension, the macrophages were removed, and the cells were fractionated using discontinuous

Percoll gradient centrifugation (Figure 2). The isolated MPCs were then collected and washed.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

A purified source of MPCs is desirable for a number of reasons. The relative ease with which large numbers of the MPCs can be purified and their distinctive phenotypic characteristics make them valuable targets for future investigations. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis in addition to aiding in bone marrow transplantation.

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Another major reason that purified cells are desirable is that Dexter cultures also contain a significant percentage of highly immunogenic macrophages that can cause onset of GvHD after transplantation. The MPCs of the present invention are purified to ~95% free of macrophages and hematopoietic cells. Note the increased survival rate in Severe Combined Immunodeficiency Disease (SCID) mice that received purified MPCs versus those that received unfractionated bone marrow stromal cells in Figure 13B. This data establishes that stromal cells in combination with engraftment or other similar procedures enhances the effectiveness of the treatment.

The present invention also provides methods of enhancing the engraftment of hematopoietic cells and of enhancing the engraftment of bone marrow. The hematopoietic support capacity of the Dexter-type cultures has been repeatedly demonstrated by a number of investigators. RT-PCR analysis showed that Dexter cultures and Friedenstein cultures expressed a similar pattern of cytokine and growth factor mRNAs; yet, Dexter cultures were found to be more efficient than Friedenstein cultures in achieving preservation of hematopoietic progenitors (Majumdar, et al., J.Cell.Physiol., 176, 57-66.). The pluri-differentiated MPC is capable of supporting hematopoiesis, as shown by its ability to express

representative hematopoietic growth factors/cytokines, i.e., G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e., ICAM-1, VCAM-1 and ALCAM (Figure 7).

Clarification of the nature of the stromal cells and the ability to purify these cells makes it possible to use them as an adjuvant in bone marrow transplantation following high-dose chemotherapy and radiation therapy. These treatment modalities not only cause damage to the hematopoietic stem cells but also to the supportive stromal cells. However, because the bone marrow microenvironment is destroyed, hematopoietic progenitor cell engraftment is delayed until the stromal environment is restored. As a result, a critical aspect of the current invention is directed to the advantages of transplanting isolated mesenchymal progenitor cells to accelerate the process of stromal reconstruction and ultimately bone marrow engraftment. The stromal cells present in the standard bone marrow transplant are not sufficient in number and can be supplemented with the cultured MPCs of the present invention.

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Yet another embodiment of the current invention provides the use of MPC transplantation to major leukemic conditions, such as acute myeloid leukemia (AML), myelodysplastic syndromes (MDS), chronic myeloid leukemia (CML) and multiple myeloma (MM). This is based on applicant's determination that bone marrow stromal cells in a leukemia patient are functionally and structurally defective, regardless of the damage caused by chemotherapy and radiation therapy. Such defects in bone marrow stromal cells are likely to aid and abet leukemia development. Alternatively, stromal cell defects could be secondarily induced by surrounding leukemia cells, thus contributing to the loss of hematopoietic support function of stromal cells and hematopoietic failure, which is an invariable feature in leukemia. Regardless whether the observed stromal cell defects are primary or secondary to the leukemic process, by reason of their indisputable impact on normal hematopoiesis, these defects remain to be corrected to improve the hematopoietic function.

Stromal cells have never been carefully investigated in terms of genomics in view of the widespread belief that they represent a heterogeneous mixture of cell types. Tissue or cellular heterogeneity presents a major challenge for the application of microarray technology. The purified stromal cells of the present

invention represent a single pluridifferentiated MPC which allows for genomic study of the stromal cells and the development of new, more objective diagnostic tools for patients suffering from leukemia conditions.

The present invention provides a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time. These findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency and are extremely difficult to study at the present time. The development of this phenotype forms the basis for various diagnostic tests including a comprehensive test that can be used to screen for different abnormalities of bone marrow stromal cells in various hematologic diseases and other diseases effecting stromal cells.

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Results show that isolated single stromal cells simultaneously express transcripts for osteoblasts, fibroblasts, muscle cells and adipocytes. Furthermore, there is shown that isolated single stromal cells simultaneously express transcripts for epithelial cells and neural/glial cells as well as transcripts for CD45, CD19, CD10, CD79a, and representative proto-oncogenes and transcription factors, typically known to be affiliated with normal and neoplastic hematopoietic cells. These findings are evidence of existence of a progenitor cell that is common to nonhematopoietic mesenchymal cells and hematopoietic cells, particularly B-lymphocytes. "Lineage burst" characterized by simultaneous activation of diverse differentiation pathways within the same cell appears to be the signature profile of a stromal cell, indicating that a "pluripotent" cell is "pluridifferentiated" at the molecular level. That is, prior to a selective and full-fledged lineage differentiation, progenitors express genes associated with multiple lineages to which they might possibly commit, thus providing insight into the molecular basis of cellular plasticity.

Transcriptomic analysis has been undeniably contributing to the molecular definition of new disease categories with demonstrable therapeutic benefit. The present invention contributes to the further definition of the stromal cell by refining its molecular signature. The *in vivo* identification of the stromal cell and its possible ontogenic variants as they might occur in different hematological diseases and subsequent targeting of these cells holds the key to ultimately treating some, if not all, of these diseases.

By comprehensively defining the gene expression profile of these cells, the present invention demonstrates the technical applicability of single-cell genomics toward understanding the physiology and pathology of both hematopoietic and nonhematopoietic microenvironments. Classically, the adventitial reticular cells located on the abluminal side of the vascular endothelium within the bone marrow microenvironment were thought to represent the stromal cells or their precursors. As with hematopoietic stem or progenitor cells, the stromal progenitor cells are rare in bone marrow occurring at an estimated frequency of 1 in 10⁵ nucleated cells. Cultured stromal cells represent the progeny of the stromal cell, and not necessarily the stromal cell itself, for which no *in vivo* assay exists as yet. The technology of single-cell genomics and the blueprint as described in the present invention allows screening for the abnormalities of bone marrow stromal cells in fresh marrow samples that reflect on the ultimate *in vivo* context.

The ability to purify culture-expanded MPCs from both normal individuals and patients afflicted with various leukemias also allows testing of the hematopoietic supportive role of MPCs in mice models. These systems provide an *in vivo* model in which to examine the role of human bone marrow microenvironment in normal and leukemic hematopoiesis.

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The SCID mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice has required either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments. As disclosed herein MPCs are a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow.

Unlike prior methods, the isolated MPCs of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral neuronal ganglia of SCID mice (Figures 10A-H and Figures 11A-C). By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment (Figure 13A and Figure 13B).

The present invention also provides for a method of preventing or treating GvHD. The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified whole marrow stroma and the bone marrow mononuclear cells. The increased mortality observed is related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse (see Figure 14A). While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). In contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

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The above results indicate that purified MPCs can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. The evidence shows that the increased survival is due to a reduction in GvHD.

Allogeneic bone marrow transplantation is the preferred method of treatment for a variety of malignant and genetic diseases of the blood and blood forming cells. However, failure of hematopoietic cell engraftment can occur for a number of reasons. These include, microenvironmental defects as part of the underlying disease itself (e.g., aplastic anemia), and/ or stromal cell damage caused by chemoradiotherapy and/ or microenvironmental damage as part of GvHD which is a dreaded complication following bone marrow transplantation. In GvHD, donor T cells present in the hematopoietic cell graft destroy host tissues. GvHD can involve multiple organs such as skin, liver, GI system etc. The current treatment modalities for preventing or treating graft failure or GvHD are cumbersome, costly and involve some form of immunosuppression. Stromal cell lesions, either primary to the disease process or secondarily induced by allogeneic bone marrow transplantation, play a prominent role in the success or failure of the hematopoietic cell graft. Cotransplantation of MPC not only enhances hematopoietic cell engraftment but

also prolongs the life of graft recipients by minimizing GvHD. Co-transplantation of healthy, culture-expanded MPC is a viable option in these situations.

The human bone marrow used in the Dexter-type cultures of the present invention can be obtained from a number of different sources in accordance with the procedures known in the art, including from plugs of femoral head cancerous bone pieces or from aspirated marrow. The cells used in the Dexter culture can be autologous, from the tissue donor, or from other individuals.

Modes of administration of MPCs include, but are not limited to, systemic intravenous injection and injection directly to the intended site of activity. The MPCs can be administered by any convenient route, for example by infusion or bolus injection, and can be administered together with other biologically active agents. Administration is preferably systemic.

The methods of the present invention can be altered, particularly by (1) increasing or decreasing the time interval between administering MPCs and implanting the tissue, cells, or implanting the organs; (2) increasing or decreasing the amount of MPCs administered; (3) varying the number of MPC administrations; (4) varying the method of delivery of the MPCs; and/or (5) varying the source of MPCs.

The MPC preparations are used in an amount effective to promote engraftment of hematopoietic progenitor cells or bone marrow cells; or for the treatment or prevention of GvHD in the recipient. The pharmaceutically effective amount for the purposes herein is thus determined by such considerations as are known in the art. In general, such amounts are typically at least 1x10⁴ MPCs per kg of body weight and most generally need not be more than 7x10⁵ MPCs/kg.

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The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of MPCs and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to McCoy's medium, saline, buffered saline, dextrose, water, and combinations thereof. The formulation should suit the method of administration as is known by those of skill in the art.

In one embodiment, the MPC preparation or composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous

administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a local anesthetic to ameliorate any pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a cryopreserved concentrate in a hermetically sealed container such as an ampoule indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

The present invention paves the way for applications of mesenchymal progenitor cells in the field of transplantation with respect to hematopoietic support, immunoregulation, and graft facilitation. MPCs can be used as a supporting cell type in bone marrow transplantation, particularly in diseases where defects in the hematopoietic stromal microenvironment are believed to prevail, such as aplastic anemia, myelofibrosis, and bone marrow failure following high dose chemotherapy and radiation therapy.

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Another aspect of the invention provides a method for diagnosing various disease states in mammals by identifying new diagnostic markers, specifically the classification and diagnosis of leukemia. Prior to the present invention, stromal cells were not carefully investigated in terms of genomics because of the widespread belief that they represent a heterogeneous mixture of cell types and cellular heterogeneity presents significant challenges for the application of genetic analysis such as microarray technology. The isolated MPCs of the present invention represent a single cell type and allow for genomic study of the stromal cells.

Using the methods of the present invention, it has been determined that bone marrow stromal cells in leukemia patients are functionally and structurally defective regardless of the damage caused by chemotherapy and radiation therapy. Given the almost 25 year history and intense interest in bone marrow stromal cell cultures, previous documentation of stromal cell abnormalities has been disappointingly low (Martinez & Martinez, Exp. Hematol 11:522-26 (1983); Budak-Alpdogan, et al., Am.J.Hematol, 62:212-20 (1999); Nagao, et al., Blood, 61:589-92

(1983); Peled, et al., Exp.Hematol 24:728-37 (1996); Bhatia, et al., Blood 85:3636-45 (1995); Agarwal, et al., Blood 85:1306-12 (1995); Diana, et al., Blood 96:357a(2000)). By identifying gene sets that are unique to a given state, these differences in the stromal cells can be utilized for diagnostic purposes.

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In one embodiment of the invention, isolated MPCs from a patient are assayed for expression of a large number of genes. The gene expression profile is projected into a profile of gene set expression values according to the definition of gene sets. A reference database containing a number of reference projected profiles is also created from the isolated MPCs of patients with known states, such as normal and various leukemic disease states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the patient matches best with the profile of a particular disease state in the database, the patient is diagnosed as having such disease state. Various computer systems and software (see Example 5) can be utilized for implementing the analytical methods of this invention and are apparent to one of skill in the art. Some of these software programs include Cluster & TreeView (Stanford, URLs: rana.lbl.gov or www.microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: http://www.spotfire.com/products/scicomp.asp#SAE) and GeneSpring (Silicon Genetics Inc, URL: http://www.sigenetics.com/Products/GeneSpring/index.html) (for computer systems and software, see also U.S. Patent No. 6,203,987).

The methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment.

One aspect of the present invention provides methods for therapeutic and drug discovery utilizing bone marrow derived isolated mesenchymal progenitor cells. The present invention can be utilized to identify stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function, which is constantly compromised, in leukemic patients. In one embodiment, gene sets are defined using cluster analysis. The genes within a gene set are indicated as potentially co-regulated under the conditions of interest. Co-regulated genes are further explored as potentially being involved in a regulatory pathway. Identification

of genes involved in a regulatory pathway provides useful information for designing and screening new drugs.

Some embodiments of the present invention employ gene set definition and projection to identify drug action pathways. In one embodiment, the expression changes of a large number of genes in response to the application of a drug are measured. The expression change profile is projected into a gene set expression change profile. In some cases, each of the gene sets represents one particular pathway with a defined biological purpose. By examining the change of gene sets, the action pathway can be deciphered. In some other cases, the expression change profile is compared with a database of projected profiles obtained by perturbing many different pathways. If the projected profile is similar to a projected profile derived from a known perturbation, the action pathway of the drug is indicated as similar to the known perturbation. Identification of drug action pathways is useful for drug discovery. See, Stoughton and Friend, Methods for Identifying pathways of Drug Action, U.S. patent application Ser. No. 09/074,983.

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The present invention provides a genomics strategy method for identifying genes differentially expressed in MPCs. The method begins with the preparation of total RNA from MPC samples, which leads to the generation of cDNA. From the cDNA, ds DNA can be prepared for *in vitro* transcription into cRNA. The cRNA is then fragmented for the hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray). Finally, analysis of differentially expressed genes is accomplished using appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type (e.g., up-regulation or down-regulation).

Up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. The combination enables those of skill in the art to identify gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also

provide insights into pathogenesis and targets for design of new drugs. For example, the method allows one to establish transcriptional profiles of MPC genes that are pathologically altered.

Those of skill in the art can use the data and methods contained herein for the following: a) study select gene or sets of genes that are relevant to hematopoietic disease conditions by using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc depending on the research interests of the individual investigators.

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The present invention also provides a large-format 2-D gel electrophoretic system for the reproducible separation of MPC proteins and for preparing 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF- α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/ premalignant and leukemic/ malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lyinphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples consist of culture supernatants/secreted proteins, extracellular matrix (ECM) proteins, plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The 2-D system described herein utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini non-denaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample

loads (up to 1.5 to 2.0 mg of total protein in up to 350 µl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for the purpose of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

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EXAMPLES

The examples presented herein can be summarized as follows. The data disclosed herein demonstrate that Dexter cultures consist of only three cell types macrophages (~35%), hematopoietic cells (~5%), and nonhematopoietic cells (~60%). Using a percoll gradient centrifugation technique, the nonhematopoietic mesenchymal progenitor cells were isolated, free of macrophages and hematopoietic cells. A variety of techniques were used to identify the isolated cells as a multi-differentiated mesenchymal cell lineage co-expressing genes specific for multiple mesenchymal cell lineages including adipocytes, osteoblasts, fibroblasts and muscle cells.

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Evidence that this multi- or pluri-differentiated mesenchymal progenitor cell is capable of supporting hematopoiesis is shown by the expression of a number of hematopoietic growth factors and extracellular matrix receptors. The SCID mouse experimental data provides evidence that since the MPCs can be purified to near

homogeneity (95%) with relative ease, MPCs can be of value for enhancing engraftment of hematopoietic stem cells and bone marrow transplants. Additionally, increased survival rate in the SCID mouse model indicates that isolated MPCs can also be useful for the treatment of GvHD. An example of the administration of bone marrow cells and MPCs to breast cancer patients treated with chemotherapy is also provided.

A stepwise genomics strategy and an example of the genomic changes observed in leukemia associated MPCs is also provided. Cluster analysis was performed to show gene expression patterns in isolated MPCs of a normal individual and individuals with different leukemic conditions. The approach presented provides the basis for a new more objective means to diagnose patients suffering from leukemic conditions.

EXAMPLE 1

Isolation and Characterization of MPCs from Dexter-Type Bone Marrow Stromal Cell
Culture Systems

Bone marrow culture:

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Bone marrow samples were obtained from posterior superior iliac crest under general anesthesia for standard marrow transplantation. Marrow stromal cell cultures were set up using the residual cells recovered from the filters of Fenwal Bone Marrow Collection System after complete filtration of the marrow samples. The filters were rinsed with phosphate-buffered saline without Ca²⁺ and Mg²⁺ (PBS-CMF). The cell suspension was subjected to Ficoll gradient isolation of the mononuclear cells (bone marrow MNCs). The bone marrow MNCs were washed (x2) in PBS-CMF and suspended in McCoy's 5A with HEPES medium containing 12.5% fetal bovine serum (FBS), 12.5% horse serum, 1 µM/L hydrocortisone and 1% penicillin/streptomycin (for this study McCoy's complete medium) and cultured under standard stromal-cell culture conditions (Figure 1) (Seshi, *et al. Blood* 83, 2399 (1994) and Gartner, *et al. Proc Natl Acad Sci USA* 77, 4756 (1980). After two weeks, confluent stromal cell cultures were trypsinized (first passage), followed by splitting each T75 flask into two T150 flasks.

Morphologic and phenotypic characteristics of MPCs as uncovered by staining for representative mesenchymal cell lineage markers:

Two weeks after the first passage (above), confluent stromal cells were again trypsinized. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains.

Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers. As illustrated in Table 1 and Figures 3 and 4A, Wright-Giemsa staining revealed three morphologically identifiable cell populations in Dexter type stromal cell cultures, macrophages, hematopoietic cells, and nonhematopoietic cells (labeled 4, 3, and 5, respectively).

The identity of macrophages was confirmed by immunostain using anti-CD68 antibody (Figure 4B) and cytochemical stains for acid phosphatase and Sudan black. The identity of hematopoietic cells (including macrophages) was confirmed by immunostain using anti-CD45 antibody (Figure 4C).

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The remaining nonhematopoietic cells stained intensely positive for Periodic acid-Schiff, which was diastase sensitive, signifying the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

In terms of lineage markers, up to 100% of the nonhematopoietic cells expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the nonhematopoietic cells were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31 (data not shown).

The results indicate that the nonhematopoietic cells of the Dexter cultures are in fact a single, pluri-differentiated cell type co-expressing multiple mesenchymal cell lineage markers. The pluri-differentiated mesenchymal progenitor cells reported here are to be distinguished from the pluri-potential, but

undifferentiated, MSCs that are generated in the absence of hematopoietic cells, such as in Friedenstein-type cultures.

Table 1. Reactivity patterns $\,$ f bon $\,$ marrow stromal c $\,$ lis based $\,$ n cyt $\,$ l $\,$ gical, cytochemical and $\,$ immunocytochemical stains*,***

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	Figure Test Utilized		Macrophages Hematopoletic cells		Mesenchymai progenitor cells	
1	3 and 4A	Wright- Giemsa (Harleco)	Large cells with a small round minimal amount of cytoplasm: 35% of total cells		Large cells with a relatively irregular nucleus & cytoplasm compartmentalized into ectoplasm and endoplasm: 60% of total cells	
2	4D	Periodic acid-Schiff (PAS) (Sigma)	0	0	~100% MPCs: staining restricted to ectoplasm in a ring-like fashion; and completely abolished by diastase digestion	
3	4C	CD45 (Dako, PD7/26 & 2B11)	100% macrophages (M Φ)	100% HCs	0	
4	4B	CD68 (Immunotec h, clone PG-M1)	100% MΦ 0 -		0	
5		Sudan Black (Sigma)	~100% МФ 0		0	
6		Acid phosphatas e (Sigma Kit No. 387)	100% MΦ; positive granules packed throughout cytoplasm	0	100% MPCs; positive granules in moderate amounts; staining restricted to endoplasm	
7	4E	Nile Red (Sigma)	0	0	~100% MPCs: staining restricted to endoplasm	
8		Oil Red O (Sigma)		0	~ 95% MPCs: variable number of positive granules; staining preferentially in the endoplasm	
9	4F	Alkaline phosphatas e (Sigma Kit No. 85)	0	0	~100% MPCs: variable number of positive granules; staining restricted to endoplasm & plasma membrane**	
1 0	4G	Fibronectin (Immunotec h, clone 120.5)	0	0	~100% MPCs: staining restricted to endoplasm	
1		Prolyl-4- hydroxylase (Dako,	0	0	~100% MPCs: staining preferentially in the ndoplasm	

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		clone 5B5)			
1 2	4H	Muscle actin (Ventana, clone HUC 1-1)	0	0	> 85% MPCs: variable staining restricted to ectoplasm

*The lineages of the markers tested above are: 3, hematopoietic cell marker; 4, 5 and 6, monocyte/macrophage markers; 7 and 8, adipocyte markers; 9, osteoblast marker; 10 and 11, fibroblast markers; 12 muscle marker.

**One earlier study (Simmons, et al., Nature 328, 429-432) interpreted the localization of alkaline phosphatase staining as confined to the plasma membrane when in fact it is predominately present within the endoplasm (compare Figure 1C of this reference with Figure 4F).

*** While well-accepted mesenchymal lineage markers were used, these markers do not necessarily lend themselves to simultaneous assessment of the same cell. For example, muscle-specific actin antibody worked only on formalin-fixed, paraffin embedded material, whereas stains like alkaline phosphatase, Oil Red and Nile Red are not anti-body based and involve varying fixing and staining conditions. Thus, the evidence shows that close to 100% of members of a morphologically distinct population express multiple lineage markers of interest.

Bone marrow mesenchymal progenitor cell (MPC) purification:

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To further investigate the characteristics of the MPCs, the nonhematopoietic stromal cells were then purified from the macrophages (~95% pure), the dominant "contaminating" cell type using the following method. Confluent monolayers of stromal cells resulting from first passage, above, were washed for three minutes in Ca²⁺/Mg²⁺ free Hanks' balanced salt solution. Cells were incubated at room temperature for 45 minutes with intermittent mixing in serum-free McCoy's medium containing 10 mM L-leucine methyl ester (LME, Sigma). LME is a lysosomotropic agent that selectively kills and detaches macrophages. The detached macrophages were removed by washing the monolayers twice in McCoy's complete medium, followed by trypsinization of the monolayers. The resulting single cell suspensions were fractionated by discontinuous Percoll gradient (70%, 50%, 30%, 20%, 10%) centrifugation at 800xG for 15 minutes at 4°C in a fixed angle rotor (Avanti-J25 Beckman centrifuge) (Figure 2). Low-density cells representing the

macrophages resistant to detachment by LME separate as a band at the interface of serum and 10% Percoll and were discarded (1). High-density nonhematopoietic cells representing MPCs form a layer in the region of 30-50% Percoll (2). These were collected and washed twice by centrifugation through PBS-CMF. This protocol is conservatively expected to yield, >2.5x10⁶ MPCs per T-150 flask (i.e., >50x10⁶ MPCs per batch of 20 flasks). The purity of these preparations, typically about 95%, was routinely monitored by Wright-Giemsa staining.

Northern Blotting:

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Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization. The sources of the gene probes employed and the major transcripts observed are outlined in the brief description of the figures.

Total RNA was prepared by dissolving the high-density cell pellets in Trizol (Life-Technologies). Total RNA samples from unfractionated stromal cells and BM MNCs were similarly prepared. The RNA samples were electrophoresed in a standard 1% agarose gel containing 2% formaldehyde in MOPS/EDTA buffer and blotted onto Immobilon-Ny+ membrane. Probes were labeled using Prime-A-Gene Kit (Promega) and a³²P dCTP (NEN). Hybridization was performed at 65°C in modified Church's hybridization solution using 3x10⁶ counts/ml in 10 ml (Millipore, 1998).

In Figures **6A-M**, Northern blot analysis was performed side-by-side on fractionated stromal cells, non-hematopoietic cells freed of macrophages, and initial bone marrow mononuclear cell samples. Lanes 1 and 2 represent total RNA samples (10µg each) from unfractionated stromal cells (subjects S1 and S2, respectively). Lanes 3 and 4 represent total RNA samples (10µg each) from purified stromal MPCs (subjects S1 and S2, respectively). Lanes 5 and 6 represent total RNA samples (10µg each) from bone marrow mononuclear cells, the starting cells for bone marrow cell cultures (subjects S3 and S4, respectively).

The large transcripts, especially of collagen (lane 1, Figure 6G) and fibronectin (lane 1, Figure 6J), in RNA extracted from unfractionated stromal cells of subject 1 showed difficulty migrating into the gel. This observation correlates with the presence of an artifact of unresolved positive material in lane 1, Figure 6A. Since

the RNA extracted from unfractionated stromal cells of the subject 2 did not present this problem (lane 2, Figure 6G, Figure 6J and Figure 6A), the observation does not impact on the overall interpretation of the results (see text). The lineages of markers tested were: monocyte/macrophage markers, CD68 and cathepsin B; adipocyte marker, adipsin; osteoblast markers, osteoblast-specific cadherin-11, chondroitin sulfate proteoglycan 2, collagen type I alpha 1 and decorin; fibroblast marker, fibronectin; muscle markers, caldesmon and transgelin. Marker signals were normalized to the amount of RNA loaded, which was based on densitometry of the GAPDH signals on the corresponding blot (Bio-Rad Model GS-700 Imaging Densitometer). Attenuation or enhancement of the marker signals in the purified stromal MPCs (i.e., lanes 3 and 4) relative to unfractionated stromal cells (i.e., lanes 1 and 2, respectively) is shown as fold Δ (decrease/increase) underneath the lanes 3 and 4; ND, means not determined.

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The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

No trace of osteoblast, fibroblast, or smooth muscle cell markers were detected in the bone marrow mononuclear cells, suggesting a less than detectable level of stromal cells or their precursors in bone marrow mononuclear cells. However, the fat cell marker, adipsin, was detected in all samples including the bone marrow mononuclear cells.

Taken together, the morphologic, cytochemical and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter

cultures co-express markers specific for at least four different mesenchymal cell lineages.

This finding is especially intriguing because pluri-differentiation is often a feature of neoplastic cells (Brambilia and Brambilia, *Rev. Mal. Respir.* 3,235 (1986); Pfeifer et al., *Cancer Res.* 51, 3793-3801 (1991); Tolmay *et al.*, *Virchow's Arch* 430, 209-12 (1997). However, a cytogenetic analysis of the Percoll-gradient purified MPCs showed a normal GTW banding pattern.

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RT-PCR Analysis for expression of representative hematopoietic growth factors and extracellular matrix receptors by MPCs

RT-PCR was conducted in a total reaction volume of 100 μ l using 2 μ g each of total RNA; corresponding primers; and a master mix of the PCR reagents. The RT conditions included sequential incubations at 42°C for 15 minutes, 99°C for five minutes, and 5°C for five minutes. The PCR conditions included: initial melting at 94°C for four minutes; and cyclical melting at 94°C for 45 seconds, annealing at 55°C for 45 seconds and extension at 72°C for 45 seconds with 34 cycles. PCR was terminated after final extension at 72°C for ten minutes. Reaction products (G-CSF, SCF, each 25 μ l; VCAM-1, ALCAM, each 50 μ l; ICAM-1, 75 μ l) were concentrated as necessary; electrophoresed along with a 100-bp DNA ladder (GIBCO-BRL) in a standard agarose (1%) gel in TAE buffer; and stained with ethidium bromide.

PCR products, shown in Figure 7 lanes labeled 1-2, were generated using aliquots of the same RNA samples from purified stromal MPCs, as used for Northern blotting shown under Figure 6 lanes 3 and 4 respectively. The gene transcripts amplified were as follows: G-CSF (granulocyte-colony stimulating factor); (Tachibana et al., Br. J. Cancer, 76, 163-74 (1997); SCF (stem cell factor, i.e., c-Kit ligand); (Saito et al., Biochem, Biophys. Res. Commun., 13, 1762-69 (1994); ICAM-1 (intercellular adhesion molecule-1, CD54) and VCAM-1 (vascular cell adhesion molecule-1, CD106) (primers from R&D); and ALCAM (activated leukocyte cell adhesion molecule, CD166) (Bruder et al., J. Bone Miner. Res., 13, 655-63 (1998)).

The observed PCR products for G-CSF (600 bp, i.e., the top bright band) and ALCAM (175 bp) were significantly different from the expected sizes (278 bp; 372 bp, respectively). However, sequencing of the gel-purified PCR bands and subsequent BLAST search showed a 99-100% identity with respective members. Attempts to detect c-Kit (i.e., SCF receptor) using primers as described (Saito et al.,

Biochem, Biophys. Res. Commun., 13, 1762-69 (1994)) amplified a PCR product of ~300 bp with no homology to c-Kit (data not shown). The observed product sizes for SCF (~730 bp); ICAM-1 (~750 bp); and VCAM-1 (~500 bp) were as expected.

As illustrated in Figure 7, RT-PCR analysis showed that purified, multidifferentiated MPCs express both critical hematopoietic growth factor/cytokines, such as G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e. ICAM-1, VCAM-1, and ALCAM.

EXAMPLE 2

Comparison of the Ability to Support in vitro Hematopoiesis by Purified MPCs vs.

Unfractionated Bone Marrow Stromal Cells

CD34+ positive cells (hematopoietic progenitor cells) were purified (Dynal kit) and cocultured with irradiated stromal monolayers for five weeks, followed by performance of standard colony assays for hematopoietic progenitors using methylcellulose medium supplemented with colony stimulating factors (using MethoCult medium from Stem Cell Technologies, Inc, Canada). Unfractionated bone marrow stromal cells and purified MPCs were prepared in the same manner as in Example 1. Data in Figure 8 represents results from three experiments. Purified MPC provides increased preservation of hematopoietic progenitor cells compared to unfractionated stromal cells.

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EXAMPLE 3

Animal Model for Enhanced Engraftment Capacity of MPCs

The Severe Combined Immunodeficiency Disease (SCID) mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice requires either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments.

There has been discovered a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow. Unlike prior methods, the isolated cells of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral

neuronal ganglia of SCID mice. By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment. Also notably, the mortality rate was highest in mice that received unfractionated whole marrow stroma whereas purified MPC increased the survival rate which can be due to reduction in GvHD.

Transplantation of human cells in SCID mice:

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Homozygous CB-17 scid/scid mice, six to eight weeks of age, were used. Lyophilized anti-asialo GM1 rabbit antibody (Wako Chemicals) was suspended in 1 ml sterile ddH₂O, followed by pretreatment of mice with an IP injection of 20 ml (600 mg) ASGM1 antibody (to specifically deplete mouse macrophages and NK cells). Alternatively, one could use NOD/SCID mice lacking NK cell function, however, in light of highly promising preliminary results it was elected to continue use of scid/scid mice. The antibody treatment schedule included four-hour pre-engraftment and every seven days thereafter for the duration of the experiment. On the day of transplantation, the mice were irradiated with 200 or 300 cGy gamma-irradiation from a ¹³⁷Cs source. Approximately 2.5 x 10⁶ MPCs suspended in 0.5 ml McCoy's medium and/ or 25x10⁶ MNCs suspended in 0.2 ml were injected per mouse, intraperitoneally. Hematopoietic cell engraftment was assessed after five weeks by harvesting and analyzing representative hematopoietic and nonhematopoietic organs including blood, spleen, bone marrow (from two femurs and tibia) from euthanized mice.

Flow Cytometric Evidence

Figure **9A** and **9B** are flow cytometric evidence of human hemopoietic cells in a SCID mouse cotransplanted with marrow MPC. Figure **9A** shows the presence of CD45+/CD34+ progenitors in the marrow. Figure **9B** shows CD45/CD34- mature hematopoietic cells circulating in the mouse's blood. *Photomicrographs of Cells*

Figures 10A-H shows engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal

areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

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Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Southern Blotting Data

Hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) shows linear signal intensity with a 2.7 Kb band (arrow; autoradiogram exposed for only 45 minutes) (Figure 12A). Lanes 1-10 contain human DNA starting 1000 ng to 100 ng admixed with 0 ng 900 ng of mouse DNA, total amount DNA loaded in each lane being 1 ug, allowing construction of a standard curve. The reported limit of detection with this technique is 0.05% human cells, which is more reliable than flow cytometry in detecting very low levels of human cell engraftment.

Figure 12B is a Southern blot of EcoR1 digest of thymic genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. There is evidence of human cell engraftment in the mouse thymus in lanes 9 and 11 and lanes 14 and 15 evidenced by the 2.7 Kb band. There was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Figure 12C isEcoR1 digest of Lymph Node genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. While there was evidence of engraftment of human cells in the mouse lymph nodes for mice that received unfractioned bone marrow stromal cells and MPCs, there was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Increased Survival and Evidence of MPC Effect on GvHD

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Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention versus unpurified bone marrow stromal cells. Mice in Figure 13A received 300 cGy irradiation dose and mice in Figure 13B received 200 cGY of irradiation. Figure 13A and Figure 13B show comparable engraftment of human hematopoietic cells in SCID mice cotransplanted with purified MPCs versus unpurified bone marrow stromal cells and the markedly enhanced survival of mice receiving purified MPCs. Notably, no engraftment was observed in mice receiving bone marrow mononuclear cells alone.

The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified stromal cells and the bone marrow mononuclear cells. The increased mortality observed can be related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, as shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Figures 14A-C demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation with human bone marrow mononuclear cells and unpurified bone marrow stromal cells. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died. Hematoxylin counterstain was applied to sections in Figure 14A and Figure

14C. Methylgreen counterstain was applied to sections in Figure 14B and Figure 14D.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse Figure 14A. While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). By contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The size of the spleens from the mice that survived and the mice that died were compared. The dead mice were observed to have small and atrophic spleens correlating with lymphoid cell depletion and apoptosis.

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The above results indicate that purified MPC can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. Evidence suggests that the increased survival can be due to a reduction in GVHD.

EXAMPLE 4

Administration of Bone Marrow Cells and Mesenchymal Progenitor Cells to Breast Cancer Patients Treated with Chemotherapy

A breast cancer patient undergoes a diagnostic posterior iliac crest bone marrow aspiration and biopsy using a local anesthetic. A small portion (2 to 3 ml) of the aliquot (10 to 20 ml) of marrow is submitted for routine histologic testing and determination of the presence of tumor cells using immunoperoxidase testing. The remainder of the cells are Dexter cultured for MPCs as described above in Example 1.

The patient also undergoes placement of a pheresis central venous catheter, and receives subcutaneous injections of G-CSF (filgrastin) 10µg/kg/day as described in Peters, et al, Blood, Vol. 81, pgs. 1709-1719 (1993); Chao, et al, Blood, Vol. 81, pgs. 2031-2035 (1993); Sheridan, et al, The Lancet, Vol. 2, pgs. 891-895 (1989); and Winter, et al, Blood, Vol. 82, pg. 293a (1993). G-CSF injections begin at least three days before the first pheresis is initiated. G-CSF therapy is withheld if the

white blood cell count rises above $40,000/\mu L$ and is resumed once the white blood cell count drops to less than $20,000/\mu L$.

If the patient is receiving only G-CSF as the vehicle for "mobilization" of peripheral blood progenitor cells, the patient must not have received chemotherapy within four weeks of the planned pheresis. If the patient has received both conventional chemotherapy and G-CSF treatment for mobilization, the patient must not have received chemotherapy within ten days of the planned pheresis, and the white blood cell count must be at least $800/\mu L$ and the platelet count at least $30,000/\mu L$.

Daily pheresis procedures are performed using a Cobe Spectra instrument (Cobe, Lakewood, Col.), and each cellular collection is cryopreserved using a controlled-rate liquid nitrogen freezer, until at least 15x10⁸ mononuclear cells/kg are collected (Lazarus, et al., Bone Marrow Transplant, Vol. 7, pgs. 241-246 (1991)). Each peripheral blood progenitor cell is processed and cryopreserved according to previously published techniques. (Lazarus, et al., J. Clin, Oncol., Vol. 10, pgs, 1682-1689) (1992); Lazarus et al., (1991)):

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Eight days before the patient is infused with the autologous peripheral blood progenitor cells, the patient receives chemotherapy over a period of 96 hours (four days), with the following chemotherapy agents: 1) Cyclophosphamide in a total dosage of 6 g/m² (1.5 g/m 2/day for four days) is given via continuous intravenous infusion at 500 mg/m² in 1,000 ml normal saline every eight hours; 2) Thiotepa in a total dosage of 500 mg/ m² /day for four days) is given via continuous intravenous infusion at 125 mg/² in 1,000 ml normal saline every 24 hours; and 3) Carboplatin in a total dosage of 1,800 mg/m² (200 mg/m² /day for four days) is given via continuous intravenous infusion at 200 mg/m² in 1,000 ml of 5% dextrose in water every 24 hours.

The patient also receives 500 mg of Mesna in 50 ml normal saline IV over 15 minutes every four hours for six days (144 hours), beginning with the first dose of cyclophosphamide.

At least 72 hours after the completion of the chemotherapy, the MPCs are harvested from the Dexter culture(s). MPCs are collected and purified as described in Example 1. Cells are resuspended at approximately 10⁶ cells/ml, and

injected slowly intravenously over 15 minutes to provide a total dosage of from 10 to about 5x10⁶ cells.

MPCs can also be frozen and thawed to use when needed. For example, unfractionated cells from a Dexter culture are frozen. Upon thawing the cells are plated for about two days. The MPCs are then purified as in Example 1 above. The MPCs are then replated with serum or in a serum free media and can remain stable for up to six days.

The day after the patient receives the MPCs, the frozen autologous peripheral blood progenitor cells are removed from the liquid nitrogen refrigerator, transported to the patient in liquid nitrogen, submersed in a 37°C to 40°C sterile water bath, and infused rapidly intravenously without additional filtering or washing steps. GM-CSF in an amount of 250 $\mu g/m^2$ then is given as a daily subcutaneous injection, beginning three hours after completion of the autologous blood progenitor cell infusion. The GM-CSF is given daily until the peripheral blood neutrophil count exceeds 1,000/ μ L for three consecutive days.

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EXAMPLE 5

Genomic Changes Observed in Leukemia Associated MPCs

The following is one example of how normal hematopoiesis might be compromised in leukemic conditions. The cellular interactions that underlie leukemic bone marrow involve stromal cells, leukemia/ lymphoma cells, and normal hematopoietic pro`genitors (including those of myelopoiesis, erythropoiesis and megakaryocytopoiesis). In addition to displacing normal hematopoietic cells, the leukemia/ lymphoma cells can potentially cause direct damage to the hematopoietic supportive stromal cells by inducing unwanted gene expression profiles and adversely affecting the normal hematopoiesis. The cellular interactions can be schematized as:

Leukemia/lymphoma cells stromal cells normal hematopoietic progenitors.

The point of this scheme is that regardless of whether stromal cell lesions are primary or secondary to leukemogenesis, the normal hematopoietic function is invariably compromised in leukemic conditions, though different leukemias affect myelopoiesis, erythropoiesis and megakaryocytopoiesis differentially. Contrary to the prevailing notion (see Marini, F et al., Mesenchymal Stem Cells from Patients with Chronic Myelogenous Leukemia Patients can be

Transduced with Common Gene Transfer Vectors at High Efficiency, and are Genotypically Normal, 42nd Annual Meeting of the American Society of Hematology, Dec. 1-5, 2000 Poster # 665), there has been observed extensive and striking gene expression changes in leukemia-associated bone marrow MPCs by using high-resolution genomics. Therefore, one embodiment of the present invention is to use transplantation of tissue-culture expanded, purified normal MPCs to improve granulopoiesis, erythropoiesis and thrombopoiesis, in for example MDS (most of MDS patients do not die from blast transformation but from complications related to cytopenias, i.e., hematopoietic failure).

The studies targeted acute myeloid leukemia (AML), chronic myeloid leukemia (CML) and multiple myeloma (MM), one case of each. The AML patient was a 57 year-old woman with 52% myeloblasts in the bone marrow with immunophenotype confirmed by flow cytometry and a karyotypic abnormality of 45, XX, -7(6)/46, XX [6]. Together with morphology, the diagnosis was AML arising in a background of myelodysplasia. The CML patient was a 35 year-old man with 2% blasts in the bone marrow and karyotypic abnormalities of Philadelphia chromosome and BCR/ABL gene rearrangement. Together with morphology, the diagnosis was CML in chronic phase. The MM patient was a 61 year-old woman with a IgA myeloma. The serum IgA level was 2.4 g/dl and the marrow plasma cell count was 37%. None of the patients was treated prior to obtaining marrow samples used in this study, to avoid any therapy-induced changes complicating the disease-associated changes.

The leukemic samples consisted of marrow aspirates that remained unused after clinical diagnostic studies were preformed. A bone marrow sample obtained from an adult healthy male who had consented to donate bone marrow for standard marrow transplantation was simultaneously studied. The normal bone marrow sample consisted of residual cells recovered from the filters after complete filtration of the marrow sample. Setting up of Dexter-type stromal cell cultures and isolation of MPC were as described in Example 1. The normal stromal cells were studied without and after stimulation with TNF α because TNF α (and IL-4) are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and

thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are considered possible mediators of hematopoietic dysregulation typical of MDS.

A stepwise genomics strategy encompassed:

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Preparation of total RNA from MPC samples → generation of cDNA → preparation of ds DNA → in vitro transcription into cRNA → fragmentation of cRNA → hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray) → analysis of differentially expressed genes using an appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type.

Cluster analysis showing gene expression patterns in bone marrow MPC isolated from a normal individual and patients with different leukemic conditions.

Genes with correlated expression across bone marrow MPC types: GeneSpring was used for cluster analysis. Prior to application of an agglomerative hierarchical clustering algorithm, microarray signals were normalized across experiments (i.e., from one MPC type to another) making the median value of all of measurements unity, so different experiments are comparable to one another. The signals were also normalized across genes in order to remove the differing intensity signals from multiple experimental readings. Genes that are inactive across all samples were eliminated from analysis. Notably, 7398 genes out of 12,626 genes (present on the Affymetrix genechip used) passed the filter of a normalized signal intensity of at least 0.1 across at least one of the five experiments performed. Cluster analysis was performed with standard correlation (same as Pearson correlation around zero) as the distance metric, a separation ratio of 0.5 and a minimum distance of 0.001 as provided by the software application. A closer relationship between CML- and MM-associated MPCs was observed, which in turn are related to AML-associated MPC, thus transforming global patterns of gene expression into potentially meaningful relationships.

Two-dimensional cluster analysis of tissue vs. gene expression vectors: A gene tree was constructed. Genes cluster near each other on the "gene tree" if they exhibit a strong correlation across MPC experiments and MPC tree branches move near each other if they exhibit a similar gene expression profile. The data indicated that the two-way clustering readjusted the location of a number of

genes resulting in accentuation of genomic signatures of each cell type. Investigators can usefully catalog genes composing any unique or signature cluster of interest by creating a gene list and disclosing their identities.

Self-organizing map (SOM) clusters (6x5) show differential gene expression in bone marrow MPC isolated from different hematopoietic conditions.

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Generation of SOM clusters involved prior normalization and filtering of the data. SOM algorithm was applied as provided by GeneSpring. Visualization of SOM clusters in combination with hierarchical clustering (i.e., MPC tree) revealed correlated meaningful patterns of gene expression. Predicated on the basis of SOM operating principle, the related SOM clusters tend to be located physically close to each other. For example, the juxtaposition of the SOM clusters with the common denominator containing genes that are up-regulated in AML/MDS-associated MPC. Whole or part of any SOM cluster can be selected to make a gene list providing the identities of the genes involved.

Genes highly expressed in normal MPC but absent or minimally expressed in leukemia-associated MPC

Lists of genes that are down-regulated in leukemia-associated MPC (AML/MDS, CML and MM) were created in comparison to normal MPC. A Venn diagram was made using these three gene lists. GeneSpring allows creation of sublists of genes corresponding to union, intersection and exclusion. Transcriptional profiles of any of these sublists of genes can be visualized across MPC samples of interest. The following is one such sublist of genes containing genes that are highly expressed in normal MPC and down-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: putative, wg66h09.x1 Soares Homo sapiens cDNA clone, Homo sapiens mRNA for CMP-Nacetylneuraminic acid hydroxylase, Homo sapiens cDNA clone DKFZp586G0421 (symptom: hute1), Human mRNA for histone H1x, Putative monocarboxylate transporterHomo sapiens gene for LD78 alpha precursor, Interacts with SH3 proteins; similar to c-cbl proto-oncogene product, wg82b12.x1 Soares Homo sapiens cDNA clone, Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, Homo sapiens hMmTRA1b mRNA, Human G0S2 protein gene, Preproenkephalin, Human guanylate binding protein isoform I (GBP-2) mRNA, Human gene for

hepatitis C associated microtubular aggregate protein p44, 17-kDa protein, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, GS3686, Human monoamine oxidase B (MAOB) mRNA, Insulin-like growth factor II precursor, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, Similar to ribosomal protein L21, X-linked mental retardation candidate gene, and Homo sapiens mRNA; cDNA DKFZp434A202. Genes not expressed in normal MPC but highly expressed in leukemia-associated MPC

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Lists of genes that are upregulated (instead of down-regulated) in leukemia-associated MPCs (AML/MDS, CML and MM) were created in comparison to normal MPC and a Venn diagram was made. The following is one such sublist of genes containing genes that are inactive in normal MPC but up-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: Beta- tropomyosin, Homo sapiens clone 24659 mRNA sequence, Human mRNA for DNA helicase Q1, OSF; contains SH3 domain and ankyrin repeat, ym22b12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone, Human mRNA for pre-mRNA splicing factor SRp20, Human mRNA for golgi alpha-mannosidasell, OSF-2os, Homo sapiens gene for Proline synthetase, hk02952 cDNA clone for KIAA0683, wi24g10.x1 Homo sapiens cDNA clone, Lysosomal enzyme; deficient in Sanfilippo B syndrome, CTP synthetase (AA 1-591), WD repeat protein; similar to petunia AN11, Human mRNA for 5'-terminal region of UMK, complete cds, Homo sapiens chemokine exodus-1 mRNA, complete cds, Human GPI-H mRNA, complete cds, Homo sapiens mRNA encoding RAMP1, Transforming growth factor-beta-2 precursor, and Homo sapiens mRNA for KIAA0763 protein.

Visualizing expression of phenotypically & functionally relevant genes across samples of normal & disease-associated BM MPC.

Although GeneSpring is a highly flexible and user-friendly software application, it lacks the facility to create functionally relevant gene lists containing user-defined key words. This limitation was overcome by devising the following method via Microsoft Excel. A stepwise protocol to create such a gene list using Excel includes: Open the annotated microarray genome file (e.g., Affymetrix U95A) in Excel \rightarrow select the column with gene names \rightarrow select Data from pull-down menu \rightarrow Filter \rightarrow AutoFilter \rightarrow Custom \rightarrow enter key words (e.g., cell adhesion or cell cycle) \rightarrow OK \rightarrow generates a new Excel worksheet with the list of genes containing the key

words. Copy and paste the list of genes containing the key words into GeneSpring and save the gene list with a meaningful name. Twenty-two (22) such functionally relevant gene lists (Table 2) were created.

The resulting approach is a simple and powerful way to peer into the expression profiles of focused sets of functionally relevant genes across samples of interest. For example, the human vascular cell adhesion molecule-1 (VCAM-1) gene is completely down-regulated in AML/MDS and the human insulin-like growth factor binding protein (hIGFBP1) gene is up-regulated in AML compared to all other samples. Similarly, *Homo sapiens* gene for LD78 alpha precursor is down-regulated in all of leukemia-associated MPCs. Finally, the lineage markers CD45 and CD68 are essentially absent from the leukemia-associated MPCs attesting to the high degree of purity achieved by the sample preparation technique of the present invention.

Results

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The genomic changes observed in leukemia-associated MPCs are striking. As shown in Table 2, the changes (up-regulation and/ or down-regulation) involved hundreds of genes. These changes were most dramatic in MPC associated with AML arising in a background of MDS and involved multiple classes of genes (Tables 1-2). Expectedly, the TNFa-induced changes were extensive. Given the high level of purity of MPC preparations, the enormous genomic changes observed are reflective of the underlying pathologic lesions in the MPCs themselves (and not due to the contaminating leukemic cells and/ or macrophages). These studies strongly support the hypothesis that stromal cells in a leukemic patient are functionally defective and therefore purified MPCs are of value in restoring the loss of hematopoietic function in leukemic patients.

Table 2. Magnitude of global gene expression changes in leukemia-associated and TNFa-stimulated MPCs in comparison to normal MPC

	AML/MDS MPC	CML MPC	ММ МРС	TNFa MPC
# of genes up- regulated	234	112	108	279
# of genes down- regulated	379	208	251	164

Table 3. Functional classes of genes analyzed across normal and leukemiaassociated MPCs

Annexins (14) Caspases & apoptosis- related transcripts (33) Cadherins (50) Calmodulins/ calmodulin- dependent kinases (25) Cell adhesion molecules (20) Cathepsins (19) Collagens (71)	Cell division cycle-related transcripts (36) Cytokines (19) Epidermal growth factors and related transcripts (22) Fibroblast growth factors (21) Fibronectins (6) Galectins (6) Growth factors (136)	IGF system (24) Interleukins/ receptors (76) Integrins/ disintegrins (70) Lineage-related markers (19) Laminins (13) Platelet-derived growth factors & receptors (12) TNF alpha-related transcripts (29) TGF beta-related transcripts (25)
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The gene lists in Table 3 were created as described above and analyzed using GeneSpring. The numerical value in parenthesis refers to the number of transcripts in the corresponding class of genes analyzed.

Example 6

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The present invention provides the following benefits: a) identification and documentation of BM stromal cell gene expression patterns under varied, normal, and leukemic hematopoietic conditions; b) identification of stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function that is constantly compromised in leukemic patients, and identification of similar targets for arresting the growth and progression of neoplastic clones since stromal cells provide the necessary support for preferential growth of leukemic cells (CLL, MM) within BM and protect the leukemic cells from chemotherapy-induced death (MM); and c) identification of new biological bases and new diagnostic markers for refinement of the classification and diagnosis of leukemia. This present invention can also lead to important insights into the pathogenesis of leukemia. In broad terms, analysis of global gene expression or transcriptome (transcriptional profile composed of all transcribed regions of the genome) is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of gene expression. A stepwise genomic strategy encompasses preparation of total RNA from cells of interest, to generation of cDNA, to preparation of ds DNA, to in vitro transcription into cRNA, to fragmentation of cRNA, to hybridization of target RNA, to a microarray of known genes (and/or ESTs), to analysis of

differentially expressed genes using an appropriate software to discern the patterns of gene expression or genomic signatures by a given disease-associated cell type.

Further test utility of sample preparation technology applied to normal EM-derived MPCs (untreated and treated with representative cytokines) and MPCs derived from patients with representative pre-leukemic and leukemic conditions for performance of high-resolution DNA microarray technology (Affymetrix genechip containing DNA from 12,000 known human genes, e.g., U95A oligonucleotide microarray).

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Representative cytokines which are pathologically altered in hematopoietic conditions and that can be used in this study include TNF-α, TGF-β and interferon-γ. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), acute lymphocytic leukemia (ALL), and multiple myeloma (MM).

The front-end strategy of microarray analysis involves the use of Percoll-gradient purified MPCs. As a follow-up strategy, to validate the stromal cell origin of the differentially expressed genes, MPCs obtained from cytospins of BM stromal cells by laser-capture microdissection (LCM) selected on the basis of morphology (Figure 3) are used followed by "real-time" quantitative polymerase chain reaction (PCR). This can be performed with an LGM system as well as a "real-time" QPCR system. Validation can be performed on at least one sample from each of 6 normal BM M7NC/ MPC types and on one sample from each of 5 leukemia-associated MPC types. Validation is considered successful if the microarray results and PCR results on a given MPC sample match using a suite of 20 genes selected based on median pattern of microarray results for the given cell type. This approach not only validates the microarray results but also ascertains the stromal cell origin of the expressed genes. The standard published protocols involving LGM and "real-time" quantitative PCR and the instructions accompanying the equipment are used for performing the experiments.

Stepwise LCMJ real-time QPCR protocol entails the following. Cytospins are made from BM stromal cells. The cytospins are stained with hematoxylin and MPC is selected for based on morphology. Microdissect up to 1,000 MPC from each sample. RNA is extracted and reverse transcribed into cDNA.

The cDNA is amplified using gene-specific primers and "real-time" quantitative PCR.

By applying the combined power of different analytical techniques (such as hierarchical clustering and self-organizing maps) together with the recently developed sample preparation technology for stromal cells the present invention provides a molecular biological basis that can allow refinement of the classification and diagnosis of leukemias and lymphomas, uncovering the suspected disease heterogeneity. This enables the deciphering of the genomic expression profiles or signatures of bone marrow stromal cells in about 10 different physiologic states and about 20 different leukemic states. In addition to aiding in refinement of the classification and diagnosis of the hematopoietic malignancies, the data provides clues to potential novel drug targets and insights into pathogenesis.

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The present invention functions by identifying the MPC genes that are differentially expressed after stimulation with different hematopoietic cytokines implicated in the pathogenesis of pre-leukemic conditions (MDS); in actual pre-leukemic disorders (MDS); and in overt leukemias (CML, AML, CLL, ALL, MM) as well as in lymphomas that have a leukemic phase with involvement of BM.

The present invention is accomplished by first determining the median gene expression profiles for MPCs associated with each disease and stimulated by each cytokine of interest (this objective can be achieved by treating the gene expression vectors of individual cases in each MPC category as replicates; this capability is available in GeneSpring software application). Then the gene groups that are up regulated and down regulated and that are common to all the members in a given MPC category are identified (this is accomplished using a series of Venn diagrams and creating required gene lists via GeneSpring). Finally, the up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. This allows the identification of gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can also be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets can be of immense diagnostic value as they can be routinely used in an assay simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets can additionally provide insights into pathogenesis and possible targets for design of new drugs.

Determine expression profiles of MPC genes which are regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4; interferon γ , TGF β ; PDGF; FGF; EGF; and calmodulin.

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TNF α , IL-4 and IFN γ are potent negative regulators of hematopoiesis. Notably these cytokines, especially TNF a, are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. Studies regarding these regulators can uncover the molecular pathways leading to cytopenias in MDS patients. As indicated earlier, myeloproliferative disorders are another, in some ways similar, group of hematopoietic disorders that are clonal in origin but not overtly malignant clinically. These MPDs include polycythemia vera. essential thrombocythemia, idiopathic myelofibrosis (agnogenic myeloid metaplasia) and chronic myelogenous leukemia. These disorders have the potential to change from one to the other at any time, however the signals that trigger such conversion remain enigmatic. Idiopathic myelofibrosis (IMF), in which stromal cells seem to play a profound pathogenetic role, is characterized by fibrosis of the marrow cavity, extramedullary hematopoiesis, splenomegaly, and anemia and leukoerythroblastic features in the peripheral blood. While myeloproliferation is known to be a clonal process, the accompanying stromal cell proliferation and fibrosis are believed to be a polyclonal reactive process that is likely to be due to increased intramedullary activity of a number of cytokines including TGF B, PDGF, FGF, EGF and calmodulin, as shown by other investigators.

Cancer genomics is a rapidly expanding area of investigation. The focus is unique however in emphasizing not the leukemic cells themselves but rather BM stromal cells that provide a haven to various types of pre-leukemia and leukemia cells, non-Hodgkin's lymphomas (NHLs) and metastatic cancers (METs). Pre-leukemic clonal neoplastic conditions include myelodysplastic syndromes (MDSs) and myeloproliferative disorders (MPD5). Stromal cells are known to produce and/or respond to growth factors such as EGF, PDGF, FGF, VEGF, and cytokines such as IL-I or TNF a, partially explaining the interactive relationship between stromal cells

and cancer cells, especially in MDS and CML.

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In spite of similarities between BM stroma and non-BM stroma, certain sharp distinctions do stand out. Non-BM stromal cells are terminally differentiated fibroblasts, while BM stromal cells represent a unique pluripotent or pluridifferentiated mesenchymal cell type, thus exhibiting preserved developmental "plasticity". Using 5-10 cc BM aspirate samples from adult leukemic patients and 3-5 cc BM samples from pediatric patients with ALL, the study can analyze the BM stroma. One cc of marrow sample can produce at least 1 T-150 flask of stromal cells. One concern is that it can be hard to obtain marrow samples from cases like CML and myelofibrosis. In such cases stromal cells are grown using peripheral blood samples as described in the prior art. At least one flask of stromal cells (i.e., 1 cc marrow) to yield the RNA required for analysis. About 10 cases of each type of leukemia/lymphoma were studied. The study provided important insights into the functioning of the BM microenvironment in normal and leukemic hematopoiesis.

A database including all of the above information and that can include age, gender and associated major illness in terms of clinical/pathologic diagnosis for each subject/patient can be created. This can also include information on cytogenetic, molecular and flow cytometric studies. Finally, also included can be the information on clinical course in terms of disease progression and response to treatment exercising adequate care to protect the identity of individual patients. The study analyzed genomic expression profiles or signatures of bone marrow stromal cells derived from about 12 different normal bone marrow states and about 19 different leukemia/lymphoma states, approximately 10 cases of each as shown in Table 4, accounting for a total of 310 samples.

Using the information of the present invention, those of skill in the art can: a) study select gene or sets of genes as relevant to hematopoietic disease conditions using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) reanalyze the primary data by using newer and more powerful bioinformatic tools as they become available; and/or c) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc.

Table 4 Scope of human BM samples targeted for DNA microarray analysis (approximately 10 cases of each)

Normal BM mononuclear cells (NMNC)

Normal BM stromal cells, unfractionated and unstimulated (NBMS)

Normal purified mesenchymal progenitor cells, unstimulated (NMPC)

NMPC stimulated with 9 different cytokines:

5 NMPC stimulated with TNFα (TNFα MPC)

NMPC stimulated with TGFβ (TGFβ MPC)

NMPC stimulated with interferon y (IFNy MPC)

NMPC stimulated with 1L-4 (IL-4 MPC)

NMPC stimulated with TNF α + IL-4 (TNF α + IL-4 MPC)

10 NMPC stimulated with PDGF (PDGF MPC)

NMPC stimulated with EGF (EGF MPC)

NMPC stimulated with FGF (FGF MPC)

NMPC stimulated with calmodulin (calmodulin MPC)

MDS - Refractory anemia (MDS-RA MPC)

15 MDS - Refractory anemia with ringed sideroblasts (MDS-RARS MPC)

MDS - Refractory anemia with excess blasts (MDS-RAEB MPC)

MDS - Chronic myelomonocytic leukemia (M1)S-CMML MPC)

MPD - Polycytheniia vera (MPD-PV MPC)

MPD - Essential thrombocythemia (MPD-ET MPC)

20 MPD - Myelofibrosis (MPD-LMF MPC)

CML (CML MPC)

AML-MO/M1/M2 (AML-MOJM1JM2 MPC)

AML-M3 (APL) (AML-M3 MPC)

AML-M4/M5 (myelomonocytic) (AML-M4i'M5 MPC)

25 ALL-L1/L2 (lymphoblastic) (ALL-L1/L2 MPC)

ALL-L3 (Burkitt's) (ALL-L3 MPC)

Multiple myeloma (MM MPC)

CLLISLL (CLL/SLL MPC)

Follicle center cell lymphoma (FCL MPC)

30 Mantle cell lymphoma (MCL MPC)

Lymphoplasmacytic lymphoma (LPL MPC)

Marginal zone lymphoma (MZL MPC).

Human Subjects

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This study involves the use of bone marrow (BM) samples from human subjects. BM samples can be obtained from normal subjects (male and female 20-45 years) as well as leukemic patients after informed consent is obtained. Leukemic cells can be obtained from diagnostic samples of BM of adult and pediatric patients (in those cases in which cells remain unused after clinical diagnostic studies are

preformed; i.e., about 90% of cases).

Example 7

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In broad terms, global gene expression analysis is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of protein expression. A stepwise proteomics strategy encompasses: solubilization of proteins from cells of interest; 2-D gel electrophoresis (IPG DALT); staining and image analysis of gels; excision of protein spots of interest; trypsin digestion of proteins; mass spectrometry (MALDI-TOF MS and/or ESI MS/MS) performed on tryptic fragments; identification of proteins by database searching. The present invention provides a method to analyze the population of expressed proteins (i.e., proteome) of BM MPCs in relation to hematopoiesis in collaboration with a state-of-the-art mass spectrometry facility.

The large-format 2-D gel electrophoretic system is used for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/premalignant and leukemic/malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The system of the present invention can be used to differentially express MPC proteins (i.e., those that increased or decreased in intensity as compared to 2-D PAGE protein maps of normal, unstimulated MPCs) using mass spectrometry (MALDI-MS and/or nanoelectrospray ionization MS/MS) and/or Western blotting and/or Western-ligand blotting.

Using high-resolution proteomics with the added power of high-

throughput robotics, enables the system to identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

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The system of the present invention enables the identification of MPC proteins whose expression is regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4; interferon γ , TGF β ; PDGF; FGF; EGF; and calmodulin.

The system of the present invention also enables the identification of MPC proteins for which expression is altered as a result of exposure of normal MPCs to agents that are clinically used for mobilization of hematopoietic stem cells from BM into peripheral blood to facilitate easy collection and subsequent transplantation, e.g., G-CSF and G-CSF plus cyclophosphaniide.

Further, the system of the present invention enables the identification of Identify the MPC proteins whose expression is pathologically altered in hematopoietic disease states such as: MDS, CML, AML, CLL, ALL and MM by matching the 2-D PAGE protein maps of disease-associated MPCs with the 2-D PAGE database of normal MPCs. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been characterized, then such proteins can be identified by MALDI-MS and/or Nano ESI MS/MS.

The system facilitates understanding of the pathogenetic mechanisms by identifying the phosphoproteins involved in cell signaling pathways. The systems immunoblots the whole cell lysate proteins of normal MPCs, untreated and treated with respective cytokines, using antibodies to phosphotyrosine, phosphoserine, and phosphothreonine. The system then locates the corresponding putative phosphoprotein spots on the gel and identifies the proteins by MALDI-MS and/or Nano ESI MS/MS. Similarly, the system can locate the altered phosphoproteins by immunoblotting the whole cell lysate proteins of untreated MPCs derived from leukemic patients. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been identified,

then MALDI-MS and/or Nano ESI MS/MS can identify the protein.

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Bone marrow MPCs derived from a leukemia background express distinctively different patterns of cell adhesion molecules from normal MPCs.

BM stromal cells provide the background required for homing and subsequent proliferation and differentiation of hematopoietic stem cells. BM stromal cells also provide a rich microenvironment for metastases and growth of various leukemias. Based on the hypothesis that homing of normal hematopoietic cells and leukemic cells to marrow utilize the same adhesion mechanisms, it was questioned whether there are fine regulatory distinctions in terms of quantitative differences in the expression of the adhesion molecules in normal vs. leukemic BM microenvironments. In a pilot study 11 cell adhesion molecules (CAMs) and several lineage-associated markers for Northern blot analysis were targeted. Dexter-type cultures were grown under standard stromal cell culture conditions using bone marrow samples from a normal individual and from one patient diagnosed with and treated for acute myelogenous leukemia (AML). Representative cultures were treated with cytokines such as TNF α alone, IL-4 alone, and TNF α plus IL-4. MPCs from unstimulated and cytokine-treated cultures were purified using Percoll gradient techniques disclosed above. Total RNAs were extracted by a standard method and analyzed by Northern blotting. This study demonstrated expression by MPCs of several CAMs, heretofore unsuspected of expression by BM stroma. These include an embryonic endothelial cell protein Dell (developmental endothelial locus 1), galectin-I, human milk fat globule protein (RMFG, lactadherin), and epithelial membrane protein I (EMP 1). Secondly, MPCs from the AML patient expressed significantly lower levels of mRNA for three CAMs Del- 1, galectin- 1, and collagen type 1 as well as for the adipocyte marker adipsin, and to a minor degree the muscle-associated protein caldesmon. On the other hand, mRNA for CAMs like TGF beta-inducible BiGH3, HMFG, osteoblast-specific cadherin 11, and VCAM1 were dramatically increased in AML-associated MPCs. CAMs such as integrin beta 5, fibronectin, EMP 1 and the muscle-associated molecule transgelin are variably increased in diseased MPCs and appear to be unaffected by treatment with cytokines tested. ICAM I was undetectable at basal level in either patient or normal samples, but was slightly elevated by TNF α and markedly elevated by TNF α plus

IL-4. VCAM1 was mildly up regulated by TNF α alone or IL-4 alone, but markedly up regulated by TNF α /IL-4 in combination. Also, the MPCs from the patient were much more sensitive to stimulation by these inflammatory cytokines than were the normal MPCs. These studies establish that stromal cells in a leukemic patient are functionally defective.

Role of leptin receptor in hematopoiesis using human marrow stromal cells as a model.

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The receptor for the product of the obesity gene, leptin, is widely distributed in tissues ranging from central nervous system to reproductive system to hematopoietic system. Within hematopoietic system, OB-R is reportedly expressed on diverse cell types ranging from early CD 34+ hematopoietic stem cells to circulating monocytes. Leptin acts on monocytes to induce production of TNF α and IL-6, which are powerful regulators of hematopoiesis. However, literature reports on the expression of leptin or its receptor on stromal cells are infrequent. To date, one particular report suggests that leptin acts on the stromal cells to enhance their differentiation into osteoblasts and to inhibit differentiation into adipocytes. Because leptin is an adipocyte-generated hormone and because marrow stromal cells represent a unique pluridifferentiated mesenchymal cell type expressing some adipocytic features, the expression of the leptin receptor by these cells was investigated in the hope of revealing its role in hematopoiesis.

By Northern blotting marrow stromal cells showed abundant expression of OB-R, consistent with their adipocytic nature. In terms of regulation, exposure of the stromal cultures to different cytokines revealed an interesting pattern of OB-R. As shown, G-CSF and TNF α down-regulated OB-R while IL-4 upregulated OB-R expression by stromal cells. Simultaneous treatment of stromal cultures with TNF α and IL-4 nearly abolished OB-R expression. The expression of OB-R was also analyzed at the protein level by a high-resolution, high capacity 2-D PAGE system, followed by Western blotting.

More specifically, the method provides the identification of leptin receptor in human BM stromal cell membrane protein extracts using 2-D Western blotting. The expression of OB-R was investigated at protein level using 2-D PAGE, followed by Western blotting. Two isoforms differing in molecular weight of 2.2 kDa (60.2; 62) and an isoelectric point of 0.2 pH unit (5.78; 5.98, respectively) have been

identified (the pH was determined by using the values specified by the IPG strip manufacturer). The ability to subsequently stain the same Western blot with gold stain allowed precise localization of the immunoreactive protein spots of interest on the blot. The gold staining of the blot, by revealing other protein spots in addition to the immunoreactive spots, has provided the necessary landmarks in turn facilitating subsequent alignment with the silver-stained gel using an appropriate 2-D analysis software program (Melanie 3).

This technique has identified two OB-R isoforms that differ in molecular mass by 2.2 kDa (60.2; 62.4) and differ in their isoelectric point by 0.2 pH units (5.78; 5.98). The level of macrophage contamination is determined by two macrophage markers, CD68 and cathepsin B. The studies include the determination of OB-R expression in a) unfractionated stromal cells vs. isolated pluri-differentiated mesenchymal progenitor cells; b) unstimulated cultures vs. cultures stimulated with a variety of cytokine/hormones including leptin itself. The studies also include mass spectrometric characterization of the two OB-R isoforms detected by Western blotting in order to establish their exact structural differences.

Proteome analysis of 2-D PAGE separated human BM stromal cell membrane proteins.

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BM stromal cells support the growth and development of normal blood cells as well as providing a haven for malignant leukemia/lymphoma cells. Focusing on stromal cell-surface proteins as potentially playing a role in cell-to-cell communication in normal as well as in abnormal hematopoiesis, the mixtures of stromal-cell plasma membrane, and plasma membrane-associated proteins were analyzed by a high-resolution, high-capacity 2-D gel electrophoresis. The 2-D system described utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini nondenaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample loads (up to 1.5 — 2.0 mg of total protein in up to 350-µl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have

been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins. The protein digests are then submitted in a near-ready state for mass spectrometry. Upon receiving the MS data the group performs the database searching. MALDI/MS has been used, which identifies a protein on the basis of its characteristic mass sizes, as well as MS/MS studies that provide amino acid sequences of selected masses to identify proteins with enhanced specificity and confidence level. This work represents the first systematic attempt to analyze BM stromal cell proteins by high-resolution 2-D gel electrophoresis and provides the basis for a full-scale proteome mapping of the marrow stromal cells. The present work can facilitate the long-term goal of deciphering the hematopoietic support functions of BM stromal cells.

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Modulation of stromal cell plasma membrane protein expression by TNF α /IL-4.

The effects of TNF α /TM on bone marrow stromal cell plasma membrane protein expression has been tested using the described system. TNF α and IL-4 are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. TNF α /IL-4 treatment of the stromal cultures induced dramatic changes in the protein profile. Initial studies using plasma membrane protein samples show reduced expression of at least 7 proteins and enhanced expression of 13 proteins.

Analyzing the insulin-like growth factor system in human marrow stromal cells

by 2-D PAGE analysis of BM stromal cell culture supernatants.

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Proliferation and development of normal and leukemic hematopoietic cells within bone marrow is regulated by interplay of various classes of molecules. These include cell adhesion molecules (CAMs), colony stimulating factors (CSFs), and cytokines as well as growth factors including insulin-like growth factors 1 and 2 (IGF 1 and IGF 2), which are small peptide homologs of prolinsulin. IGF 1 has known erythropoietic activity, whereas the function of IGF 2 is less clear. IGF 1 and 2 exert their activities through two types of receptors. The type I IGF receptor, a tyrosine kinase receptor highly homologous to the insulin receptor, binds to IGF 1 and IGF 2 with high affinity. The type II IGF receptor, a mannose 6-phosphate receptor that lacks intrinsic kinase activity, binds IGF 2 with high affinity and IGF I with low affinity. The type and number of receptors expressed on a target cell determine the strength of the IGF signal. One important key to understanding the IGFs' role in hematopoiesis is to appreciate how biological effects of receptors are modulated by larger soluble proteins, the IGF binding proteins (IGFBPs), which share no homology with the IGF receptors. Because IGFs and IGFBPs play important roles in cell growth and proliferation in many tissues, and because marrow stromal cells support hematopoietic growth and development, the patterns of expression of the IGF system components by marrow stromal cells cultured under serum-free conditions is necessary. To this end, unfractionated and purified stromal cells were analyzed, side-by-side, by Northern blotting, under varied stimulatory conditions for expression of IGFs and IGFBPs with surprising results. IGF 2 is constitutively expressed at a high level by macrophages in Dexter cultures; it is down regulated markedly by TNF α alone; moderately by TNF α plus IL-4; and unaffected by IL-4 alone. On the other hand, IGF 2 is minimally expressed by unstimulated MPCs, but is markedly up regulated by TNF α alone or IL-4 alone; and moderately up regulated by combined TNF α and IL-4. IGFBP4 is abundantly expressed both by macrophages and MPCs and is unaffected by cytokine treatment. In contrast, IGFBPs 5, 7, and 10, selectively expressed by MPCs, show no evidence of expression by macrophages and are unaffected by cytokine treatments. IGF 1 and the precursor to IOFBP 3 are not expressed in either macrophages or MPCs, either constitutively or after stimulation with TNF α , IL-4 or both. In initial studies, bone marrow mononuclear cells expressed none of the IGFs or IGFBPs tested. These

results provide important insights into the operation of the IGF system in stromal cells and it is likely that potentially novel IGFBPs can be uncovered by ligand blotting studies.

The present invention provides a large-format 2-D gel electrophoretic system for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g. TNF α or IL-4) and for MPCs derived from patients with representative pre-leukemic and leukemic conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

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Molecular analysis assay involving the high-resolution 2-D PAGE and mass spectrometric identification of gel-separated proteins.

The completion of human genome project has provided a huge proteome database including the theoretical mass databases generated on the basis of site-specific cleavage employing proteolytic enzymes, such as trypsin and others. The availability of highly sensitive biological mass spectrometers together with the capability of bioinformatics to search extremely large amounts of data and identify the relevant proteins matching the mass spectrometry data provides the basis for the current excitement in proteomics. The focus of the interest is the BM MPC proteome as expressed under varied functional and disease states. The goal of the present invention is to identify BM MPC proteins that have possible functional and/or pathologic significance, that is, those proteins that show altered levels of expression in response to cytokine treatments and various leukemic states.

Until recently, the focus of the laboratory has centered on isolation and characterization of BM stromal cell adhesion molecules using a novel 2-D cell

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blotting technique. For this purpose, applicants have established an analytical 2-D mini gel system that separates stromal cell plasma membrane proteins using 18-cm long 4-7 pH range IPG strips in the 1St D (Amersham Pharmacia Biotech). Subsequent to IEF, the IPG strip is cut into appropriately small pieces and subjected to 2 D separation using nondenaturing lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDSPAGE) and mini gels. The reason for using mini gels in the 2nd D is that they are compatible with a downstream functional assay involving cell adhesion. The stromal cell membrane proteins are blotted on to a PVDF membrane and assayed for hematopoietic cell-binding proteins directly on the blotting membrane. The system can be extended using 17-cm long 3-10 pH range IPG strips (Bio-Rad) for separation of stromal cell culture supernatants, ECM proteins, and whole cell lysates. As detected by silver staining of the gels, and analyzed by appropriate software (GelLab II or Melanie 3) this 2-D system has resolved greater than 800 membrane protein spots within a pH interval of 2.5 units (4.25-6.75) and a MW range of 10-150 kDa. Similarly, the ECM samples showed 475 spots; and conditioned media from BM stromal cell cultures grown under serum free conditions showed 524 spots. Not surprisingly, the total cell lysate of BM stromal cultures showed only 553 spots, most likely representing the abundant housekeeping proteins and masking detection of many functionally relevant proteins. These observations provide the rationale for the proposed subproteome approach involving the use of differential solubilization of sample proteins and multiple large gels. Membrane proteins thus far identified by mass spectrometry followed by database searching; proteins are identified by standard Western blotting. Select IGF binding proteins were identified by ligand Western blotting. The blotting shows the identification of IGF-binding proteins (IGFBPs) using 2-D ligand blotting. The conditioned media from BM stromal cultures grown under serum-free conditions were concentrated using Microcon concentrator, and proteins were fractionated using a high-resolution 2-D PAGE. The separated proteins were electroblotted onto PVDF membrane and subjected to Western ligand-blotting assays using 1-125 labeled IGF-2, resulting in the identification of a series of IGFBPs (up to 30 spots). Notably, TNF α treatment of the cultures down-regulated two LGFBPs and upregulated IGFBP labeled 6.

By necessity the protein work began on BM stromal cells using a

nondenaturing (LDS-PAGE) mini gel system that contained no reducing/alkylating agents. To preserve the function of 2-D gel separated proteins many otherwise powerful sample preparation methodologies designed for proteomic studies (such as multiple surfactant solution, MSS) were avoided. While mini gels are convenient and allow comparison and information transfer to large-format gels, they are less sensitive.

Subproteomes according to sample prefractionation.

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In order to be able to identify the low-abundance proteins implicated in the regulatory and pathologic processes, a number of approaches to prefractionation of the whole cell lysates have been described. Applicant studied the subproteomes of secreted proteins from BM stromal cell culture supernatants as well as ECM proteins. Notably, the ECM protein samples can be a rich source of functionally relevant cytokines and chemokines since the latter are known to mediate function by binding to ECM. In addition, the plasma membrane and whole cell samples were subjected to the 3-step sequential solubilization protocol shown. The solubilizing solutions can be prepared in-house or purchased commercially (Bio-Rad). The first step involves the use of Tris base, which can solubilize the peripheral membrane proteins and cytosolic proteins. These proteins are lyophilized and subsequently solubilized prior to 2-D PAGE in a standard solubilizing medium (the modified O'Farrell cell lysis solution containing urea, CHAPS, DII, Iris, ampholytes and appropriate protease inhibitors). The resulting pellet can also be solubilized in the standard 2-D solubilizing medium and subjected to 2-D PAGE. Because—the standard solution cannot solubulize some proteins, the membrane-rich pellet is finally solubilized in a potent multiple surfactant solution (MSS) consisting of urea, thitheea, CI-LAPS, zwittergent 3-10 and tributyl phosphine (TBP) in addition to Iris base and ampholytes that is compatible with subsequent IEF. The MSS has been shown to solubilize the hydrophobic proteins with as many as 12 transmembrane regions (TMRs), facilitating their 2-D analysis. Another final step incorporating 1% SDS in boiling sample buffer can be used to test by 1-D SDS-PAGE if any proteins remained unsolubilized after these extractions (notably, SDS extract is unsuitable for 2-D PAGE analysis since SDS interferes with IEF). The prefractionation step clearly reduces the complexity of the sample. Thus, the serial extractions not only simplify the gel images and reduce spot overlapping frequently encountered in single-step

extractions but also correlate closely with the cellular location of specific proteins, providing clues to their function. The prefractionation strategy can be extended to enriching low-abundance proteins in culture supernatants by selective removal of contaminating albumin using an Albumin Depletion Kit (containing Cibachron Blue resins) (Genomic Solutions, mc). Similarly membrane glycoproteins can be enriched by a Glycoprotein Enrichment Kit (containing lectins) prior to 2-D PAGE analysis (Genomic Solutions, Inc.).

Subproteomes according to overlapping pH gradients.

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Using a series of medium-range and partially overlapping pH gradients (3-6, 5-8, 7-10, each 17-cm long) (Bio-Rad) can enhance reproducibility and resolution by creating "virtual" gels with up to 40 cm equivalent of PI separation across a pH 3-10 range. Alternatively, a combination of two pH gradients, pH 4-7 and pH 6-11, each 24 cm-long (Amersham Pharmacia Biotech) can be used, also providing a "virtual" separation distance of 40 cm across a pH range of 4-11. These strips accept micropreparative sample loads (1-2 mg). Notably, a given sample of cells yields a total of 8 protein samples. These samples include one protein sample composed of conditioned medium, one protein sample comprising of ECM proteins, three protein samples derived from plasma membrane lysates and three protein samples derived from total cell lysates, following application of a three-step protein extraction protocol to purified plasma membranes and total cells. Eight protein samples can thus translate into 24 large format (18 cm) gels corresponding to three overlapping 1st D gels; or 16 extra large format gels (24 cm) corresponding to two overlapping 1st D gels. Proteomics is no longer considered a single 2-D gel study. Taking advantage of the common spots in the 2nd D corresponding to overlapping regions, PDQUEST software can allow "stitching together" of the constituent gels, creating the so-called "cyber gel" providing a composite map for each protein sample. The data generated can be stored in an internet-accessible 2-D PAGE database in the form of 8 submaps. Three of these submaps correspond to plasma membrane proteins representing 3-step solubilization; one of them corresponds to secreted proteins; one of them corresponds to ECM proteins; and 3 of them correspond to total cell lysate proteins representing 3-step solubilization. These submaps can be linked to a master synthetic gel, a conglomerate of the submaps, representing the so-called "cyberproteome" of MPCs. Given the ability to run up to

12 IPG strips per 1st D gel (using IPGPhor) and 10 to 12 large or extra large SDS-PAGE gels per 2nd D gel run (using Hoefer DALI and Ettan DALI II, respectively), the resulting number of gels can be well within the manageable workload of one person (36). Although not easily accessible now, some innovative technological developments are on the horizon, e.g., development of fluorescence 2-D difference gel electrophoresis (DIGE), which could minimize the tedium. Unlike the current practice of running different protein samples on separate gels, and then staining and comparing the gels, DIGE technology uses matched, spectrally resolvable dyes (e.g., Cy2, Cy3 and Cy5) to label protein samples prior to 2-D separation. Differentially labeled protein samples are mixed and co-separated by 2-D electrophoresis, allowing analysis of at least three samples on a single gel. Gels are scanned and proteins are subjected to image analysis using appropriate software. Alternatively, one can use a highly sensitive silver stain to visualize the proteins after electrophoretic separation. Notably, the silver stain is compatible with subsequent mass spectrometry analysis.

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Follow-up strategy for 2-D PAGE using the so-called ultrazoom LPG gels with narrow-range pH gradients.

Commercially available narrow-range IPG strips include pH 3.54.5; 4.0-5.0; 4.5-5.5;5.0-6.0; 5.5-6.7. These are available as 18 cm and 24 cm-long strips, consequently allowing spanning of 1 pH unit over a distance of 18-24 cm and providing extraordinary resolution. By using narrow pH gradients (IpH unit) up to 10mg of protein would be loaded onto a single IPG gel strip, either by repeated sample cup application or by in-gel rehydration without incurring vertical or horizontal streaking. Employing a combination of such narrow-range overlapping IPG strips, one study utilized up to 40 2-D gels for analysis of a single protein sample. The preference is not to follow such extreme approach but rather to use these gradients as a backup in situations where a functionally relevant protein is first detected by the front-end strategy but could not be studied by mass spectrometry for lack of adequate resolution or due to overlapping spots. The 24-cm long narrow IPG strips can be subjected to 2nd D using correspondingly extra large slab gels (the required precast, plastic-backed gels can be purchased from Amersham Pharmacia Biotech). However, the "giant 2-DE" 30 X 40cm size gels are impractical to handle. The situations for the use of narrow range pH gradients include situations like detection

of proteins by Western blotting using anti-phosphotyrosine antibodies or Western ligand blotting using labeled IGF 1 or 2, which are probably more sensitive than silver staining. Consequently, these assays identify the functionally relevant proteins but without providing the actual identity of the individual proteins. Because the frontend strategy can at least provide the range of the phosphoprotein or the IGF-binding protein identified, on the basis of this information samples can be subjected 2-D PAGE using the appropriate ultrazoom IPG strip, which as indicated above can permit loading of several mg of protein sample. Extra large precast slab gels (26x20 cm) with plastic backing suitable for running the 24-cm long ultrazoom IPG strips and the appropriate electrophoretic system (Ettan DALI II 2 dimension electrophoresis system) that runs up to 12 of these gels are commercially available (Amersham Pharmacia Biotech).

Summary of subproteome strategy.

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The subproteome approach involves: 1) Cellular fractionation involving isolation of purified MPCs. 2) Subcellular fractionation involving preparation of functionally relevant protein sets. These include: 2a) secreted proteins such as colony stimulating factors (CSFs), cytokines, etc in the conditioned media; 2b) ECM proteins such as cell adhesion molecules (CAMs), etc; 2c) plasma membrane proteins such as various receptor molecules, CAMs and components of cell signaling systems, etc; 2d) finally, whole cell lysate proteins that include some of these proteins plus cytosolic and nuclear proteins. The cytosolic and nuclear proteins can be a rich source of target proteins for phosphorylation with a regulatory function.

2-D PAGE data capture and analysis

2-D PAGE data capture and analysis can be performed using standard equipment and protocols. Silver-stained gels can be scanned using an imaging densitometer and processed with QuantOne software (Bio-Rad) whereas gels stained with fluorescent Sypro Ruby (with 450 nm in the excitation range) can be scanned using a STORM 860 gel and blot imaging system and processed with ImageQuant Solutions software (Amersham Pharmacia Biotech). A number of factors, including differences in sample preparation and loading, staining and image acquisition can influence the reproducibility of 2-D gel protein separation. Quantitative data are reported as spot volumes (integrated spot densities). In

experiments comparing replicate 2-DE patterns of the same sample or 2-DE patterns of samples from different individuals, the spot volumes in each pattern are scaled to correct for differences in the total amount of protein loaded onto each gel. These variations are compensated by accurately comparing the quantity of any spot across multiple gels. These operations can be performed using a dedicated 2-D gel analysis software, Melanie 3. This program can analyze such variations by scatter analysis and can compensate for varying staining absorption across proteins by normalizing protein expression change. Varying stain intensities and sample sizes can be compensated for by relative spots quantification. The Melanie 3 software also has the capability to merge several gel electrophoretic patterns from the same sample into a composite gel, providing fine control over the included proteins. Finally, the software can compensate for gel distortions caused by variations in protein migration through alignment of the gels.

Mass spectrometric instrumentation.

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Examples of such mass spectrometers include, but are not limited to, Voyager DE Pro (Applied Biosystems, formerly Perceptive Biosystems, Inc.) and QSTAR (Applied Biosystems). Voyager DE Pro is a matrix-assisted laser desorption time-of-flight mass spectrometer (MALDI-IOF) that can be operated in a linear mode for the analysis of large biomolecules or in a reflector mode for high-resolution analysis of smaller molecules, i.e., peptides. The MALDI-TOF instrument also utilizes delayed extraction technology that results in greatly increased resolution, sensitivity and mass accuracy. This is the instrument of choice for high throughput analysis, with a capacity of up to 100 samples per sample plate. On the other hand, the QSTAR is a hybrid quadrupole-quadrupole-time-of-flight mass• spectrometer. Samples are introduced in solution and are ionized by electrospray. For samples requiring the highest sensitivity, Dr. Jackson utilizes a low flow rate (25 nl miff') electrospray called nanoelectrospray, typically requiring only 1-2 μl of a solution for sample analysis. The QSTAR instrument yields data quite similar to those obtained from the MALDI-TOF instrument, except that the QSTAR data analysis is somewhat more complex due to the multiple charging of peptides by the electrospray process compared to the single charging applied to peptides on the MALDI-TOF instrument. One important additional characteristic of the QSTAR is its ability to determine structural information from sample molecules by tandem MS/MS. This is achieved by

effectively "purifying" selected molecules within the mass spectrometer's first quadrupole section. For analysis of peptides produced by tryptic digestion, a single MS experiment is initially performed to determine the masses of components present in the mixture. Next, MS/MS experiments are carried out to select specific peptides for $de\ novo$ amino acid sequence determination. Typically 2 μ l of peptide mixture is sufficient for determining the sequences of ten to twelve peptides.

Mass spectrometric analysis by MALDI

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The scheme for mass spectrometral analysis of in-gel tryptic digests of proteins for the purpose of protein identification consists of several steps. First, the peptides extracted from the gel must be cleaned and concentrated. The cleanup is necessary to remove residual detergent and other non-peptide materials that can interfere with the analysis of the tryptic peptides. This step involves binding of the peptides to a Microcon-SCX adsorptive microconcentrator. This is a cation exchange membrane held within a microcentrifuge device. At low pH, the peptides bind to the negatively charged membrane, while uncharged or negatively charged molecules pass through. After a brief wash, the peptides are eluted from the membrane in two 25-μl steps of 1.5 N ammonium hydroxide in 1:1 methanol/water. The samples are then speed-vac dried for 10 minutes, and fresh solvent is added for additional treatment to concentrate the sample prior to MS analysis. Initially, all samples can be analyzed by MALDI-TOF MS. For this analysis, the sample from the Microcon-SCX elution can be dissolved in 0.1% trifluoroacetic acid (TFA) in water and loaded on a ZipTipC 18 Pipette tip. The tip is then washed with the same solution and the peptides are then eluted directly onto the MALDI-TOF sample plate with 2 μl matrix solution (cyano-4-hydroxy-cinnamic acid, 10 mg/mi in 0.1% TFA in 1:1 acetonitrile/water). The spotted sample is dried at room temperature for at least five minutes before the sample plate is loaded in the instrument. The instrument calibration is performed externally by the addition of a calibration mixture to the sample plate. Samples are calibrated internally if the known tryptic autodigestion peptides are observed in the sample. This can be used as long as the specific type of trypsin used in the proteolytic digestion step is known. After data collection, the data can be further processed in two ways. First, the data can be treated by noise reduction software and second, it can be deisotoped. Software for both operations of these programs are standard features of the Data Explorer system provided with the

Voyager DE Pro mass spectrometer. The obtained peptide mass data can be subjected to peptide fingerprint analysis utilizing one of the protein database search sites on the Internet, such as Mascot or MS-Fit. While each of these search sites has access to several databases, one can initially select either OWL or NCBInr. One can search the database with a standard set of criteria without using a species filter. The practice is to select three variable modifications to allow for conversion of peptide N-terminal glutamine to pyroglutamate, and oxidation of methionine residues; allowing for up to one missed cleavage. Neither the protein MW nor the PI can be used as a search parameter (these, however, can be used for subsequent validation of the matched protein). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from analysis. Finally, the peptide mass tolerance can be set to +1-0.15 Da relative to the monoisotopic MW of the singly charged peptide ion. Positive database hits are scored with a MOWSE number. The higher the number of hits the greater the confidence level. The database search algorithm relates the significance level for a given search. If a high MOWSE score is obtained indicating an unambiguous match, one can consider the protein positively identified, otherwise the sample can be subjected to analysis by use of the QSTAR mass spectrometer.

Mass spectrometric analysis by Nano ESI MS/MS.

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Samples that require analysis utilizing the QSTAR, following cleanup by Microcon-SCX adsorptive microconcentrator, can be concentrated by binding the peptide mix to a small amount of POROS R12 reversed-phase C18 chromatographic support packed into a nanopurification capillary. The packed capillary column volume is ~ 10-15 nl. The sample, dissolved in 10-p.l of 5% acetic acid in water, is applied to the capillary by use of a ten-µl gel loading pipette tip. A brief centrifugation forces the liquid down the capillary so that the peptides can bind to the support. The support is then washed with 10-15 p.1 of 0.5% acetic acid in 1:50 methanol/water. The peptides are eluted from the purification capillary into a nanospray capillary by the addition of 2 µ1 of 0.5% act id in 1:1 methanol/water followed by brief centrifugation with the nanospray capillary stacked just below the purification capillary in a micropurification holder (MDS Protana). Initially, data for a single MS run is collected. The peak masses are labeled and peptides are selected for potential MS/MS sequencing by locating those that appear to be doubly charged.

Most peptides resulting from a tryptic digest can have a significant doubly charged form, which is ideal for MS/MS sequencing. The first quadrupole of the QSTAR is tuned to pass a 2 Dalton window for the pre-selected doubly charged peptide ions, one at a time, for fragmentation by collision with low-pressure argon gas in the second quadrupole. Collision energy is adjusted for each peptide to obtain the best possible MS/MS spectra. Data are collected long enough to get good quality spectra. After MS/MS spectra are collected for all selected peptides, the data are manually interpreted. Internet protein database searches are performed similar to that for MALDI-TOF peptide fingerprint, except that the search is a partial amino acid sequence search with mass information (i.e., Mascot, employing Sequence Query format). The search criteria cannot screen for a species or a protein MW or PI (which, however, can be used for subsequent validation of the protein matched). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from MS/MS analysis. One missed cleavage can be allowed and two variable modifications can be selected, carbamidomethylation of cysteine and oxidation of methionine. The tolerance of the peptide monoisotopic mass can be set to +1- 0.3 and the MS/MS tolerance can be set at +1- 0.2. This type of search generally requires only two or three peptide sequences consisting of three of the amino acids per peptide to obtain a statistically significant match (a high MOWSE score). Once a match is identified, a list of the matched peptide's theoretical MS/MS fragments can be generated to compare with the observed fragments to further confirm the correctness of the match.

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Establishment of large-format 2-D PAGE protein maps for MPCs derived from normal BM.

The normal cell samples include, A) Untreated normal MPCs; B) Normal MPCs treated with TNF α ; C) Normal MPCs treated with TNF- α and IL-4. Each cell sample can generate a total of 8 protein samples, 1) culture supernatants/ secreted proteins (1 protein sample); 2) extracellular matrix (ECM) proteins (1 protein sample); 3) plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility (3 protein samples); 4) whole cell lysate proteins similarly solubilized using a 3-step differential extraction protocol (3 protein samples). Each protein sample can generate 3 large format 2 D gels (corresponding to 3 medium-range, overlapping

IPG gradient gels, pH 3-6; 5-8; 7-10). This means each cell sample can generate 24 large format 2 D gels, leading to generation of at least 72 large format gels for analysis of normal MPCs. To account for duplicate or triplicate samples, the gel number falls in the range of 200-300.

Establishment of large-format 2-D PAGE protein maps for MPCs derived from BM involved with representative pre-leukemic and leukemic conditions.

The disease-associated MPCs include those from MDS, CML, AML, CLL, ALL, and MM. As above, each MPC sample can generate 24 large-format 2 D gels. With 6 such diseases being studied, the gel number can reach 144. To account for duplicate or triplicate samples, the gel number falls within the range of 400-500. The use of IPGPhor, together with ready-made IPG strips, permits sample in-gel rehydration and performance of unattended IEF overnight by adding automation to the 2-D procedure.

Using high-resolution proteomics and with the added power of high-throughput robotics, identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

A robotically guided system facilitates excision of protein spots (by a spot cutter or picker) from 2-D PAGE gels, transfer of protein samples to 96-well microplates, and automated protein digestion in the microwells. Such a system reduces the time and labor relative to manual procedures and provides high throughput while minimizing keratin contamination from human skin, a frequent problem in proteomics research. The preferred method is to excise all spots from a gel but to process only the spots of interest, storing the remaining excised proteins frozen at -70°C for a later use. The robotic components can include MALDI slide spotter in addition to an automated protein spot picker and digestion station.

Example 8

30 Methods

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The present study involved microarray analysis of 23 samples and a corresponding number of chips. The samples were obtained from 4 normal healthy adult human subjects, consisting of mixtures of unfractionated stromal cells

(collective USCs or cUSCs, 8 samples), Percoll gradient-purified MPCs (collective MPCs or cMPCs, 5 samples) and single-cell MPCs (sMPCs, 10 samples) obtained by laser-capture microdissection (LCM). The study design allowed for adequate controls and replicates appropriate for a comprehensive gene expression profiling of normal BM stromal cells. The isolated single stromal cells were selected on the basis of morphology. Wright-Giemsa stained cytospin preparation revealed characteristically large cells with a relatively irregular nucleus and cytoplasm compartmentalized into ectoplasm and endoplasm. Subsequently, applicant identified a hematoxylin stain as a substitute for Wright-Giemsa stain. The hematoxylin stain is simpler to use and provides morphologic detail sufficient to allow recognition and isolation of these cells by laser capture microdissection and does not interfere with the downstream microarray testing (see details under Materials & Methods). The photomicrographs of 10 stromal cells that have been subjected to microarray testing are shown in Figure 15. To serve as controls and facilitate comparison, applicant analyzed side-by-side 8 samples of unfractionated stromal cells that are "contaminated" by up to 35% macrophages and 5% hematopoietic cells (referred to collective USC, or cUSC), and 5 samples of Percollgradient purified stromal cells, up to 95% pure (referred to collective MPC, or cMPC to distinguish from sMPC). RNA isolated from sMPC samples was subjected to 2 rounds of amplification using RiboAmp kit (Arcturus, Inc) prior to in vitro transcription (IVT). In contrast, RNA samples isolated from cUSCs and cMPCs were used without amplification for IVT. The subsequent steps of microarray testing were standard for all 3 types of samples and are schematized as follows: Preparation of total RNA ightarrowgeneration of cDNA → preparation of ds cDNA → in vitro transcription into cRNA → fragmentation of cRNA \rightarrow hybridization of target RNA to a microarray of known genes (Affymetrix U95Av2 oligonucleotide microarray, with 12,625 probe sets) → Signal quantification and first-tier analysis using the microarray quantification software, Microarray Suite (MAS v. 5, Affymetrix, Inc). The presence of a gene within a given a sample was determined at a detection p-value of <0.05, according to the statistical expression analysis algorithm employed by MAS v.5, and was graded absent (A), marginal (M) or present/ positive (P).

Assessment of RNA amplification method

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Since single-cell microarrays are relatively novel, applicant critically reviewed the

data with respect to two important statistics that would reflect on the reliability of RNA amplification assay procedure employed before analysis involving data-mining techniques. a) 3': 5' ratios of housekeeping control genes: As shown in Table 9, these ratios were close to 1 in the standard unamplified samples, whereas, they were increased in the amplified samples. Although this is to be expected due to preferential amplification toward 3' end, since amplification may not proceed all the way up to 5' end, applicant wanted to exclude possible sample degradation. For reasons unclear, in the case of ACTB (beta actin), the 3': 5' ratios were highly variable across single cell MPC samples. In any event, the 3': 5' ratios in case of GAPD (glyceraldehyde 3-phosphate dehydrogenase) were relatively tight, suggesting no evidence of sample degradation. Furthermore, both GAPD and ACTB gene probes that were employed as part of the standard gene probe set yielded relatively stable signals across replicates in each sample type, which is further evidence of intactness of RNA samples targeted for microarray analysis. b) Number of genes present or detected: As outlined in Table 9, the amplified single cell MPC RNA samples expectedly showed significantly lower number of genes compared to the standard RNA samples (on average 34% vs. 46% of the genes etched on the array). The fact that the number is relatively constant across single cell replicate samples is further indication of the reliability of the data. Notwithstanding the shortcomings of the amplification procedure, it is important to bear in mind that the conclusions are based only on those stromal cell genes that are detected commonly across unamplifed cMPCs and cUSCs as well as in amplified sMPCs (but do not include the genes undetected or the genes selectively detected in sMPCs).

Data mining and reproducibility of overall procedures

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The thrust of the present invention is to identify genes that are relatively uniformly expressed across normal untreated bone marrow stromal cell samples, regardless whether they are of single cell type or collective cell samples, purified or unpurified. As detailed under Materials & Methods, GeneSpring was used to achieve the following data-analysis objectives: a) Filtering for genes reliably detected in each sample group by eliminating the genes with weak expressions that are statistically close to the background estimate. b) Filtering for genes that are active or "present" across replicates in each sample group. c) Exclusion of genes

with weak expressions from genes "present" in each sample group. d) Preparation of master stromal cell gene list by intersecting gene lists from step (c) (as shown in Figure 16). These steps have led to identification of a list of 2755 genes that are detected in at least 7 of 8 cUSC samples AND 4 of 5 cMPC samples AND 9 of 10 sMPC samples, i.e., in at least 20 of 23 stromal cell samples investigated. The main conclusions of the present report are based on this "stromal cell gene list" that is broadly representative of all 3 types of stromal cell samples investigated, and not on a gene list that is selective to sMPCs. A hallmark of the quality of microarray data can be discerned from hierarchical cluster analysis of replicates, which involves the principles of vector algebra. An array of numbers representing expression levels of a particular gene in terms of normalized signal intensity in a group of samples is considered a gene expression vector. Likewise, an array of numbers showing expression levels of a group of genes by a particular tissue sample is considered a tissue expression vector. In the case, applicants have 2755 gene expression vectors and 23 tissue or sample expression vectors. These vectors are amenable to algebraic treatment, facilitating calculation of similarity between any two gene- or tissue-expression vectors on the basis of a correlative metric or a similarity-measure employed, e.g., Euclidean angle. Grouping together of two samples on the basis of these principles signifies that they are most closely related out of all the samples in terms of their overall pattern of gene expression. Construction of a bone marrow stromal cell hierarchical tree has enabled visualization of global gene expression patterns across replicates and conditions. As shown in Figure 17, stromal cell genes that are expressed at a relatively lower level in amplified samples (sMPCs) are clustered to the left of gene tree, genes that are more strongly expressed in sMPCs are prominently figured in the middle of gene tree, and genes that are expressed approximately at same level as in unamplified samples (cMPCs and cUSCs) are clustered to right of gene tree. Even more important as noticeable on the sample or experiment tree, hierarchical clustering segregated the members of each sample type into a separate group (cMPC, cUSC and sMPC). Note within each sample type, corresponding subject replicates clustered together with minor exceptions. This is a reflection on the reproducibility of the overall assay-procedures employed, which encompass a variety of stages and steps in addition to target RNA amplification prior to in vitro transcription (see Materials & Methods for details).

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Finally, it is important to keep in mind that the measured level of a transcript following amplification does not necessarily provide a quantitative estimate of gene expression, but only provides a qualitative indication that the gene is transcriptionally active, which by itself is sufficient grounds for the conclusions arrived at in the present report. As shown in Figure 18, the expression of genes within the stromal cell gene list ranges from 0.2 to 6 (on the log scale) in unamplified samples (cMPC and cUSC) and from 0.02 to 36 in amplified samples (sMPC), thus showing much greater variability in the amplified samples. For illustration purpose, the coloring of gene expression curves (following the linear color bar shown on the right) was based on the gene expression pattern of a particular single-cell sample, SCA1. Note that the genes that are detected at a low level in this sample (as indicated in blue) are not necessarily expressed at a low level in unamplified samples (as read by the log scale on Y-axis). In fact, a significant number of them are expressed at a high level in the unamplified samples. This finding together with the observation that amplified samples detected about 34% of genes as opposed to unamplified samples detecting about 46% of genes tested (Table 9), strikes a cautious note that some genes do not amplify at all by the method used, and other genes amplify to a sufficient degree to be detectable (shown in blue), while some other genes amplify to a degree equal to (in yellow) or surpassing (in red) the amounts in the collective samples. (The curve shown in white is the housekeeping gene, GAPD.) The statistical algorithm as implemented in the latest version of Microarray Analysis Suite (MAS v.5) determined that a gene within a given sample as positive, regardless of grading. To overcome the limitations of the amplification procedure employed, applicant focused only on genes that were positive in at least 20 of the 23 stromal cell samples investigated.

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A stromal cell gene list is expected to be representative of typical stromal cell gene expression profile. Such master gene list forms the basis for derivation of all other stromal cell gene lists, organized in accordance with lineage or functional categories. As depicted in Figure 19A & 19B, and listed in Tables 10 through Table 17, that were prepared according to lineage/ functional assignment, the findings show that isolated single cells simultaneously express genes associated with diverse mesenchymal cell lineages, namely osteoblasts, muscle cells, fibroblasts, adipocytes, epithelial cells, endothelial cells, nerve cells and glial cells,

providing confirmation of the existence of a pluridifferentiated progenitor cell type. By definition the stromal cell genes are present in at least 4 of 5 collective MPC samples AND 7 of 8 collective USC samples AND 9 of 10 single cell MPC samples; consequently, they are active in at least 20 of 23 samples tested, representing a typical genomic profile of stromal cells. The following gene lists are sub-lists of the master stromal cell gene list consisting of 2,755 genes. The stromal cell gene list contains a number of genes that are capable of causing endothelial differentiation and vasculogenesis within the marrow microenvironment; however, these genes themselves are not necessarily endothelial cell markers. In fact, stromal cells express a gene, EDF1, the expression of which inversely correlates with endothelial cell differentiation within the stromal cells. Of the 67AFFX control genes present on the U95A v2 chip, 22 genes are detected in at least 7 of 8 cUSC samples, 24 genes are detected in 4 of 5 cMPC samples and 19 genes are detected in at least in 9 of 10 sMPC samples. Thirteen of these genes are present in the stromal cell gene list, i.e., in 20 of the 23 samples investigated.

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As evident from these gene lists, note that an isolated single stromal cell simultaneously expresses transcripts for epithelial and neuroectodermal cell types as well. Departing even further from the initial thinking, the findings add to the evidence that the MPCs within the Dexter system might represent a form or stage of the progenitor cell that is common to nonhematopoietic and hematopoietic cells. As depicted in Figure 20, and listed in Table 18 through Table 21, the isolated single stromal cells express transcripts that are typical of hematopoietic cells, in particular precursor B cells. That BM stromal cells express CD10 (CALLA) is not novel since BM stromal cells as well as endometrial stromal cells and normal breast myoepithelial cells are known to express CD10. However, the expression of CD19, CD79A and immunoglobulin enhancer binding factors E12/E47 (proto-oncogene TCF3) by BM stromal cells is unforeseen, and forms the basis for postulating the existence of a common progenitor with B cell lineage. B-cell progenitors typically display the phenotype, (CD45 +/-, CD34 +/-, CD20 +/-), (CD10 +, CD19 +, CD79A +, HLA-Dr +), which as reported here is also displayed by isolated single stromal cells at least at the transcriptome level.

CD45 positivity by cMPC and cUSC samples is attributable to coexisting or contaminating hematopoietic cells in these samples as evidenced by

concurrent positivity for myelomonocytic markers CD13, CD33 and CD14 (Table 21). However, a similar explanation cannot hold true in case of isolated single stromal cells. The protein products or transcripts for CD45 and CD19 are most likely present in stromal cells at a basal level that is beyond the detection limits of conventional techniques, e.g., immunocytochemistry and Northern blotting, respectively. Conceivably, two rounds of amplification prior to IVT sufficiently increased their transcript levels to be detected by microarray analysis. In fact, the CD45 levels were several-fold lower in cMPC and cUSC compared to CD45 levels in sMPC, and CD19 was undetectable in unamplified samples. Finally, note that CD45 and CD19 are not isolated examples in this regard since applicant has identified at least 200 other genes that are uniquely present across sMPC samples but undetectable in cMPC and cUSC (Figure 16).

The issue of stromal cell – B cell connection

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Although no anlage of Bursa of Fabricius exists in mammals, bone marrow is generally regarded as the site of B-cell generation. While the Dexter type stromal cell culture system was devised for investigation of hematopoiesis. specifically myelopoiesis (see Introduction), Whitlock and Witte developed another system for the study of B-lymphopoiesis. Whitlock-Witte cultures, like Friedenstein cultures, are grown in the absence of hydrocortisone and horse serum. When stromal cell layers in W-W cultures are seeded with fresh bone marrow as a source of B cell precursors or with purified B cell precursors, the latter then differentiate into mature B cells. On the other hand, although Dexter cultures do not promote B cell maturation, Dexter cultures do contain B cell precursors, which upon switching of culture conditions from those of Dexter to Whitlock-Witte, differentiate into mature B cells. While BM stromal cells in one form or another are definitely known to support B-lymphopoiesis, it has not been so clear as to whether stromal cells actually give rise to B-cell precursors. Evidence for a progenitor cell common to stromal cells and hematopoietic cells has been coming to light piecemeal in the form of isolated reports. 1) Singer JW et al in 1984 in the course of investigating bone marrow cultures from human patients with clonal myeloproliferative disorders showed that the nonhematopoietic stromal cells were derived from the same clonal progenitors that were involved by the hematopoietic neoplasm, as revealed by G6PD marker analysis. 2) Huss R et al in 1995 in the course of investigating a canine BM stromal

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cell line showed that the adherent stromal cells had "turned" into nonadherent hematopoietic cells, especially when the latter were cultured in presence of stem cell factor. 3) Pessina et al in 1997 showed that a particular murine stromal cell line upon stimulation with bFGF, expressed a B-cell phenotype, including CD45R and surface 5 immunoglobulin. Although not by design, applicant shows for the first time that isolated single stromal cells express transcripts that are typically associated with hematopoietic lineage, namely, CD45 and CD19, as well as relevant protooncogenes and transcription factors. These results are strongly supportive of the existence of a progenitor cell common to bone marrow stromal cells and hematopoietic cells, particularly the bone marrow-derived (B) lymphocytes. Note that the study involves no feeder cells, no embryonic stem cells, no cell lines and no colonies of cells. Contrasting with the existing literature, the present study embarks on a new path of investigation entailing gene expression analysis of single, primary, normal human stromal cells that suggest a broad capacity for multilineage differentiation. On this model, progenitor cells express genes that are characteristic of any of the lineage fates that these cells are capable of adopting.

Perspective on pluripotentiality vs. pluridifferentiation

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The present investigation involves isolated single stromal cells, consisting of 10 cells from 4 different individuals (Figure 15). The cell culture system has been earlier characterized at light microscopic level, ultrastructural level and by karyotypic analysis, showing no evidence to suggest the artifacts discussed. Spontaneous cell fusion most likely involves monocytes/macrophages, forming multinucleated giant cells; however applicant observed no expression of myelomonocytic marker genes by isolated single stromal cells (Table 12). Keep in mind that the readout of in vivo transdifferentiation studies involves localization of different lineage cells in different tissues or organs; such a situation only requires fusion between two cell types (one donor cell and one recipient cell) for the investigators to believe the artifact as transdifferentiation. In contrast, applicant shows here presence of genes for a variety of cell-lineages simultaneously within the same cell. The probability of an array of different cell types fusing into one cell which then masquerading as a pluridifferentiated cell, and that too happening with 10 of 10 cells investigated, is in the opinion close to zero. There has never before been an opportunity to assess the extent of differentiation within these multipotential

progenitor cells in molecular terms at the single-cell level. Theoretically, a) A stem cell can directly become a terminally differentiated cell, or b) A stem cell can enter a phase of multilineage differentiation prior to becoming a single-lineage, mature cell. To the knowledge, this study is the first systematic attempt to answer these questions at the single cell level by using the marrow stromal cells as a model. Although numerous forward-looking reviews exist on the topic of single-cell genomics, only a rare report is available on the actual application of this technology. Applicant has applied this frontier technology to show that a phase of multilineage differentiation indeed exists at least in Dexter-type stromal cells. Pluripotentiality of the bone marrow mesenchymal stromal cells in terms of their ability to become muscle cells, bone cells, fat cells and fibroblasts under select culture conditions has been described by other investigators. Instead of documenting another example of the phenomenon per se, the results provide an independent validation of the studies on transdifferentiation by casting light at the molecular basis of cellular plasticity. Finally, to borrow a concept from the clinical practice setting, a morphologically "poorly" differentiated neoplasm expressing hematopoletic markers is classified as a leukemia/ lymphoma and treated as such. Similarly, a morphologically "undifferentiated" neoplasm marking for epithelial gene expression is diagnosed as a carcinoma and treated according to the protocols designed for a carcinoma. It is in this sense that applicant uses the term "pluridifferentiated" as opposed to "pluripotential" to characterize the BM stromal cells. Notwithstanding the semantics, applicant shows that the pluripotent stromal cells are pluridifferentiated, at least at the molecular level.

Conclusions

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The findings of the present study clarify the on-going controversy as to the co-existence of multiple stromal cell types vs. one stromal cell type with co-expression of multiple phenotypes within the Dexter system of BM stromal cell cultures. An isolated single stromal cell from these cultures simultaneously expresses an array of phenotypes, i.e., osteoblasts, fibroblasts, muscle cells, adipocytes, epithelial cells, endothelial cells, neural cells/glial cells and even hematopoietic cells, in particular, B-lymphoid progenitors, thus documenting its wide differentiation repertoire. The significance of the findings is three-fold, 1st) They validate the hypothesis that the BM stromal cells express a pluridifferentiated

progenitor cell phenotype, providing insight into the molecular basis of cellular plasticity as well as establishing the utility of single-cell genomics, 2nd) They provide evidence for a common progenitor for mesenchymal progenitors and BM-derived (B) lymphoid progenitors, 3rd) By establishing a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time, the findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency.

Materials & Methods

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Second-tier data-analysis/ data mining

The microarray data outputted by MAS v.5 (in the form of tab delimited text files) were imported into GeneSpring[™] software version 4.2.1 (Silicon Genetics, Redwood City, CA). Following instructions accompanying GeneSpring, each gene was normalized to itself (per-gene normalization) by using the median of the gene's expression values over all the samples of an experimental group (or groups) and dividing each measurement for that gene by the corresponding median value, assuming that it was at least 0.01. The ratios were then log transformed to base e. No per-sample normalization was performed in GeneSpring since it was already accomplished as part of MAS v.5 analysis. The purpose of the above data transformations, including scaling and normalization, was to remove systematic error within and across conditions or experimental groups prior to further analysis. GeneSpring was used to achieve the following data-analysis objectives. a) Filtering for reliably present genes by eliminating the genes with weak expressions that are statistically close to the background estimate. As per the instructions accompanying GeneSpring, random error was estimated from control strength or median measurement level using the two-component global error model of Rocke-Lorenzato that assumes variability between replicates as being similar for all genes showing similar measurement level. The formula for the error model of normalized expression levels can be written as follows:

$$S (norm)^2 = a^2/C^2 + b^2$$

Where, $S = \text{standard error of normalized expression data, a \& b are the two error components, a = an absolute or fixed error component impacting at lower measurement values, b = a relative or proportional error component impacting at higher measurement levels, and <math>C = \text{control strength.}$ According to the

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manufacturer, a curve is fitted for each group of replicates, with standard error of normalized data on Y-axis vs. control strength on X-axis. At lower end of control strength, the normalized standard error would be high and as the control strength increases, the standard error would decrease reaching a point where the curve flattens and data become more reliable. Control strength for each condition or sample group at which the above-referred two error components contribute equally, was calculated as follows, for collective MPCs, C = 128.68; collective USCs, C = 253.52; single-cell MPCs, C = 348.32. Each condition was filtered for genes expressing signals greater than the respective control strength, thus eliminating the genes with weak expressions from each group. Note 7,196 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 7,287 genes in case of cUSCs and 5,937 in case of sMPCs. Corresponding gene lists were created. b) Filtering for genes "present" across replicates in each sample group. GeneSpring's "Add data file restriction" feature was used to prepare the respective lists of genes that were present (or expressed or active) in a least 7 of 8 cUSC samples, 4 of 5 cMPC samples, and 9 of 10 sMPC samples. Note 5,204 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 4,763 genes in case of cUSCs, and 3,124 genes in case of sMPCs. Corresponding gene lists were created. c) Exclusion of genes with weak expressions from genes "present" in each sample group. Respective gene-lists for each sample group from steps (a) and (b), were intersected via Venn diagrams. Note 5,204 genes passed the restriction in case of cMPCs, 4,761 genes in case of cUSCs, and 3,124 genes in case of sMPCs, which are almost identical to the numbers obtained as under step (b), except for a difference of 2 genes in case of cUSCs, thus providing no significant improvement in restricting the data beyond under step (b). This is a reflection of the high stringency of the criterion employed under step (b). The 2 genes in case of cUSCs that passed the restriction under step (b) but failed the combined restriction under step (c) did show weak expressions (raw signals ranging, 142-331). Corresponding gene lists were created. d) Preparation of master stromal cell gene list. Respective gene lists for the three sample groups from step (c) were intersected via Venn diagrams, resulting in identification of a list of 2,755 genes that are uniformly present or expressed in at least 20 of 23 stromal cell samples investigated. The stromal cell gene list thus arrived at contained genes that

are representative of diverse mesenchymal lineages. Parenthetically, intersecting of gene lists corresponding to the three sample groups from step (b) resulted in a stromal cell gene list consisting of 2,756 genes, thus differing by 1 gene from the "official" master stromal cell gene list. e) Two-way hierarchical clustering of 2755 stromal cell genes based on expression profiles in 23 stromal cell samples. Only the data that were "cleaned up" of genes with weak expressions as outlined under step (a) were used for hierarchical clustering. This necessitated further processing of data in Microsoft Access prior to analysis by GeneSpring. Note that the data for each individual sample as outputted by MAS v.5 contained probe IDs, quantitative and qualitative data, as well as other information such as annotations and are readily recognizable by GeneSpring. In contrast, the gene list, resulting from step (a), contained only probe IDs and could not contain the data associated with each individual sample and was not recognizable by GeneSpring for inputting as part of an Experiment. Therefore, the microarray data for each group of individual samples (in Excel format) as well as the corresponding gene list for that group from step (a) (also in Excel format) were imported into an Access database. The genes that did not pass the test under step (a) were deleted from the microarray data for each individual sample by querying and intersecting with the appropriate post-cleanup gene list. The resulting data files were saved first as Excel files, then re-saved as tab delimited text files and then imported into GeneSpring. Per-gene normalization and log transformation were applied as described above. "Gene Tree" and "Experiment Tree" were constructed by applying a method similar to that of Eisen et al as implemented in GeneSpring and by using the stromal cell gene list and the following parameters: standard correlation as similarity measure; a minimum distance of 0.001; and a separation ratio of 0.5 in case of Gene Tree and 1.0 in case of Experiment Tree. f) Preparation of stromal cell gene lists as relevant to different cellular phenotypes and/ or functions. The gene lists associated with distinct mesenchymal cell lineages or phenotypes, i.e., osteoblasts, fibroblasts, muscle cells and adipocytes, etc, were prepared using a combination of methods. These include 1) Visually inspecting the entire stromal-cell gene list for relevant key words. 2) Directly searching the stromal cell gene list by using key words of interest via "Advanced Find Genes" feature under Edit menu in GeneSpring and by selecting "Search Only Current Gene List". 3) Intersecting the stromal cell gene list with gene

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lists of interest from Gene Ontology lists, e.g., list of oncogenes, via Venn diagrams. g) Visualization of gene-expression plots. The expression pattern of a gene across a given group (or groups) of samples of interest was pictured via Gene Inspector window, utilizing desired display options.

Throughout this application, various publications, are referenced by author and year. Full citations for the publications are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

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The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

The preceding descriptions of the invention are merely illustrative and should not be considered as limiting the scope of the invention in any way. From the foregoing description, one of ordinary skill in the art can easily ascertain the essential characteristics of the instant invention, and without departing from the spirit and scope thereof, can make various changes and/or modifications of the inventions to adapt it to various usages and conditions. As such, these changes and/or modifications are properly, equitably, and intended to be, within the full range of equivalence of the following claims.

Tables

Table 5

Summary of bone marrow stromal cell samples targeted for microarray analysis with an outline of the corresponding indicators of assay quality performance

·	Unfractionated stromal cells (Collective USC, 8 replicates)	Percoll gradient- purified stromal cells (Collective MPC, 5 replicates)	LCM-dissected single cell samples (Single Cell MPC, 10 replicates)
Subject A	UNFR A	MPC A	SCA1, SCA2, SCA3
Subject B	UNFR B, UNFR B RI, UNFR B R2	MPC B R2	SCB1, SCB3
Subject C	UNFR C R1, UNFR C R2	MPC C R2	SCC1, SCC3
Subject D	UNFR D R1, UNFR D R2	MPC D R1, MPC D R2	SCD1, SCD2, SCD3
Amplification of RNA before IVT	No	No	Two rounds
Number of genes present (% of 12,625)	Mean: 46.63 SD: 5.95	Mean: 46.54 SD:3.66	Mean: 33.93 SD: 3.94
3':5' ratio, GAPD M33197 (Probe used as part of housekeeping control gene probe set)	Mean: 0.89 SD: 0.33	Mean: 1.23 SD:0.53	Mean: 6.76 SD: 2.97
GAPD signal 35905_s_at (Probe used as part of standard gene probe set)	Mean: 130,723 SD: 36,990	Mean: 164,593 SD: 40,204 (See Figure 5B.)	Mean: 43,235 SD: 14,413 (See Figure 5B.)
3':5' ratio, ACTB X00351 (Probe used as part of housekeeping control gene probe set)	Mean: 1.44 SD: 0.60	Mean: 2.29 SD: 1.57	Mean: 57.92 SD: 67.82
ACTB signal 32318_s_at (Probe used as part of standard gene probe set)	Mean: 86,104 SD: 18,458	Mean: 100,383 SD: 28,427 (See Figure 5B.)	◆Mean: 4,445 ◆SD: 884 (See Figure 5B.)

Footnote to Table 5

Replicate samples shown under each sample type as indicated correspond to each subject. The replicates of collective USC and collective MPC represent cell-culture or biological replicates of stromal cells grown in parallel flasks (instead of technical replicates). We started with 27 samples of which 2 collective MPC samples and 2 single cell MPC samples failed either at the test chip stage or produced unusual results in terms of the number of genes present and/ or 3':5' ratios and were therefore excluded as outliers. Only those samples that were targeted for the data mining analysis are represented in this table. The statistics shown (means and SDs) were based on the number of sample replicates indicated in the top row of the table except for ACTB-signal for single cell MPCs (noted in the table by \spadesuit), which were based on 9 replicates instead of 10.

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Table 6:. Osteoblast/bon cell/bone dis rders (S shi, B)

Systematic	Common	Genbank	Descripti n	Phenotype/ Function
38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	
38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	•
38126_at	BGN	J04599	biglycan	
36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	·
37315_f_at	8M036	A1057607	uncharacterized bone marrow protein BM036	
36996_at	OS-9	U41635	amplified in osteosarcoma	
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	
2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	
1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	OMIM Notes: c-fos restricted to perichondrial growth regions of the cartilaginous skeleton.
1915_s_at	c-fos	V01512	Human cellular oncogene c-fos	
1388_g_at	VDR	J03258	(complete sequence). vitamin D (1,25- dihydroxyvitamin D3) receptor	?Osteoporosis, involutional; Rickets, vitamin D-resistant
1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like)	
32094_at	CHST3	AB017915	carbohydrate (chondroitin 6) sulfotransferase 3	•
32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic

32305_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
34321_i_at	GS3786	D87120	predicted osteoblast protein	•
34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	
34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan 6 (barnacan)	•
222_at	EXT1	S79639	exostoses (multiple) 1	Chondrosarcoma; Exostoses, multiple, type 1
36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	Chondrosarcoma, extraskeletal myxoid
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, class B, 2; OMIM Notes: Alternative title, DEC1, expressed primarily in differentiated chondrocytes.	/ transcription factor

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Table 7: Muscl / muscle disorders (Seshi, B)

Syst matic	Common 1	Genbank	Description	Phenotype/ Function
38251_at	MLC1SA	Al127424	myosin light chain 1 slow a	,
38923_at	FRG1	L76159	FSHD (Facioscapulohumoral	·
00000_0.	11,00	• • • • • • • • • • • • • • • • • • • •	muscular dystrophy) region gene 1	
•			,	
37012_at	CAPZB	U03271	capping protein (actin filament)	
07012_d\			muscle Z-line, beta	•
37279_at	GEM	U10550	GTP binding protein overexpressed	/ GTPase
0.2.0_0.		-,	in skeletal muscle	
36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial
			, , , , , ,	hypertrophic, 3
36790_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial
				hypertrophic, 3
36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	
36678_at	TAGLN2	D21261	transgelin 2	
36641_at	CAPZA2	U03851	capping protein (actin filament)	•
. —			muscle Z-line, alpha 2	
36931_at	TAGLN	M95787	transgelin	
37631_at	MYO1E	U14391	myosin IE	
41439_at	MYO1B	AJ001381	myosin IB	
40910_at	CAPZA1	U56637	capping protein (actin filament)	/ binds barbed ends of
			muscle Z-line, alpha 1 -	actin filaments
41187_at	MLC-B	U26162	myosin regulatory light chain	
41747_s_at	MEF2A	U49020	Human myocyte-specific enhancer	· .
•			factor 2A (MEF2A) gene, last coding	9
			exon, and complete cds.	·
				·
41738_at	CALD1	M64110	caldesmon 1	•
41739_s_at	CALD1	M83216	caldesmon 1	Dorior discosso
39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac	Dariel disease
00700	470040		muscle, slow twitch 2 ATPase, Ca++ transporting, cardiac	Darier disease
39790_at	ATP2A2	M23115	muscle, slow twitch 2	. Darrer diocase
20270 -	DECNI	U17999	beclin 1 (coiled-coil, myosin-like	
39378_at	BECN1	017333	BCL2 interacting protein)	
40488_at	DMD .	M18533	dystrophin (muscular dystrophy,	Becker muscular
40400_at	DIVID	14110555	Duchenne and Becker types)	dystrophy;
			Bushing and Beener types,	Cardiomyopathy, dilated,
				X-linked; Duchenne
				muscular dystrophy
	_			ONAINA NIMANI DIMININA
40438_at	PPP1R12A	D87930	protein (myosin) phosphatase 1,	OMIM Notes: Regulates
•	•		regulatory (inhibitor) subunit 12A	the interaction of actin
				and myosin downstream
				of the guanosine triphosphatase Rho.
	•			imphosphatase nho.

			• ,	
32838_at	smooth muscle myosin heavy chain isoform SMemb	S67247	Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA	
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
33994_g_at	MLC	M22919	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	
33447_at	MLCB	X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
35362_at 34306_at 36989_at	MYO10 MBNL DAG1	AB018342 AB007888 L19711	myosin X muscleblind-like (Drosophila) dystroglycan 1 (dystrophin- associated glycoprotein 1)	···
40022_at	FCMD	AB008226	Fukuyama type congenital muscular dystrophy (fukutin)	?Walker-Warburg syndrome; Muscular dystrophy, Fukuyama congenital
39031_at	COX7A1	AA152406	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	oongome.
35729_at	MYO1D	AB018270	myosin ID	
32378_at	PKM2	M26252	pyruvate kinase, muscle	
40375_at	EGR3	X63741	early growth response 3; OMIM Notes: Expressed in developing muscle spindles.	
1637_at	МАРКАРК3	U09578	mitogen-activated protein kinase- activated protein kinase 3; OMIM Notes: Expressed especially high in heart and skeletal muscle.	
40399_r_at	MEOX2	A1743406	mesenchyme homeobox 2 (growth arrest-specific homeobox).OMIM Notes: Important regulator of myogenesis.	
39565_at	BMPR1A.	Z22535	bone morphogenetic protein receptor, type IA. OMIM Notes: Alternative title, activin receptor-like kinase 3; ALK3. Expressed almost exclusively in skeletal muscle with weak expression in heart and placenta.	Polyposis, juvenile intestinal
41449_at	SGCE	AJ000534	sarcoglycan, epsilon	Dystonia, myoctonic

Table 8: Fibroblast (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
39333_at	COL4A1	M26576	Human alpha-1 collagen type IV gene, exon 52.	
37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4 dioxygenase (proline 4-hydroxylase),	
36666_at	P4HB	M22806	alpha polypeptide I precursor; Human prolyl 4- hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	•
41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	
39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface- associated, fibroglycan)	
39945_at	FAP	U09278	fibroblast activation protein, alpha	OMIM Notes: Expressed in fetal normal mesenchymal tissues and stromal fibroblasts within common types of epithelial tumors.
32835_at	MAFF	AA725102	v-maf musculoaponeurotic - fibrosarcoma oncogene homolog F (avian)	
32535_at	FBN1	X63556	fibrillin 1 (Martan syndrome)	Ectopia lentis, familial; Marfan syndrome; MASS syndrome; Shprintzen- Goldberg syndrome
2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	Jackson-Weiss sydnrome; Pfeiffer syndrome
1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	OMIM Notes: May play a role in mesenchymal stimulation of epithelial cell proliferation.
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
31720_s_at	FN1	M10905	fibronectin 1	·
31720_s_at	FN1	X02761	fibronectin 1	•
35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
34390_at	P4HA2	U90441	procollagen-proline, 2-oxoglutarate dioxygenase (proline 4-hydroxylase) alpha polypeptide II	

Table 9: Adipocyte (Seshi, B, et al)

Prob ID	Gene Name	Genbank ID	Description	OMIM Notes
343,78_at	ADRP	X97324	adipose differentiation-related protein (adipophilin) / lipid-droplet binding/ adipocyte-specific	mRNA levels are induced rapidly and maximally after triggering adipocyte differentiation.
40282_s_at	DF	M84526	D component of complement (adipsin)	High level of expression in fat.
33337_at .	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	
39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	• • • • • • • • • • • • • • • • • • • •
39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	
31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	
37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like	
36073_at	NDN	U35139	necdin homolog (mouse)/ Prader- Willi syndrome	
37122_at	PLIN	AB005293	Perilipin (Did not meet the criteria to be included in stromal cell gene list because it was positive in 5 of 5 cMPC and 9 of 10 sMPCs, but only 6 of 8 cUSc instead of 7 of 8 cUSC samples).	Plays an important role in adipocyte metaboloism. Has significant sequence relationship with ADRP.

Table 10::Epithelial cell/ carcin ma (S shi, B)

Systematic	Common	G nbank	Description	Phenotype/ Function
38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38589_i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	Epidermolytic hyperkeratosis
37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	·
36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance	
36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Pancreatic cancer; Polyposis, juvenile intestinal
36852_at	N33	U42349	Putative prostate cancer tumor suppressor	
36851_g_at	N33 [*]	U42360	39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.	?Prostate cancer, susceptibility to
37762_at	EMP1	Y07909	epithelial membrane protein 1	/ receptor
37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 15	
40856_at	SERPINF1; PEDF; EPC		PEDF; Human pigment epithelium- derived factor gene, complete cds.	
41431_at	ICK	AB023153	intestinal cell kinase	
· 39363_at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	
39631_at	EMP2	U52100	epithelial membrane protein 2	
39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	e / associates with p110(RB)
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	
32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	-
32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	
32329_at 34005_at	KRTHB6 PIGR	X99142 X73079	keratin, hair, basic, 6 (monilethrix) polymeric immunoglobulin receptor, expressed in glomerular epithelial cells	Monilethrix / Binds and transports . polymeric immunoglobulin
1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8); OMIM Notes: Expressed in prostate carcinoma cells but only rarely in prostatic hypertrophy.	1

Table 11: Endoth lial cell (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
39315_at 1929_at	ANGPT1 ANGPT1	D13628 U83508	angiopoietin 1 angiopoietin 1	/ ligand for the TIE2 receptor
40387_at	EDG2	U80811	endothelial differentiation, lysophosphatidic acid (LPA) G- protein-coupled receptor, 2	·
40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1; OMIM Notes: EDF1 level inversely correlates with the level of endothelial differentiation. Inhibition of EDF1 expression promotes endothelial cell differentiation. It is postulated that EDF1 may function as a bridging molecule that interconnects regulatory proteins and the basal transcriptional machinery, thus modulating the transcription of the genes involved in endothelial differentiation.	•
37907_at	F8A; DXS522E	M34677	Factor VIII-associated gene 1; CpG island protein; Human nested gene	
41433_at	VCAM1	M73255	protein gene, complete cds. Human vascular cell adhesion molecule-1 (VCAM1) gene,	
36988_at	TNFAIP1	M80783	complete CDS. tumor necrosis factor, alpha-induced protein 1 (endothelial); OMIM Notes: Involved in the promary response of the endothelium to TNF.	
583_s_at 1953_at 36100_at 37268_at	VCAM1 VEGF VEGF VEGFB	M30257 AF024710 AF022375 U43368	vascular cell adhesion molecule 1 vascular endothelial growth factor vascular endothelial growth factor vascular endothelial growth factor B	
159_at	VEGFC ·	U43142 .	vascular endothelial growth factor C	/ ligand and activator of the receptor tyrosine kinase Flt4

Table 12: Nerve cell/ neuro ndocrine/ neurologic disorders (Seshi, B)

			,	
Systematic	Common	G nbank	Description	Phenotype/ Function
37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	
37692_at	DBI GABARAPL	Al557240	A binding protein) GABA(A) receptor-associated	
35767_at	2 GABARAPL	Al565760	protein-like 2 GABA(A) receptor-associated	
35785_at	1	W28281	protein like 1	
38406_f_at	PTGDS	Al207842	prostaglandin D2 synthase (21kD, brain)	
38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca), brain specific insertion sequences	
38653_at	PMP22	D11428	peripheral myelin protein 22	Charcot-Marie-Tooth disease with deafness; Charcot-Marie-Tooth neuropathy-1A; Dejerine- Sottas disease; Neuropathy, recurrent, with pressure palsies
38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3'flank.	
39072_at	MXI1	L07648	MAX interacting protein 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
38841_at	GDBR1	AF068195	putative glialblastoma cell differentiation-related	•
38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	Neuropathy, hereditary sensory and autonomic, type 1
36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase), neuron- specific. OMIM Notes: Highly specific to neurons and to cells of the diffuse neuroendocrine system and their tumors.	Parkinson disease, familial
37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	
37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	
36667_at	PYGB	U47025	phosphorylase, glycogen; brain	
36965_at	- ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	/ peripheral proteins believed to act as membrane-cytoskeleton
				linker molecules

38040_at 37958_at 41221_at	SPF30 BCMP1 PGAM1	AF107463 AL049257 J04173	splicing factor 30, survival of motor neuron-related brain cell membrane protein 1 phosphoglycerate mutase 1 (brain)	
40936_at 41091_at	CRIM1 FALZ	Al651806 U05237	cysteine-rich motor neuron 1 fetal Alzheimer antigen. OMIM Notes: Abnormally expressed in fetal brain. The corresponding antibody ALZ50 recognizes neurofibrillary pathology associated with Alzheimer's disease.	
41136_s_at	APP	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	Alzheimer disease-1, APP- related; Amyloidosis, cerebroarterial, Dutch type; Schizophrenia, chronic
763_at 641_at	GMFB PSEN1	AB001106 L76517	glia maturation factor, beta presenilin 1 (Alzheimer disease 3)	Alzheimer disease, familial, with spastic paraparesis and unusual plaques; Alzheimer disease-3
39793_at 40023_at 39687_at 39686_g_at 39542_at	GBAS BDNF E46L E46L ENC1	AF029786 X60201 AI524873 AL050282 AF059611	glioblastoma amplified sequence brain-derived neurotrophic factor like mouse brain protein E46 like mouse brain protein E46 ectodermal-neural cortex (with BTB- like domain)	/ associates with p110(RB). OMIM Notes: Expressed highest in brain.
40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	
40121_at	HIP2	U58522	huntingtin interacting protein 2	
40467_at	SDHD	AB006202	succinate dehydrogenase complex, subunit D, integral membrane protein	Paragangliornas, familial central nervous system; Paragangliornas, familial nonchromaffin, 1, with and without deafness; Pheochromocytoma
40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	,
32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	Ceroid-lipofuscinosis, neuronal 2, classic late infantile
32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	

33817_at	D10S102	S63912	FBRNP; heterogeneous	
			ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP (human, fetal brain, mRNA, 3043 nt).	
- 33942_s_at	STXBP1	AF004563	syntaxin binding protein 1	/ implicated in vesicle trafficking and neurotransmitter release
1659_s_at 1695_at	RHEB2 NEDD8	D78132 D23662	Ras homolog enriched in brain 2 neural precursor cell expressed, developmentally down-regulated 8	
2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	
216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7, brain	
32102_at	SACS	AB018273	spastic ataxia of Charlevoix- Saguenay (sacsin)	Spastic ataxia, Charlevoix- Saguenay type
31896_at 35681_r_at	NAG ZFHX1B	AL050281 AB011141	neuroblastoma-amplified protein zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease- mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without
e .	:		-	Hirschsprung disease
35268_at	AXOT	AL050171	axotrophin	•
36190_at	CDR2	M63256	cerebellar degeneration-related protein (62kD)	
36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	
35973_at 36142_at	HYPH SCA1	AB023163 X79204	Huntingtin interacting protein H spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	Spinocerebellar ataxia-1
34817_s_at	A2LP	U70671	ataxin 2 related protein	•
34777_at	ADM	D14874 AB018327	adrenomedullin activity-dependent neuroprotector	
34394_at 32606_at	ADNP BASP1	AA135683	brain abundant, membrane attached signal protein 1	
38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	
36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	Spinocerebellar ataxia-2
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	Immunodeficiency with hyper-IgM, type 3
34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L- proline), member 7	

34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (782 protein)	
654_at	MXI1	L07648	MAX interacting prot in 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
37945_at 39685_at	BACH E46L	U91316 AL050282	brain acyl-CoA hydrolase like mouse brain protein E46	•
33769_at	MPZL1	AF087020	myelin protein zero-like 1	
39356_at	NEDD4L	AB007899	neural precursor cell expressed, developmentally down-regulated 4- like	
38800_at	STMN2	D45352	stathmin-like 2; OMIM Notes: Neuronal growth-associated protein SCG10.	
36933_at	NDRG1	D87953	N-myc downstream regulated gene	Neuropathy, hereditary motor and sensory, Lom type
40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse); OMIM Notes: Alternative title, KF1, expressed in normal cerebellum and Alzheimer disease cerebral cortex, but not in normal cerebral cortex.	76-
1452_at	LMO4	U24576	LIM domain only 4	OMIM Notes: is highly expressed in the cranial neural crest cells, somite, dorsal limb bud
		•		mesenchyme, motor neurons, Schwann cell progenitors, and T-
1058_at	WASF3	S69790	WAS protein family, member 3	lymphocyte lineage.

Table 13: Drosophila and/ or homeotic genes (S shi, B)

Systematic	Common	Genbank	D scription	Ph notype/ Function
38288_at	SNAI2	U69196	snail homolog 2 (Drosophila). OMIM Notes: Neural crest transcription factor SLUG. A zinc fanger protein that plays an important role in the transition of epithelial to mesenchymal characteristics within the neural crest.	
39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	
39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila). OMIM Notes: Positive in dendritic cells of lymph nodes and Reed-Sternberg cells.	
39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila). OMIM Notes: Upregulated during retinoic acid-induced granulocytic differentiation of APL cells.	
38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila). OMIM Notes: Promotes the differentiation of astroglia from multipotent progenitors.	Cerebral (autosomal dominant) arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL)
38944_at	марнз	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD3 signal transduction important in the regulation of muscle-specific genes.
37693_at	NUMB	L40393	numb homolog (Drosophila)	OMIM Notes: Numb directs neuronal cell fate decisions.
40004_at	SIX1	X91868	sine oculis homeobox homolog 1 (Drosophila)	OMIM Notes: Expressed in adult skeletal muscle, and in multiple tumors including mammary carcinoma.
39610_at	HOXB2	X16665	homeo box B2	OMIM Notes: Essential for motor neuron development. Within the hematopoietic compartment, expressed specifically in erythromegakaryocytic cell lines.

				•
40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	OMIM Notes: Expressed in prostate gland epithelial cells.
40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	Rhabdomyosarcoma, alveolar. OMIM Notes: Activates myogenic transcription program.
40127_at	PMX1	M95929	paired mesoderm homeo box 1	OMIM Notes: Expressed in cardiac, skeletal and smooth muscle tissues.
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	OMIM Notes: Expressed in many epithelial, some endothelial and smooth muscle cells.
40328_at	TWIST	X99268 .	twist homolog (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)	Saethre-Chotzen syndrome. OMIM Notes: Required for cranial neural tube morphogenesis.
33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	OMIM Notes: Highest expression adult skeletal muscle and fetal kidney. FZD7 dependent PKC signaling controls cell sorting behaviour in the mesoderm.
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila); adipocyte associated.	
1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	OMIM Notes: MAD proteins were originally defined in Drosophila as essential components of the signaling pathways of the TGF-beta receptor family (e.g., TGFBR1). MADH7 and MADH6 as shown by IHC and ISH are predominantly expressed in vascular endothelium.
1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	/ inhibitor of BMP signaling

PCT/US02/31662

1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	OMIM Notes: SMAD5 plays a critical role in the signaling pathway by which TGF-beta inhibits the proliferation of human hematopoietic progenitor cells.
1453_at	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	
1433 <u>g</u> _at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD2/ SMAD3 signal transduction appears to be important in the regulation of muscle-specific genes.
35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease- mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease
35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	OMIM Notes: Expressed in extensor tendons, and in lens fibers and participates inconnective tissue patterning.
36308_at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	OMIM Notes: Specifically expressed in nervous tissue and in particular cerebellar granule cells, potential biomarker for cerebellar granule cell lineage and
34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	medulloblastoma. OMIM Notes: Expressed in skeletal muscle myoblasts, also in lymphoblastoid cell lines.
33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	OMIM Notes: Expressed in fibroblasts and hepatocytes.

Table 14:	B-cell/ B-c II n oplasms (Seshi, B)				
Systematic	Common	Genbank	Description	Phenotype/ Function	
41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene	
37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative		
38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis 1	
37730_at	p100	U22055	EBNA-2 co-activator (100kD); OMIM Notes: EBNA-2 activates transcription of specific genes and is essential for EBV-mediated Blymphocyte transformation.	nuclear protein 2 acidic	
466_at	GTF2I	U77948	general transcription factor II, I; OMIM Notes: Alternative title, BTK-associated protein, 135kD (BAP135). Bruton's tyrosine kinase (BTK) is essential for B-cell		
	. •		activation and phosphorylates BAP135 in B cells.		
36875_at 38438_at	IBTK NFKB1	AL050018 M58603	inhibitor of Bruton's tyrsoine kinase nuclear factor of kappa light polypeptide		
39730_at	ABL1	X16416	gene enhancer in B-cells 1 (p105) v-abl Abelson murine leukemia viral oncogene homolog 1	Leukemia, chronic myeloid	
38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog 1	· · · · · · · · · · · · · · · · · · ·	
36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)		
41436_at	ZNF198	AJ224901	zinc finger protein 198; OMIM Notes: ZNF198 involves T- or B-cell lymphoblastic lymphoma, myeloid hyperplasia, and eosinophilia and evolves toward AML. This multilineage involvement suggests the malignant transformation of primitive hematopoietic stem cell.	Stem-cell leukemia/lymphoma syndrome	
40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51); OMIM Notes: BCL6 is predominantly expressed in the B-cell lineage, especially mature B cells (centrocytes and centroblasts).	Lymphoma, B-cell, Diffuse Large	
32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	· :	
32696_at 33791_at	PBX3 DLEU1	X59841 Y15227	pre-B-cell leukemia transcription factor 3 deleted in lymphocytic leukemia, 1	. •	

34005_at	PIGR	X73079	polymeric immunoglobulin receptor	/ Binds and transports polymeric immunoglobulin
1636_g_at	ABL	U07563	ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia.	Leukemia, chronic myeloid
1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene
2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis 1
1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
1377_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	/ IkB-like activity
1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	
35350_at	GALNAC4 S-6ST	AB011170	B cell RAG associated protein	
35992_at	MSC	AF087036	musculin (activated B-cell factor-1, ABF1); OMIM Notes: Downstream target of B-cell receptor signal transduction pathway. Also expressed in proliferating undifferentiated myeloblasts.	/ basic helix-loop-helix transcription factor
34344_at	IKBKAP	AF044195	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex- associated protein	Dysautonomia, familial
34350_at	RSN .	X64838	restin (Reed-Sternberg cell-expressed intermediate filament-associated protein); Note R-S cell is a form of B-cell.	
36204_at	PTPRF	Y00815	protein tyrosine phosphatase, receptor type F; OMIM Notes: Alternative title, Leukocyte antigen-related tyrosine phosphatase (LAR) Both LAR and LCA (CD45) map to chromosome 1. LCA is protein-tyrosine phosphatase, receptor-type C, PTPRC, whereas LAR is PTPRF.	
34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1.	IGBP1, a marker for early B-cells

1373_at	TCF3	M31523	proto-oncogene or transcription factor 3 TCF3 (E2A immunoglobulin enhancer binding factors E12/E47); OMIM Notes: E2A mutant mice will have selective failure to develop B cells, all other hematopoietic c_ll lineages being intact. The block to B cell development occurs before immunoglobulin D(H)-J(H) rearrangement.	contributing the DNA binding domain of the t(1:19) translocation
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5; OMIM notes: Alternative title, B-cell associated molecule CD40; expressed on the surface of all mature B cels, most mature B-cell malignancies and some early B-cell ALL.	Immunodeficiency with hyper-IgM, type 3
38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1; OMIM Notes: Alternative title, BERG36 (B-cell early response gene encoding a 36 kD protein).	
37026_at	COPEB .	AF001461	core promoter element binding protein; OMIM Notes: Alternative title, B-cell-derived 1, BCD1. The expression of BCD1 was limited to two tissues, CD19+ B-cells and testis of normal individuals. B-cell maturation is associated with BCD1- expression.	/ transcription factor involved in hepatic wound healing
38050_at	BTF	D79986	Bcl-2-associated transcription factor	
32696_at	PBX3 .	X59841	pre-B-cell leukemia transcription factor 3	

Table 15: Myel id cell/ myeloid leukemia (Seshi, B) Phenotype/ Function Description **Systematic** Common Genbank myeloid/lymphoid or mixed-lineage 39037_at MLLT2 L13773 leukemia (trithorax homolog, Drosophila); translocated to, 2 Meis1, myeloid ecotropic viral 37486_f_at MEIS3 U68385 integration site 1 homolog 3 (mouse) Leukemia, acute 37685_at **PICALM** U45976 phosphatidylinositol binding clathrin myeloid; Leukemia, assembly protein acute T-cell lymphoblastic MLL septin-like fusion; a fusion partner Leukemia, acute MSF AB023208 41220_at gene of MLL myeloid, therapyrelated: Ovarian carcinoma Myeloid leukemia, core-binding factor, beta subunit 41175_at **CBFB** L20298 acute, M4Eo subtype Leukemia, acute 943_at **RUNX1** D43968 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 myeloid; Platelet disorder, familial, with oncogene) associated myeloid malignancy Leukernia, chronic v-abl Abelson murine leukemia viral 39730_at ABL1 X16416 myeloid oncogene homolog 1 myeloid cell leukemia sequence 1 33146_at MCL1 L08246 (BCL2-related) Leukemia, chronic ABL is the cellular homolog proto-1636_g_at ABL U07563 oncogene of Abelson's murine myeloid leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia. myeloid cell leukemia sequence 1 277_at MCL₁ L08246 (BCL2-related) 41388_at MEIS2 AF017418 Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) SET translocation (myeloid leukemia-40189_at SET M93651 associated, M2/M4 AML); SET stands for suppressor of variegation, enhancer of zeste and trithorax. Leukemia, acute 38992_at DEK X64229 DEK oncogene (DNA binding) nonlymphocytic Leukemia, acute 36941_at AF1Q U16954 ALL1-fused gene from chromosome myelomonocytic 1q

Table 16:	T cell/ NK ce	NK cell (Seshi, B)					
Systematic	Common	Genbank	D scripti n	Phenotype/ Function			
37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic			
498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1				
40822_at	NFATC3	L41067	nuclear factor of activated T- cells, cytoplasmic, calcineurin- dependent 3	·			
34003_at	·CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	/ T-cell coreceptor; involved in antigen recognition; participant in signal transduction pathway			
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell (T-ALL)			
35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	,			
34234_f_at	NKTR	Al688640	natural killer-tumor recognition sequence; OMIM Notes: The protein product of the NKTR gene is present on the surface of LGLs and facilitates their binding to tumor targets.				
39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	/ HIV-1 Tat transcriptional coactivator			
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell			

Table 17
Stromal cells showing expression of genes that are typically affiliated with B-cell progenitors

Gene	Probe ID	GenBank ID	cMPC	cUSC	sMPC
CD45	40518_at		Positive in	Positive in	Positive in
			4/5 samples	8/8 samples	6/10 samples
CD34	538_at		4/5	5/8	4/10
CD19	1116_at		0/5	0/8	10/10
CD20	619_at		1/5	0/8	3/10
CD22	38521_at		0/5	2/8	1/10
*CD10 (CALLA)	1389_at		5/5	8/8	10/10
Common acute	· .		·		
lymphoblastic					
leukemia antigen.		,			·
*Transcription	1373_at		5/5	8/8	9/10
factor 3 (E2A)			-		
Immunoglobulin					
enhancer binding					
factors E12/E47					
*CD79A (IGBP1)	34391_at		5/5	8/8	9/10
Immunoglobulin					
binding protein 1, a					
marker for early B-					
cells				· .	
*HLA class II,	37039_at	<u> </u>	5/5	8/8	9/10 .
Dr alpha					

*HLA class II,	33261_at	 5/5	8/8	10/10
Dr beta 1				
*B2M	34644_at	5/5	8/8	10/10
Beta-2				
microglobulin				
CD2	40738_at	1/5	2/8	2/10
CD5	32953_at	0/5	0/8	0/10
CD7	771_s_at	0/5	0/8	0/10
CD13	39385_at	5/5	8/8	0/10
CD33	36802_at	2/5	4/8	0/10
CD14	36661_at	3/5	8/8	0/10

Footnote to Table 17

Genes marked with asterisk (*) have met the criteria for inclusion in stromal cell gene list.

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CLAIMS

What is claimed is:

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1. Isolated mesenchymal progenitor cells that are pluri-differentiated.

- 2. A therapeutic composition comprising an isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective for treating a disease state in a mammal in need thereof.
- 3. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance hematopoietic progenitor cell engraftment in a mammal in need thereof.
- 4. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said pluri-differentiated mesenchymal progenitor cells are present in an amount effective to treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.
- 5. A method for purifying pluri-differentiated mesenchymal progenitor cells comprising the steps of:
 - a) providing a cell culture preparation by the Dexter method;
 - b) treating the cells to obtain a cell suspension;
 - c) removing macrophages;
 - d) fractionating the cells; and
 - e) collecting the fraction of pluri-differentiated mesenchymal progenitor cells.
- 6. A method for enhancing bone marrow engraftment in a mammal in need thereof which comprises administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

7. The method according to claim 6, wherein said administrating step includes intravenously injecting or directly injecting the isolated pluri-differentiated mesenchymal progenitor cells to the site of intended activity.

- 8. A gene in an MPC for detecting the presence of cancer or pre-cancer in a cell population.
 - 9. A pharmaceutical for modulating the gene of claim 10.

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- 10. A method for enhancing engraftment of cells in a mammal in need thereof which comprises administering to the mammal isolated pluri-differentiated mesenchymal progenitor cells wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the cells in the mammal.
- 11. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered by intravenous injection or by injecting directly to the site of intended activity.
- 12. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered prior to administration of the hematopoietic progenitor cells.
- 13. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are introduced in a cell suspension also containing hematopoietic progenitor cells.
 - 14. A SCID mouse model for investigating MPC function.
- 15. Phenotypic cultured bone marrow stromal cells capable of being analyzed at single cell level.
- 16. A diagnostic test for screening for abnormalities of bone marrow stromal cells.
 - 17. The diagnostic test according to claim 16, wherein said test can be used for screening for various hematologic diseases and other diseases effecting stromal cells
- 18. The diagnostic test according to claim 16, wherein said abnormalities are phenotypic abnormalities that can be discerned at a single cell level.
 - 19. Stromal cells for use in combination with engraftment or other similar procedures for enhancing the effectiveness of the treatment.

20. A method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

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- 21. A method for diagnosing a disease state comprising the steps of:
 - a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
 - b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
 - c) identifying gene sets that are unique to a given state; and
 - d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to said gene sets.
- 22. A method for identifying therapeutic targets for treatment of hematopoietic function comprising the steps of:
 - a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest;
 - b) identifying gene groups that are up-regulated, down regulated, and common to each disease state; and
 - c) identifying gene sets that are unique to a given state.

Figure - 1

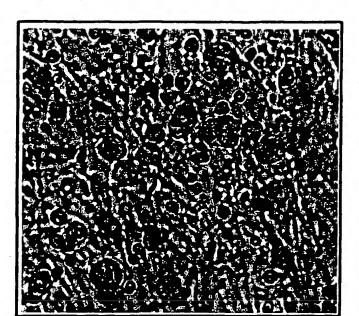
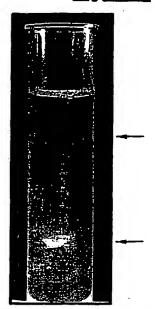


Figure - 2



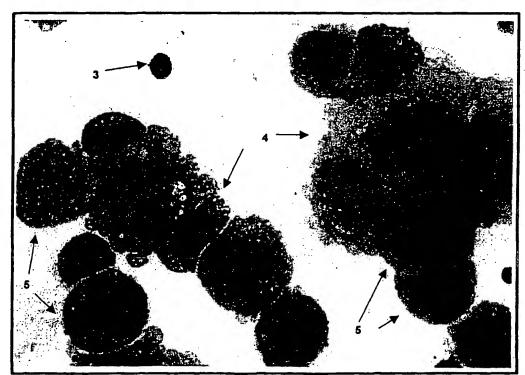
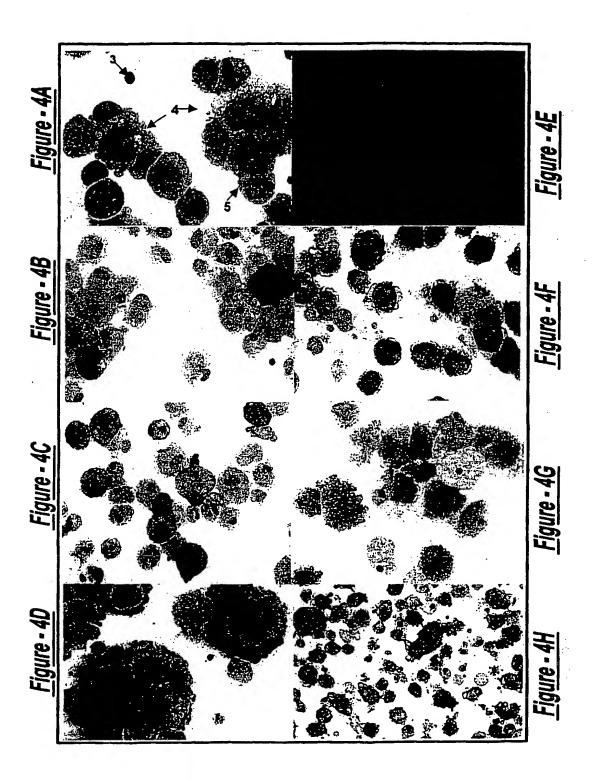


Figure - 3



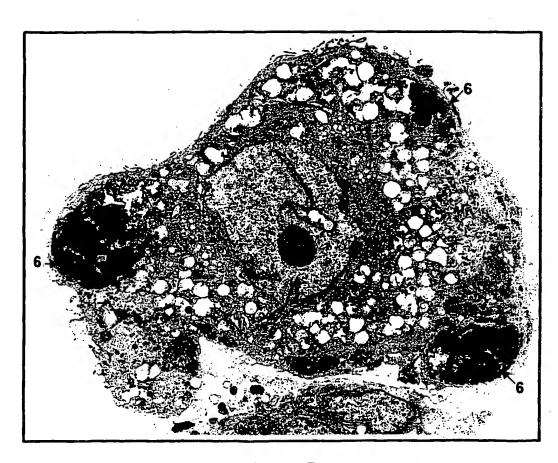
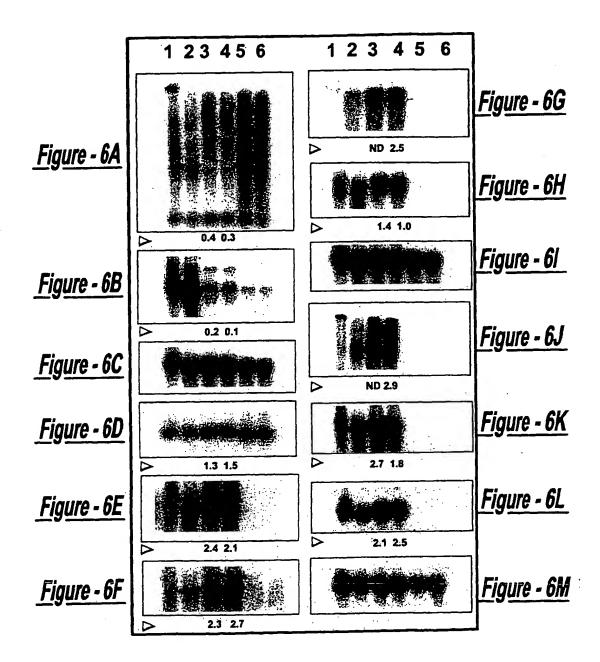


Figure - 5



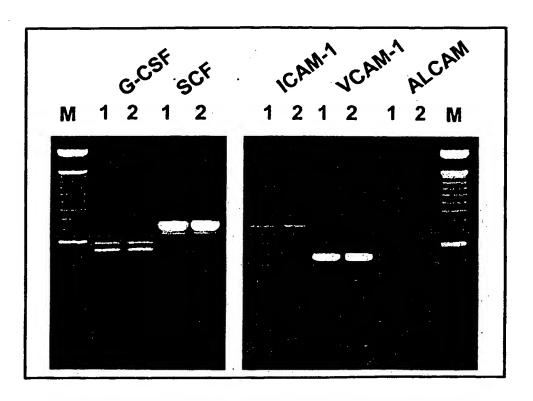


Figure - 7

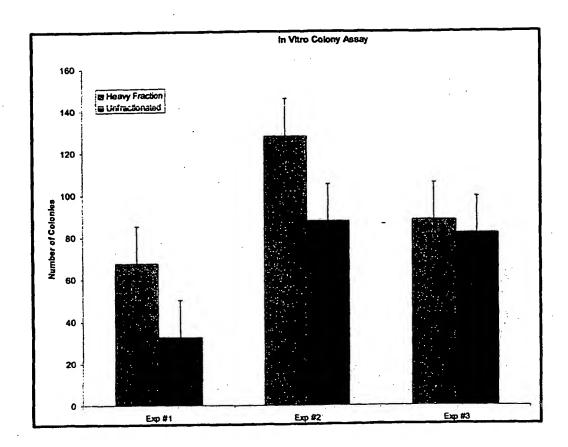


Figure - 8

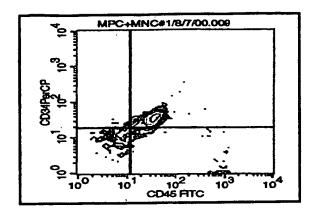


Figure - 9A

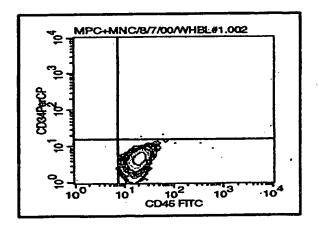


Figure - 9B

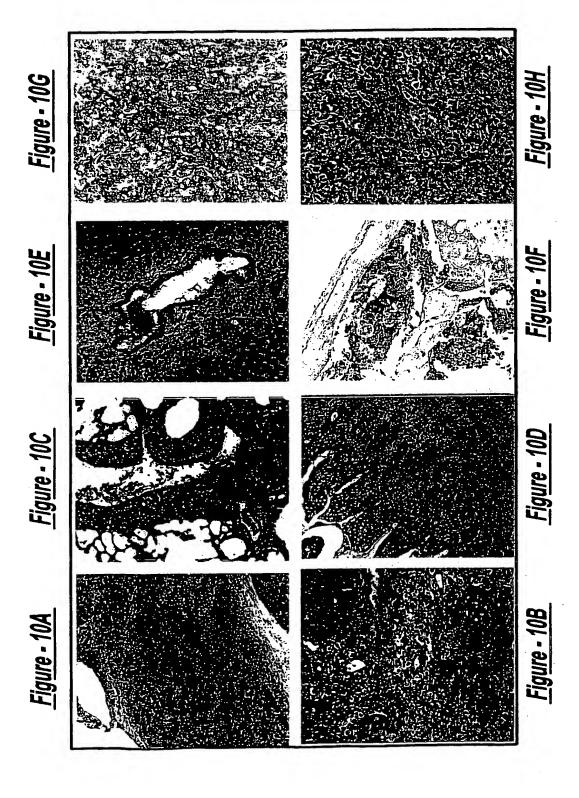


Figure - 11A

Figure - 11B

Figure - 11C

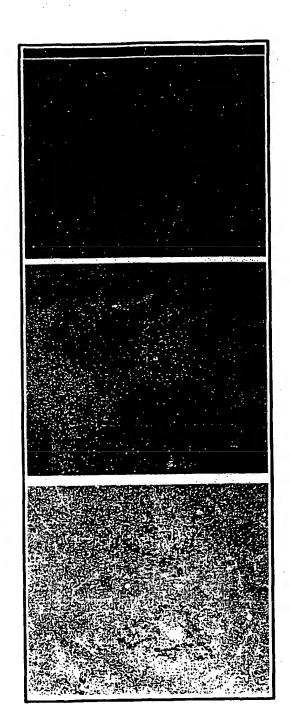


Figure - 12A

Figure - 12B

Figure - 12C

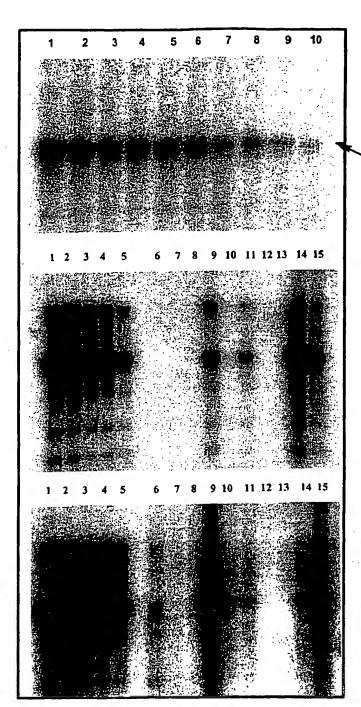


Figure - 13A

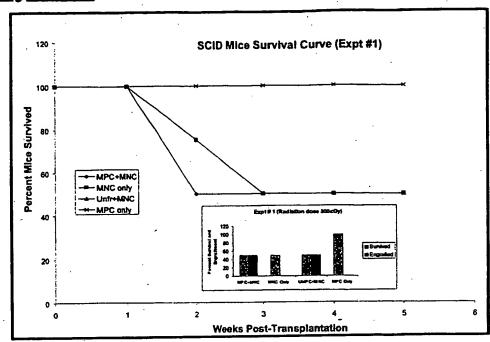
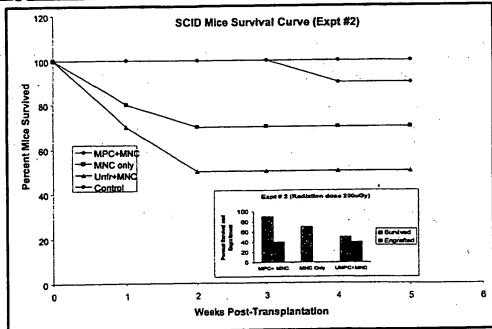
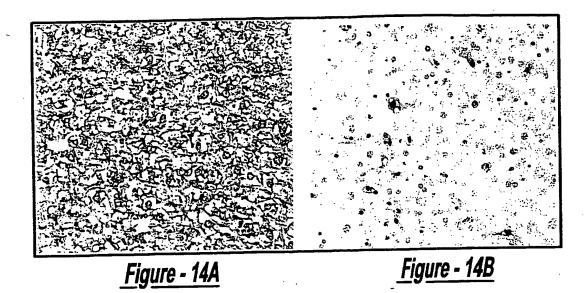


Figure - 13B





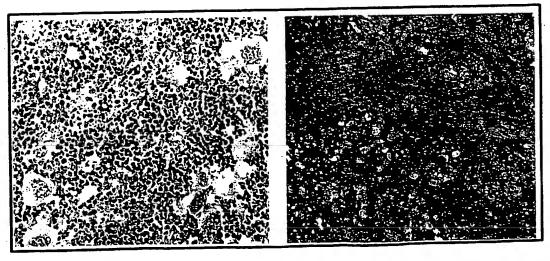
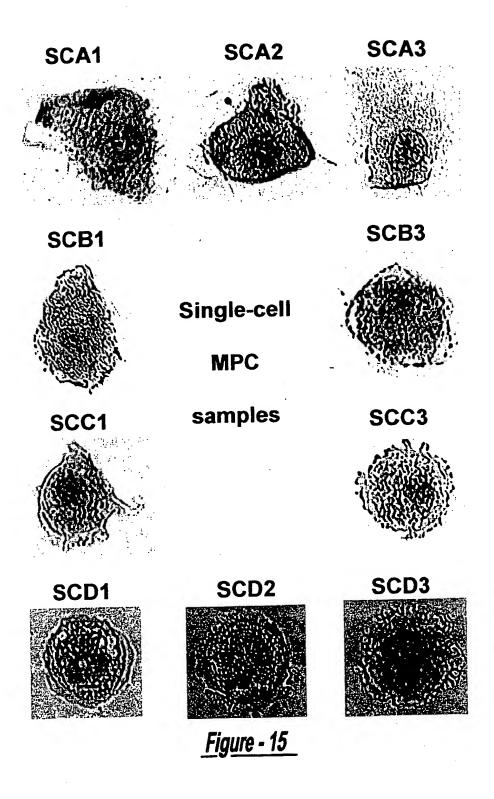


Figure - 14C

Figure - 14D



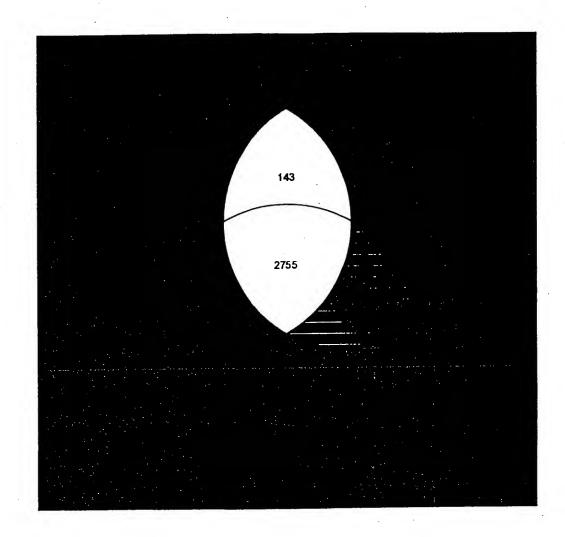


Figure - 16

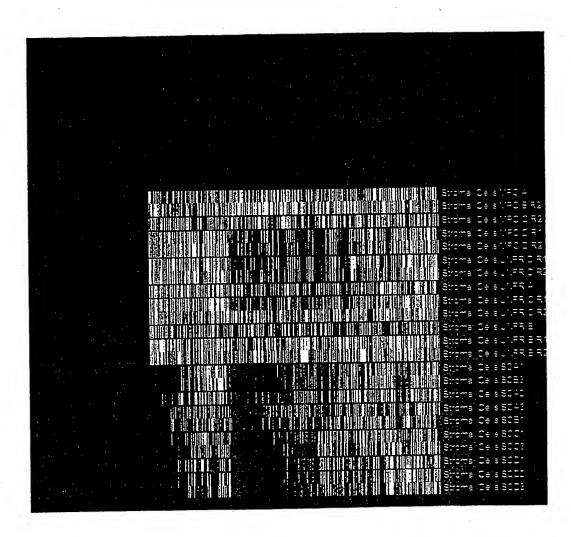


Figure - 17

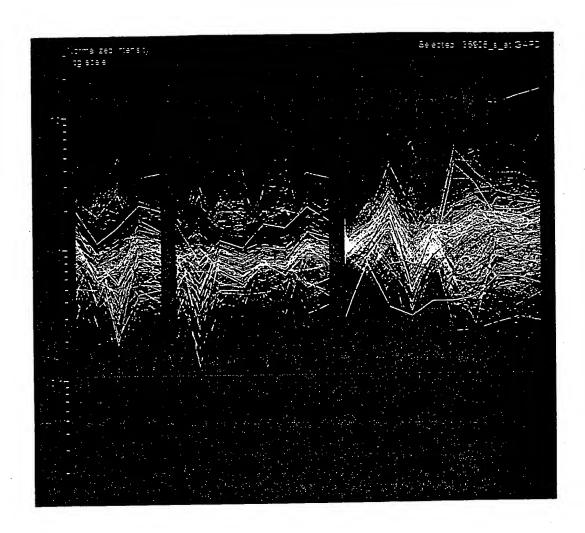
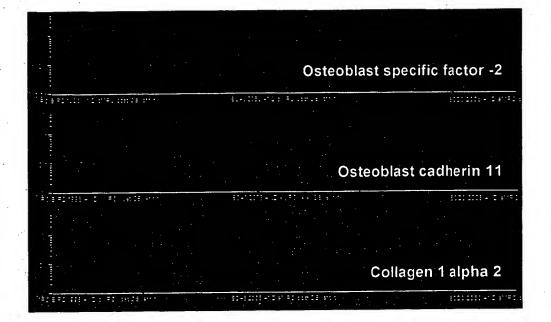


Figure - 18

Collective MPCs (Samples 1-5)

Single cell MPCs (Samples 6-15)



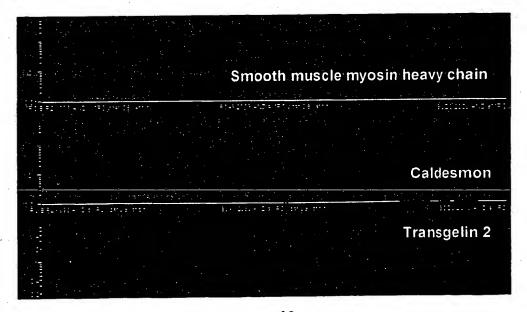


Figure - 19

C llective MPCs (Samples 1-5)

Single c II MPCs (Samples 6-15)

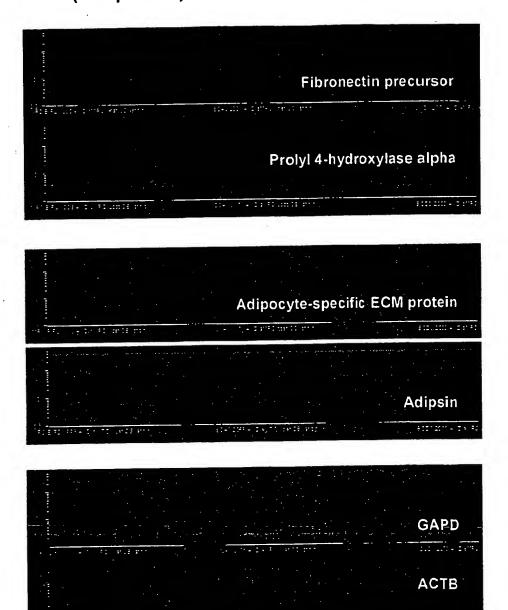


Figure - 20

Collective MPCs (Samples 1-5)

Single cell MPC (Samples 6-15)

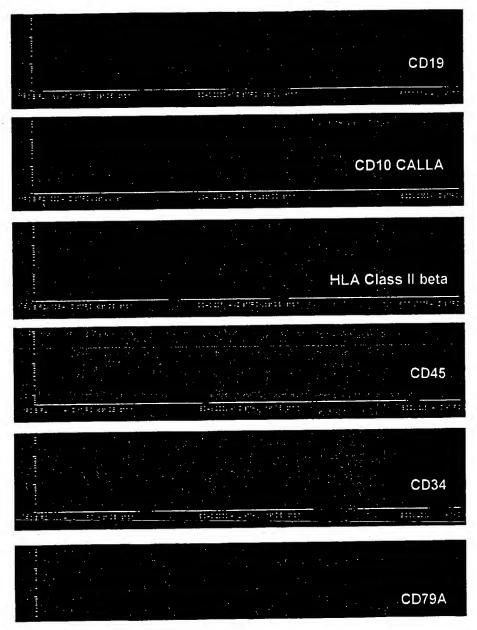


Figure - 21

	A	8	ပ	Q	ш
-	Systematic	Common	Genbank	Description	Product
				***ALU WARNING: Human Alu-Sq	
7	AFFX-hum_alu_at		U14573	subfamily consensus sequence.	
3	38820_at	15-Sep	Sep AF051894	15 kDa selenoprotein	15 kDa selenoprotein
				26S proteasome-associated pad1	
4	33247_at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
		-		factor, arginine/serine-rich 7 (SFRS7)	
2	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein; Human N33 protein form	,
9	36851_g_at	N33	U42360	2 (N33) gene, exon 11 and complete cds.	N33 protein form 2
				3-hydroxy-3-methylglutaryl-Coenzyme A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328_at	HMGCR	M11058	reductase	reductase
					succinyl CoA:3-oxoacid CoA transferase
8	41142_at	охст	U62961	3-oxoacid CoA transferase	precursor
				3'-phosphoadenosine 5'-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
9	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
Ξ	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formyttransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811_at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
				5-methyltetrahydrofolate-homocysteine	
13		MTR	U73338	methyltransferase	methionine synthase
14	39025_at	LOC54543	AI557912	6.2 kd protein	

									7
ш	divalent cation tolerant protein CUTA	delta7-sterol reductase	ADAM10		metalloprotease/disintegrin/cysteine-rich protein precursor	gravin		KIAA0629 protein	KIAA0920 protein
0	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04342 P18077 P05744 P41056 CE04352 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA52649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05704 P3465 145758	7-dehydrocholesterol reductase	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein 10	A kinase (PRKA) anchor protein 11	A kinase (PRKA) anchor protein 2
0	0.001366	AF034544	AF009615	AA142964	U41766	U81607	AA114830	AB014529	AB023137
8	10K07971	DHCR7	ADAM10	ADAM17	ADAM9	AKAP12	AKAP10	AKAP11	AKAP2
V	9,000	39059 at	40797_at	41601_at		_		34657_at	35985_at
	r.	9	7	\$	19	8		22	23

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				_						\neg	\neg	-
E	proto-oncogene tyrosine-protein kinase	accessory proteins BAP31/BAP29	mitochondrial 3-oxoacyl-CoA thiolase	acetyl-coenzyme A transporter		acidic nuclear phosphoprotein pp32	APRIL	okadaic acid-inducible phosphoprotein	KIAA0785 protein	iron regulatory factor	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
Q	ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; atternative splicing using alternative first exon 1b; ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto- oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.	accessory proteins BAP31/BAP29	acetyl-Coenzyme A acyttransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	acetyl-Coenzyme A transporter	acetylserotonin O-methyttransferase-like	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	acid-inducible phosphoprotein	Ac-like transposable element	aconitase 1, soluble	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
O		X81817	D16294	D88152	AA669799	U73477	Y07969	AF069250	AB018328	Z11559	D25248	U50523
В	ABL	DXS1357E	ACAA2	ACATN	ASMTL	ANP32A	ANP32B	OA48-18	ALTE	ACO1	AFAP	ARPC2
V	1636 g at	41724 at	41530 at	34668 at		_	_		39168_at		37578_at	
	24	25	26	27	28	29	8	3	32	အ	发	35

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	٨	20	٥		
90	34602 7 24	7000	A EOOGOB7	actin related protein 2/3 complex, subunit	p20-Arc
7	04036_1_ai	5	10000	and protein 2/3 complex subunit	
75	38392 at	ABPCS	AFOOGORR		p16-Arc
_		ACTA2	X13839	ha 2, smooth muscle, aorta	alpha 2 actin
Т	AFFX-HSAC07/MACTB		X00351		beta actin
T	AFFX-HSAC07/XACTB		X00351		beta actin
т	32318 s at	ACTB	X63432	actin, beta	mutant beta-actin (beta'-actin)
Г	34160 at	ACTG1	X04098	actin, gamma 1	gamma-actin
£		ACTN1	X15804		actinin, alpha 1
44		ACTN4	U48734	actinin, alpha 4	alpha actinin
45	38642 at	AI CAM	Y10183	activated leucocyte cell adhesion molecule MEMD protein	MEMD protein
	31			activated RNA polymerase II transcription	
46	36171_at	PC4	AI521453	cofactor 4	
47	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162_s_at	ACVR2	D31770	activin A receptor, type II	activin typell A receptor precursor
49	34394_at	ADNP	AB018327		KIAA0784 protein
				ıydrogənase,	
ည	40673_at	ACADSB	U12778		acyl-CoA dehydrogenase
21	40459_at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
				adaptor-related protein complex 1, beta 1	
52	40745_at	AP1B1	L13939	subunit	beta-prime-adaptin
L				adaptor-related protein complex 1,	
23	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
				-related protein complex 2, mu 1	adaptor-related protein complex 2, mu 1
24	39795_at	AP2M1	D63475	Π	Subunit
				adaptor-related protein complex 2, sigma	
22	39347_at	AP2S1	X97074	1 subunit	clathrin-associated protein
L				adaptor-related protein complex 3, beta 1	
56	32039_at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
				adaptor-related protein complex 3, delta 1	,
24	36172_s_at	AP3D1	AF002163	subunit	delta-adaptin
L				adaptor-related protein complex 3, sigma	
28		AP3S1	U91932	1 subunit	AP-3 complex sigma3A subunit
23	33102_at	ADD3	D67031	adducin 3 (gamma)	adducin-like protein

	V	6	,	T		u
1		۵		Ī		
						adenosine deaminase, RNA-specific,
						isoform ADAR-a; adenosine deaminase,
						RNA-specific, isoform ADAR-b; adenosine
8	38014_at	ADAR	X79448	aden		deaminase, RNA-specific, isoform ADAR-c
				aden	adenosine deaminase, RNA-specific, B1	
61	38748_at	ADARB1	U76421	(REO	(RED1 homolog rat)	dsRNA adenosine deaminase DRADA2b
23	168_at	ADK	U50196	aden	adenosine kinase	adenosine kinase
အ	33865_at	BS69	AA127624	aden	adenovirus 5 E1A binding protein	
	33134 at	ADCY3	AB011083	aden	adentylate cyclase 3	KIAA0511 protein
4	40585_at	ADCY7	D25538	aden	adentylate cyclase 7	adenylate cyclase 7
	33800_at	ADCY9	AF036927	aden	aderlylate cyclase 9	adenylyl cyclase type IX
	40788_at	AK2	U84371	aden	adenylate kinase 2	adenylate kinase 2A
88	36639_at	ADSL	AF067853	aden	adenylosuccinate lyase	adenylosuccinate lyase
	935_at	CAP	L12168	ader	aderlylyl cyclase-associated protein	adenylyl cyclase-associated protein
20	33405_at	CAP2	N90755	ader	aderlylyl cyclase-associated protein 2	
	34378_at	ADFP	X97324	adipa	adipese differentiation-related protein	adipophilin
	36861_at	DKFZp56411922	AL049946	adlican	ue	hypothetical protein
73	33987_at	ARF1	M36340	ADP	ADP-ribosylation factor 1	ADP-ribosylation factor 1
14	39336_at	ARF3	M74491	ADP	ADP ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP	ADP-ribosylation factor 4	ADP-ribosylation factor 4
				ADP	ADP-ribosylation factor domain protein 1,	
9/	37537_at	ARFD1	L04510	<u>8</u>		nucleotide binding protein
				ADP	ADP-ribosylation factor GTPase activating	
11	39905_i_at	ARFGAP1	AA402332	protein 1	in 1	
78	37296_at	ARL1	L28997	ADP	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
				ADP	ADP-ribosylation factor-fike 6 interacting	
73	36572_r_at	ARLGIP	D31885	protein	in	
				ADP	ADF-ribosyltransferase (NAD+; poly (ADP	
8	41146_at	ADPRT	J03473	ribos	ribose) polymerase)	poly(ADP-ribosyl)transferase
				ADP	ADP-ribosyttransferase (NAD+; poly (ADP-	$\overline{}$
8	1287_at	ADPRT	J03473	ribo	ribose) polymerase)	poly(ADP-ribosyl)transferase
82	34777_at	ADM	D14874	adre	adrenomedullin	adrenomedullin precursor
				AFO	AF084176 Human mRNA (Tripodis and	
				Rag	Ragoussis) Homo sapiens cDNA clone	
83	83 32218_at		AF034176	ntco	ntcoh5 contig.	

AFG312 Y18314 AFG3 ATPase famil AGRN AF016903 agrin AHNAK M80899 AHNAK nucleoprofe AARS D32050 alanyl-tRNA synthet AALDH3 U07919 member A3 ald bhyde dehydrog member A3 ald bhyde dehydrog member A1 at ALDH3A2 U46689 member A1 at ALDH3A1 U24266 member A1 at ALDH3A1 U34252 aldehyde dehydrog t AKR1A1 U34252 aldehyde dehydrog t AKR1B1 X15414 (aldehyde reductase t AKR1B1 X15414 (aldehyde reductase t AKR1B1 X15414 (aldehyde reductase) t AKR1C3 D17793 the t AKR1C3 AF10		A	8	O	Q	T)
AFG312 AFG312 AFG313 AFG313 AFG314 AFG312 AFG313 AFG312 A	1-					وأوفوه وكأنا وأوادا
33454_at AGRN AF016903 agrin AGRN AHNAK M80899 AHNAK nucleoprotein (desmoyokin) E		34315_at	AFG3L2	Y18314	AFG3 A I Pase family gene 3-like 2 (yeast)	parapiegii i-iike proteii i
37027_at AHNAK M80899 AHNAK nucleoprotein (desmoyckin) is 37027_at ALDH1A3 U07919 alianyl-tRNA synthetase is aldehyde dehydrogenase 1 family. is aldehyde dehydrogenase 2 family. is aldehyde dehydrogenase 3 family. is aldehyde dehydrogenase 3 family. is aldehyde dehydrogenase 4 family. is aldehyde dehydrogenase 4 family. is aldehyde dehydrogenase 7 fami		33454_at	AGRN	AF016903		agrin precursor
36185_at		37027_at	AHNAK	M80899	AK nucleoprotein (desmoyokin)	
ALDH1A3 U07919 member A3 ALDH2 X05409 (mitochondrial) aldehyde dehydrogenase 2 family (aldehyde dehydrogenase 2 family (aldehyde dehydrogenase 3 family (aldehyde dehydrogenase 4 family (aldehyde dehydrogenase 4 family (aldehyde dehydrogenase 4 family (aldehyde dehydrogenase 7 family (aldehyde dehydrogenase 7 family (aldehyde dehydrogenase 7 family (aldehyde dehydrogenase 9 family <td< td=""><td>1</td><td>36185_at</td><td>AARS</td><td>D32050</td><td></td><td>alanyi-tRNA synthetase</td></td<>	1	36185_at	AARS	D32050		alanyi-tRNA synthetase
ALDH1A3 U07919 member A3 ALDH2 X05409 (mitochondrial) ALDH2 X05409 (mitochondrial) ALDH3A2 U46689 aldehyde dehydrogenase 3 family. ALDH3A1 U24266 member A1 ALDH3A1 S74728 member A1 ALDH3A1 S74728 member A1 AKR1B1 S74728 member A1 AKR1B1 J04794 aldehyde dehydrogenase 7 family. AKR1B1 J04794 aldehyde dehydrogenase 9 family. AKR1B1 X15414 aldo-keto reductase family 1, member R1 AKR1B1 X15414 (aldehyde dehydrogenase 9 family. AKR1B1 X15414 (alde-keto reductase family 1, member R1 AKR1B1 X15414 (alde-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase) AKR1C3 AKR1C3 D17793 hype II) AGPS Y09443 alkydycserone phosphate synthase AFIQ U16954 ALL1-fused gene from chromosome 1q G2AN D42041 AB023234 alpha thala					se 1 family,	
ALDH2 X05409 (mitochondrial) (mitochondrial) ALDH3A2 U46689 member A2 (mitochondrial) (mitochondrial) ALDH3A2 U46689 member A2 (mitochondrial) (mitochondrial) ALDH3A1 U24266 member A1 (mitochondrial) (mitochondrial) ALDH3A1 U24266 member A1 (mitochondrial) (mitochondrial) ALDH9A1 U24266 member A1 (mitochondrial) (mitochondrial) ALDH9A1 U34252 aldehyde dehydrogenase 7 family. (mitochondrial) AKR1A1 J04794 (aldehyde dehydrogenase 9 family. (mitochondrial) AKR1B1 X15414 (aldehyde reductase family 1, member A1 (alde-keto reductase) AKR1B1 X15414 (aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, A1 AKR1C3 D17793 type II) aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, A1 (aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, A1 (aldo-keto reductase family 1, member C3 (3-alpha hydrox	_	36686_at	ALDH1A3	U07919		aldehyde dehydrogenase 6
ALDH2 X05409 (mitochondrial) ALDH3A2 U46689 member A2 ALDH3A2 U46689 member A2 aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, member A1 member A1 ALDH3A1 U34256 member A1 ALDH9A1 U34252 aldehyde dehydrogenase 9 family, aldehyde reductase family 1, member A1 AKR1A1 J04794 (aldehyde reductase family 1, member R1 AKR1B1 X15414 (aldo-keto reductase family 1, member R1 AKR1B1 X15414 (aldo-keto reductase family 1, member R1 AKR1C3 D17793 hype II) AKR1C3 D17793 hype II) AKR7A2 AF026947 (alfatoxin aldehyde reductase) AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN AF1Q ALL1-fused gene from chromosome 1q G2AN AB023234 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integin binding protein 63 ATRX U72936 cerevisiae)	Γ					aldehyde dehydrogenase 2 family
ALDH3A2 U46689 aldehyde dehydrogenase 3 family, member A2 aldehyde dehydrogenase 4 family, member A1 ALDH4A1 U24266 member A1 ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 aldehyde dehydrogenase 9 family, member A1 aldehyde dehydrogenase 9 family, member A1 AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldehyde reductase) AKR1B1 X15414 (aldeoketo reductase) AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-tused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)	_	32747_at	ALDH2	X05409	(mitochondrial)	(mitochondrial)
ALDH3A2 U46689 member A2 i ALDH4A1 U24266 member A1 indehyde dehydrogenase 7 family, indehyde dehydrogenase 7 family, indehyde dehydrogenase 9 family, indehyde deforming 1, member A1 AKR1A1 J04794 (aldehyde reductase family 1, member B1 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member A2 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member A2 aldo-keto reductase family 1, member B1 aldo-keto reductase family 1, member B2 aldo-keto reductase family					aldehyde dehydrogenase 3 family,	
ALDH4A1 U24266 member A1 ALDH7A1 S74728 aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, member A1 ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 aldehyde dehydrogenase 9 family, member A1 AKR1B1 X15414 aldo-keto reductase family 1, member B1 AKR1B1 X15414 (aldehyde reductase family 1, member B1 AKR1B1 X15414 (aldo-keto reductase family 1, member C3 AKR1B1 X15414 (aldo-keto reductase family 1, member C3 AKR1C3 D17793 aldo-keto reductase family 7, member A2 AKR7A2 AF026947 (affatoxin aldehyde reductase) AF1Q V09443 aldo-keto reductase family 7, member A2 AF1Q AF026947 (affatoxin aldehyde reductase) AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)		40409_at	ALDH3A2	U46689	member A2	aldehyde dehydrogenase
ALDH4A1 U24266 member A1 ALDH7A1 S74728 aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde reductase 6 family, aldehyde reductase 6 family 1, member A1 ALDH9A1 U34252 aldehyde reductase family 1, member A1 AKR1A1 J04794 (aldehyde reductase family 1, member B1 AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AF1Q AF026947 (aflatoxin aldehyde reductase) AF1Q D42041 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)					aldehyde dehydrogenase 4 family,	
ALDH7A1 S74728 aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldo-keto reductase family 1, member A1 aldo-keto reductase family 1, member B1 aldo-keto reductase family 1, member C3 (aldose reductase family 7, member A2 (aldose family 7, member A2 (aldose reductase family 7, member A2 (aldose family 7,		37331_g_at	ALDH4A1	U24266	member A1	pyrroline-5-carboxylate dehydrogenase
ALDH7A1 S74728 member A1 aldehyde dehydrogenase 9 family. ALDH9A1 U34252 member A1 aldo-keto reductase family 1, member A1 AKR1A1 J04794 (aldehyde reductase) aldo-keto reductase family 1, member B1 AKR1B1 X15414 (aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, pype II) AKR1C3 D17793 type II) aldo-keto reductase family 7, member C3 AKR7A2 AF026947 (aflatoxin aldehyde reductase) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha inlegrin binding protein 63 ATRX U72936 cerevisiae)					aldehyde dehydrogenase 7 family,	
ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde reductase family 1, member A1 aldo-keto reductase) AKR1B1 X15414 (aldehyde reductase) AKR1B1 X15414 (aldose reductase family 1, member B1 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, ppe II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha inlegrin binding protein 63 ATRX U72936 cerevisiae)	92	36132_at	ALDH7A1	S74728	member A1	antiquitin
ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 lddo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, (alado-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, (alado-keto reductase family 7, member R2 AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)					aldehyde dehydrogenase 9 family,	
AKR1A1 J04794 aldo-keto reductase family 1, member A1 AKR1B1 X15414 (aldehyde reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 lddo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) aldo-keto reductase family 7, member A2 AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)	93	33899_at	ALDH9A1	U34252	member A1	gamma-aminobutyraldehyde dehydrogenase
AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 ldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, lg-alpha ll) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX U72936 cerevisiae)					aldo-keto reductase family 1, member A1	aldo-keto reductase family 1; member A1
AKR1B1 X15414 aldo-keto reductase family 1, member B1 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 (3-alpha hydroxysteroid dehydrogenase, type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	94	38780_at	AKR1A1	J04794	(aldehyde reductase)	(aldehyde reductase)
AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkydglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN ALL1-fused gene from chromosome 1q G2AN ALL1-fused gene from chromosome 1q G2AN alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)					aldo-keto reductase family 1, member B1	aldo-keto reductase family 1, member B1
AKR1C3 D17793 Salpha hydroxysteroid dehydrogenase, (3-alpha hydroxysteroid dehydrogenase, type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	95	36589_at	AKR1B1	X15414	(aldose reductase)	(aldose reductase)
(3-alpha hydroxysteroid dehydrogenase, type II) aldo-keto reductase family 7, member A2 AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)					aldo-keto reductase family 1, member C3	
AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. syndrome X-linked (RAD54 homolog, S.					(3-alpha hydroxysteroid dehydrogenase,	aldo-keto reductase family 1, member C3 (3-
AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit AIA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	96	37399_at	AKR1C3	D17793	type II)	alpha hydroxysteroid dehydrogenase, type II)
AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)					aldo-keto reductase family 7, member A2	
AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	6	32510_at	AKR7A2	AF026947	(aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)						alkyl-dihydroxyacetonephosphate synthase
AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	86	39225 at	AGPS	Y09443	alkylglycerone phosphate synthase	precursor
G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	66	36941_at	AF10	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX Cerevisiae)	8	37040 at	GZAN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	101	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
Syndrome X-linked (RAD54 homolog, S. U72936 cerevisiae)					alpha thalassemia/mental retardation	
ATRX U72936 cerevisiae)					syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
	102	39147_g_at	ATRX	U72936	cerevisiae)	helicase

	A	В	၁	O	W
Ş	818 6 04	YOTA	172036	syndrome X-linked (RAD54 homolog, S.	putative DNA dependent A I Pase and
	010-9-BI	4117	015300	celevisiae)	
				afternative translation inflation; H.sapiens HI TF gene for helicase-like transcription	
104	34327_at	HLTF	246606	factor.	helicase-like transcription factor
L				aminoadipate-semialdehyde	
				dehydrogenase-phosphopantetheinyl	
105	35761_at	AASDHPPT	AL050073	transferase	hypothetical protein
9	106 39431_at	NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	107 41338_at	AES	Al951946	amino-terminal enhancer of split	
108	108 36996_at	6-80	U41635	amplified in osteosarcoma	OS-9 precurosor
				amylo-1, 6-glucosidase, 4-alpha-	
				glucanotransferase (glycogen	
				debranching enzyme, glycogen storage	
109	38253_at	AGL	U84011	disease type III)	głycogen debranching enzyme isoform 6
				amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
110	41136_s_at	APP	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
				amyloid beta (A4) precursor protein-	
111	40148_at	APBB2	U62325	binding, family B, member 2 (Fe65-like)	FE65-like protein
				amyloid beta precursor protein	
112	38471_r_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein	
113	38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein binding	
114	35364_at	APPBP1	U50939	protein 1, 59kD	amyloid precursor protein-binding protein 1
	1 0001	000	70777004	amyotrophiic tateral scienosis z (juveriile)	
115	40064_at	ALS2CH3	AB011121	chromosome region, candidate 3	KIAAU549 protein
_				androgen receptor (dihydrotestosterone	
			•	receptor; testicular feminization; spinal	
				and bulbar muscular atrophy; Kennedy	
116	3 1577_at	AR	M23263	disease)	androgen receptor
117	7 38842_at	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
118	39315_at	ANGPT1	D13628	angiopoietin 1	angiopoietin 1
119	1929_at	ANGPT1	U83508	angiopoietin 1	angiopoietin-1

att ANK3 U13616 ankyrin 3, node of Ranvier (ankyrin G) att ANXA1 X05908 annexin A1 att ANXA21 L19605 annexin A1 att ANXA2P1 M62896 annexin A2 att ANXA2P1 M62895 annexin A2 att ANXA2 J04543 annexin A2 att ARCN1		A	8		Q	ш
ANNXA1	120	36965	1	U13616		ankyrin G
36637_at ANXA21 L19605 annexin A11 36837_at ANXA22 D00017 annexin A2 31684_at ANXA2P3 M62896 annexin A2 pseudogene 1 31644_s_at ANXA2P3 M62895 annexin A2 pseudogene 3 31374_at ANXA2P3 M62895 annexin A2 pseudogene 3 41138_at ANXA2P3 M62895 annexin A2 41138_at ANXA2P3 M62895 annexin A2 41138_at ANXA7 J04543 annexin A2 41138_at MIC2 M16279 antigen identified by monoclonal antigen identified ident	121		ANXA1	X05908		annexin I
769_s_at ANXA2 D00017 annexin A2 31684_at ANXA2P1 M62896 annexin A2 pseudogene 1 31444_s_at ANXA2P3 M62895 annexin A2 pseudogene 3 31744_s_at ANXA2 M82809 annexin A4 41138_at MIC2 M16279 antigen identified by monoclonal antibodies 12E7, E21 and O13 40506_s_at ANXA7 J04543 antigen identified by monoclonal antibodies 12E7, E21 and O13 40506_s_at ANBPC4; APP1; AU75686 binding protein mRNA, complete cds. 34370_at ARCN1 X81198 arginine-glutamic acid dipeptide (HE) arginine-glutamic acid dipeptide (HE) 32253_at ARCN1 X81198 ariadne homolog 2 (Drosophila) 39164_at ARIH2 ARO99149 ariadne homolog 2 (Drosophila) 3657_at ACTR1 ARO99149 ariadne homolog ubiquitin-conjugating <tr< td=""><td>122</td><td>36637_at</td><td>ANXA11</td><td>L19605</td><td></td><td>56K autoantigen</td></tr<>	122	36637_at	ANXA11	L19605		56K autoantigen
at ANXA2P1 M62896 annexin A2 pseudogene 1 at ANXA2P3 M62895 annexin A2 pseudogene 3 ANXA4 M82809 annexin A4 annexin A7 J04543 annexin A7 antigen identified by monoclonal antigen identified ide	123	769_s_at	ANXA2	D00017		lipocortin II
ANXA2P3 M62895 annexin A2 pseudogene 3 ANXA4 M82809 annexin A4 ANXA7 J04543 antigen identified by monoclonal antigen identified by monoclonal antigen identified by monoclonal antigen identified by monoclonal APP-1; Homo sapiens polyadenylate APP-1; Homo sapiens polyadenylate archain 1 ARCN1 X8119B anchain J Form Sapiens polyadenylate archain ARCN1 ARCN1 X8119B archain J Form Sapiens polyadenylate archain ARCN1 ARCN1 X8119B archain J Form Sapiens polyadenylate archain ARCN1 ARCN1 X8119B archain J Form Sapiens polyadenylate archain ARCN1 ARIH2 ARD007927 repeats archain alpha yordinal ARCN1 ARIH2 AF099149 ariadne homolog ubiquitin-conjugating ariadne homolog 2 (Drosophila) ALEX2 ARB011084 arradillo repeat protein ALEX2 ACTR1 ARB011084 arradillo repeat protein 1 homolog (yeast) ACTR2 AF006082 (yeast) ACTR2 AF006082 (yeast) ACTR3 AF006082 (yeast) ACTR3 AF006083 (yeast) ACTR3 AF006083 (yeast) ACT	124	31684_at	ANXA2P1	M62896	annexin A2 pseudogene 1	
ANXA4 M82809 annexin A7 ANXA7 J04543 antibodies 12E7. E21 and O13 MIC2 M16279 antibodies 12E7. F21 and O13 APP-1; Homo sapiens polyadenylate APP-1; Homo sapiens polyadenylate PABPC4; APP1; AU75686 binding protein mRNA, complete cds. ARCN1 X81198 archain 1 ARRS S80343 arrighin-glutamic acid dipeptide (RE) ARHS S80343 ariadne homolog 2 (Drosophila) ALEX2 ARO93149 ariadne homolog 2 (Drosophila) ALEX2 ARD1094149 arriadne homolog 2 (Drosophila) ALEX2 ARD109571 enzyme E2 binding protein 1 (Drosophila) ACTR1 X82206 centractin alpha (yeast) ACTR2 AF006082 (yeast) ACTR2 AF006082 (yeast) ACTR2 AF00	125	31444 s at	ANXA2P3	M62895	annexin A2 pseudogene 3	
37374_at ANXA4 M82809 annexin A4 37670_at ANXA7 J04543 annexin A7 41138_at MIC2 M16279 antibodies 12E7, F21 and O13 40506_s_at M1C2 M76279 APP-1; Homo sapiens polyadenylate 40506_s_at ARBPC4; APP1; AU75686 binding protein mRNA, complete cds. 34370_at ARCN1 X81198 archain 1 32263_at ARCN1 X81198 archain 1 32263_at ARCN1 X81198 archain 1 38164_at ARCN1 ARO0327 repeats 39164_at ARIHZ AF099149 ariadne homolog 2 (Drosophila) 39164_at ARIHZ AF099149 ariadne homolog 2 (Drosophila) 36057_at ARIHZ AB011084 arriadne homolog 2 (Drosophila) 36057_at ACTR1 AB011084 arriadne homolog 2 (Drosophila) 36057_at ACTR2 AB011084 arriadne homolog 2 (Drosophila) 35733_at ACTR2 AB011084 arriadne homolog 2 (Drosophila) 35733_at ACTR2<						annexin IV (placental anticoagulant protein
37670_at ANXA7 J04543 annibacies 12E7 F21 and O13 41138_at MIC2 M16279 antibodies 12E7 F21 and O13 40506_s_at PABPC4; APP1; AU75686 binding protein mRNA, complete cds. 34370_at ARCN1 X81198 archain 1 32253_at ARCN1 X81198 arginine-glutamic acid dipeptide (RE) repeats 34370_at ARCN1 X81198 arginine-glutamic acid dipeptide (RE) repeats 34370_at ARCN1 AR007927 repeats 34370_at ARCN1 AR00343 arginine-glutamic acid dipeptide (RE) arginine-glutamic acid dipeptide (RE) 35164_at ARIH2 AF099149 arriadne homolog 2 (Drosophila) 36057_at ARIH2 AF099149 arriadne homolog 2 (Drosophila) 36057_at ALEX2 AB011084 arriadne homolog 2 (Drosophila) 36057_at ACTR1A X82206 centractin-related protein 1 homolog (PAR) 35733_at ACTR2 AF006082 (yeast) 35733_at ACTR2 AF006082 (yeast) 40516_at AHR L19872 <td>126</td> <td>37374_at</td> <td>ANXA4</td> <td>M82809</td> <td>annexin A4</td> <td>(1)</td>	126	37374_at	ANXA4	M82809	annexin A4	(1)
MIC2 MIC2 MIC29 APP-1; F21 and O13	127		ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
40506_s_at PABPC4; APP1; AU75686 binding protein mRNA, complete cds. properties of properties of protein mRNA, complete cds. protein mRNA, complete cds. properties of protein mRNA, complete cds. properties of protein mRNA, complete cds. properties of protein mRNA, complete cds. protein mRNA, complete cds. properties of protein mRNA, complete cds. protein mRNA, complete cds. protein mRNA, complete cds. <t< td=""><td>128</td><td>41138_at</td><td>MIC2</td><td>M16279</td><td>antigen identified by monoclonal antibodies 12E7, F21 and O13</td><td>antigen</td></t<>	128	41138_at	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
34370_at ARCN1 X81198 archain 1 32253_at RERE AB007927 repeats 549_at ARRS S80343 arginine-glutamic acid dipeptide (RE) 1 549_at RARS S80343 arginyl-1RNA synthetase 1 549_at ARIH2 AF099149 arriadne homolog 2 (Drosophila) 1 39164_at ARIH2 AF099771 enzyme E2 binding protein, 1 (Drosophila) 1 36057_at ALEX2 AB011084 armadillo repeat protein ALEX2 ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) ARP2 actin-related protein 2 homolog 36057_at ACTR1 AF006082 (yeast) ARP2 actin-related protein 2 homolog 35734_at ACTR2 AF006082 (yeast) ARP2 actin-related protein 2 homolog 35733_at ACTR2 AF006082 (yeast) ARP2 actin-related protein 2 homolog 3573_at ACTR2 AF006082 (yeast) ARP3 actin-related protein 2 homolog 3657_at ACTR2 AF006082 (yeast) ARP3 actin-related protein 3 homolog 3	129	40506 s. at		1U75686	APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
32253_at RERE AB007927 repeats Image of page of the peats	ا ا	34370_at		X81198	archain 1	archain
249_at RARS S80343 arginyl-IRNA synthetase 549_at RARS S80343 ariadne homolog 2 (Drosophila) 39164_at ARIH2 AF099149 ariadne homolog 2 (Drosophila) 41729_at ARIH1 AJ009771 enzyme E2 binding protein. 1 (Drosophila) 36057_at ALEX2 AB011084 armadillo repeat protein ALEX2 40052_at ACTR1A X82206 centractin alpha (yeast) ACTR2 ARP2 actin-related protein 1 homolog 35733_at ACTR2 ARP2 actin-related protein 2 homolog 35733_at ACTR2 AF006082 (yeast) ARP3 actin-related protein 2 homolog (yeast) ARP3 actin-related protein 3 homolog 35733_at ACTR2 AF006082 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 asparaginyl-tRNA synthetase 38703_at AGA AF005030 asparatylglucosaminidase	÷	22252 24	BEDE	AB007927	arginine-glutamic acid dipeptide (RE)	KIAA0458 protein
at ARIH2 AF099149 ariadne homolog 2 (Drosophila) at ARIH1 AJ009771 enzyme E2 binding protein, 1 (Drosophila) at ALEX2 AB011084 armadillo repeat protein, 1 (Drosophila) at ALEX2 AB011084 armadillo repeat protein, 1 (Drosophila) at ACTR1A X82206 centractin alpha (yeast) at ACTR2 AI935551 (yeast) at ACTR2 AF006082 (yeast) at ACTR2 AF006082 (yeast) at ACTR3 AF006083 (yeast) at ACTR3 AF006083 (yeast) ARP3 actin-related protein 2 homolog (yeast) ARP3 actin-related protein 3 homolog (yeast) ARP3 actin-related protein 2 homolog (yeast) ARP3 actin-related protein 3 homolog (yeast) at ARR3 AF006083 (yeast) at ARR3 AF006083 (yeast) at ARR3 AF006083 (yeast) at ARR3 </td <td>133</td> <td>549 at</td> <td>RARS</td> <td>S80343</td> <td>arginyl-tRNA synthetase</td> <td>arginyl-tRNA synthetase</td>	133	549 at	RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
41729_at ARIH1 AJ009771 ariadne homolog, ubiquitin-conjugating 36057_at ALEX2 AB011084 armadillo repeat protein, 1 (Drosophila) 40052_at ALEX2 AB011084 armadillo repeat protein, 1 (Drosophila) 40052_at ACTR1A X82206 centractin alpha (yeast) 35734_at ACTR2 AI935551 (yeast) 35733_at ACTR2 AF006082 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ARR AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARRS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
36057_at ALEX2 AB011084 armadillo repeat protein ALEX2 40052_at ACTR1A X82206 centractin alpha (yeast) 35734_at ACTR2 AI935551 (yeast) 35733_at ACTR2 AF006082 (yeast) 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ARNS MZ7396 asparagine synthetase 41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	13		ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	putative RING finger protein
40052_at ACTR1A X82206 centractin related protein 1 homolog A, centractin alpha (yeast) 35734_at ACTR2 AI935551 (yeast) 35733_at ACTR2 AF006082 (yeast) 3573_at ACTR2 AF006082 (yeast) 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	135	36057 at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
ARP2 actin-related protein 2 homolog 35734_at ACTR2 AI935551 (yeast) 35733_at ACTR2 AF006082 (yeast) 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ARNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 asparatyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	136	40052 at	ACTR1A	X82206	ARP1 actin-related protein 1 homolog A, centractin alpha (veast)	alpha-centractin
35733_at ACTR2 AF006082 (yeast) 35733_at ACTR2 AF006082 (yeast) 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 asparaginyl-tRNA synthetase 34181_at AGA X55330 aspartyflucosaminidase	5		ACTB2	A 025551	ARP2 actin-related protein 2 homolog	
35733_at ACTR2 AF006082 (yeast) 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-RNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase					ARP2 actin-related protein 2 homolog	
ARP3 actin-related protein 3 homolog 35271_at ACTR3 AF006083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-IRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	13		ACTR2	AF006082	(yeast)	Arp2
352/1_at ACIR3 APO00083 (yeast) 40516_at AHR L19872 aryl hydrocarbon receptor 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase			100	* T000000	ARP3 actin-related protein 3 homolog	A 22.3
40210_at ATIR L15072 at principle synthetase 36671_at ASNS M27396 asparagine synthetase 41241_at NARS D84273 asparaginyl-RNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase		35271_at	ACIRS	AF-005083	(yeast)	AH-receptor
41241_at NARS D84273 asparaginyl-tRNA synthetase 38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	= ;	1 25571 of	ACNO	L13072	asparadio synthetase	asparadine synthetase
38703_at DNPEP AF005050 aspartyl aminopeptidase 34181_at AGA X55330 aspartylglucosaminidase	= =	1 3007 I at	NABS	N673	asparadinyl-tRNA synthetase	Asparaginyl IRNA Synthetase
34181 at AGA X55330 aspart/glucosaminidase	4	3 38703 at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
	<u>-</u>	34181	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

Fig 21

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145	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379_at	APACD	AB006679	differentiation	ATP binding protein
148	40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit b,	
149	149 41228_r_at	ATP5F1	X60221	isoform 1	H+-ATP synthase subunit b
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	150 34811_at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760_at	АТР5Н	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
				ATP synthase, H+ transporting,	
152	152 38751 i_at	ATP51	Ā A426364	mitochondrial F0 complex, subunit e	
				ATP synthase, H+ transporting,	
153	36107_at	ATP5J	AA845575	mitochondrial F0 complex, subunit F6	
				ATP synthase, H+ transporting,	
154	38693_at	ATP5L	AA917672	mitochondrial FO complex, subunit g	
				ATP synthase, H+ transporting,	
				mitochondrial F1 complex, gamma	
155	155 40115_at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791_at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790_at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, type 2C,	
158	38684_at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159	35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
1 8		ATP10D	AI478147	ATPase, Class V, type 10D	
161	36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
				ATPase, Cu++ transporting, alpha	
162	36523_at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
	- 1	4004		ATPase, H+ transporting, lysosomal	
3	163 33854_at	AlP6M	AA8///95	(vacuolar proton pump)	

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				somal	
\$	37395_at	ATP6S14	D49400		vacuolar A i Pase
				somal	
165	36994_at	ATP6L	M62762		vacuolar H+ ATPase proton channel subunit
				somai	
166	36167_at	ATP6F	D89052	(vacuolar proton pump) 21kD	proton-ATPase-like protein
167	37367 at	ATP6E	X76228		vacuolar H+ ATPase E subunit
				ATPase, H+ transporting, lysosomal	
168	37948_at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting A I Pase beta-
175	32563_at	ATP1B3	U51478	polypeptide '	3 subunit
				ATP-binding cassette, sub-family A	
176	35717_at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177		ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
					hypothetical protein DKFZp586F1122 similar
181	35268_at	AXOT	AL050171	axotrophin	to axotrophin

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182	35350_at	GALNAC4S-6ST	AB011170		KIAA0598 protein
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
8	41562_at	BMI1	L13689		homolog
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
\$	1728_at	BMI1	L13689	(mouse)	homolog
1 88	185 36578 at	BIRC2	U37547	baculoviral IAP repeat-containing 2	MIHB
186	186 41278 at	BAF53A	AF041474	BAF53	BAF53a
187	33175 at	BBS4	AA156237	Bardet-Biedl syndrome 4	
				basic helix-loop-helix domain containing,	
188	40790_at	BHLHB2	AB004066	class B, 2	1-Dec
189	40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	190 40202_at	BTEB1	D31716	•	GC box binding protein
191	35055_at	BTF3	X53281	basic transcription factor 3	general transcription factor
192	38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein
				B-cell translocation gene 1, anti-	
194	37294_at	BTG1	X61123	proliferative	B-cell translocation protein 1
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060_at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010_at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
L				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436_at	BNIP3L	AF079221	protein 3-like	protein 3a
				-	glucocortoid receptor-associated protein
198	198 34798_at	BAG1	Z35491	BCL2-associated athanogene	RAP46
199	199 35291_at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
8	200 36463 at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
201	38050 at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101 at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	
				beta subunit; Human pyruvate debydronenase (FC 1.2.4.1) beta subunit	
204	204 39160 at	PDHB	D90086	gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

			\[\frac{\circ}{\circ}\]		
		9	3		
205	34644_at	B2M	AB021288		beta 2-microglobulin
206	40601_at	BBP	AI057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	
207	39340_at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
208	208 38126 at	BGN	J04599	biglycan	biglycan preproprotein
209	209 33198 at	BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
				sapiens biotindase (BTD) gene, exons 2,	
210	210 37274_at	Btq	AF018631	\neg	biotinidase
				biphenyl hydrolase-like (serine hydrolase;	
				breast epithelial mucin-associated	
211	211 40912 s at	BPHL	X81372		biphenyl hydrolase-related protein
212	212 35267 g at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	213 35266 at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	214 37700 at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
				protein receptor, type	
215	39565_at	BMPR1A	Z22535		ALK-3
216	39551_at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607_at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
				brain abundant, membrane attached	
218	32606 at	BASP1	AA135683	signal protein 1	
219	37945 at	ВАСН	U91316	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
220	37958_at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023_at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
				branched chain keto acid dehydrogenase	
				E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683 i at	ВСКОНВ	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	protein
L				brefeldin A-inhibited guanine nucleotide-	
224	38306_at	BIG1	AA477576	exchange protein 1	
225	37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
		200	4 100000	BTB and CNC homology 1, basic leucine	BTB and CNC homology 1, basic leucine
526	226 31895 at	BACHI	ABUUZBU3	Zipper transcription tactor i	Lippel danscription factor i

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227	36634	BTG2	U72649	BTG family, member 2	втаг
228	37218	BTG3	D64110		ANA
	1	i i	,	BUB3 budding uninhibited by	and an animatic charkmaint BI IR3
623	4154/_at	BUB3	AF04/4/2	BUR3 birdding uninhibited by	
230	34783_s_at	BUB3	AF047473	benzimidazoles 3 homolog (yeast)	testis mitotic checkpoint BUB3
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
232	32780 at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
233	32629 f at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	39357_E	C2F	U72514	C2f protein	CZÍ
235	40709_at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
238	36976 at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
				cadherin 11, type 2, OB-cadherin	*
239	2087_s_at	CDH11	D21254	(osteoblast)	Ob-cadnern-1
240	240 2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
3	0,00	CAMAZO	LIOAGEA	calcium/calmodulin-dependent protein	CaM kinasa II isoform
<u>;</u>	_	CAIMING	100	calcium/calmodulin-dependent protein	
242	38716_at	CAMKK2	AB018330	kinase kinase 2, beta	KIAA0787 protein
		200	0001	calcium/calmodulin-dependent serine	N. A. C.
243	31854 at	CASA CALD1	Ar035562 M64110	caldesmon 1	caldesmon
245		CALD1	M83216	caldesmon 1	caldesmon
				calmodulin 1 (phosphorylase kinase,	
440	41288_at	CALMI	ALU30/44	uelia)	
247	911_s_at	CALM2	M19311	caimoduiin z (priospriorylase kiriase, delta)	calmodulin 2 (phosphorylase kinase, delta)
248	248 40125_at	CANX	L10284	calnexin	calnexin
249	249 37001_at	CAPN2	M23254	calpain 2, (π/II) large subunit	neutral protease large subunit
250	36138_at	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunt 1

251 41257_at 252 33385_g_at 253 40953_at	A	80	Ö	3	ע
252 3338 252 3338 253 4095 254 3734		1			
252 3338 253 4095 254 3734		CAST	D16217		calpastatin
253 4095 254 3734	at	CAST	U31346	calpastatin	calpastatin
254 3734		CNN3	S80562	calponin 3, acidic	acidic calponin
		CALU	AF013759	calumenin	calumein
					cAMP responsive element binding protein 1,
255 37535 at	5 at	CREB1	M27691	CAMP responsive element binding protein	protein 1, isoform B
				cAMP responsive element binding protein	
256 4084	40849_s_at	CREB3	U88528		transcription factor LZIP
				cAMP responsive element binding protein-	•
257 39438_at	18_at	CREBL2	AF039081	like 2	Cre binding protein-like 2
					cyclic AMP-responsive element modulator
258 32065_at	55_at	CREM	S68134	cAMP responsive element modulator	beta isoform
259 32067_at	17_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
					cyclic AMP-responsive element modulator
260 3206	32066_g_at	CREM	S68134		beta isoform
				capping protein (actin filament) muscle Z-	
261 40910_at	10_at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
_				tein (actin filament) muscle Z-	
262 36641	11_at	CAPZA2	U03851	\neg	capping protein alpha
_				capping protein (actin filament) muscle Z-	
263 3701	37012_at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
_				carbohydrate (chondroitin 6)	
264 3209	32094_at	CHST3	AB017915	sulfotransferase 3	chondroitin 6-sulfotransferase
265 4144	41447_at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAA0990 protein
				carbohydrate (keratan sulfate Gal-6)	
266 4139	41395_at	CHST1	AB003791	sulfotransferase 1	keratan sulfate Gal-6-sulfotransferase
				carbohydrate (N-acetylglucosamine-6-0)	N-acetylglucosamine-6-0-sulfotransferase
267 3796	37960_at	CHST2	AB014679	sulfotransferase 2	(GicNAc6ST)
268 36454_at	54_at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
269 3487	34876_at	СРО	U65090	carboxypeptidase D	carboxypeptidase D
270 3660	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
				Cas-Br-M (murine) ectropic retroviral	
	35632_at	CBLB	U26710	transforming sequence b	q-lqo
272 4018	40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273 369	36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase I delta

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274	38019_at	CSNK1E	L37043	casein kinase 1, epsilon	casein kinase I-epsilon
				containing	
275	1211_s_at	CRADD	U84388	adaptor with death domain	death domain containing protein CHADD
276	276 11867 at	CFL AR	AF005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
				caspase 4, apoptosis-related cysteine	
277	195_s_at	CASP4	U28014	protease	cysteine protease
				caspase 8, apoptosis-related cysteine	
278	33774_at	CASP8	X98172	protease	MACH-alpha-1
279	279 41156 g at	CTNNA1	103100	catenin (cadherin-associated protein), Jaloha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein).	
280	280 41155_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
281	2085_s_at	CTNNA1	D14705	alpha 1 (102kD)	'human alpha-catenin'
				catenin (cadherin-associated protein),	
282	2069_s_at	CTNNA1	123805	alpha 1 (102kD)	alpha1(E)-catenin
				catenin (cadherin-associated protein),	
283	35331_at	CTNNAL1	U97067	alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	
284	284 40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
282	285 40444_s_at	CTNND1	AB002382	delta 1	
286	286 38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290		CAV2	AF035752	caveolin 2	caveolin-2
	-			Cbp/p300-interacting transactivator, with	
291	33113_at	CITED2	U65093	Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
				CCAAT/enhancer binding protein	
292	1052_s_at	CEBPD	M83667	(C/EBP), delta	NF-IL6-beta protein
203	293 39219 at	SEBPG	1190940	CCAAT/enhancer binding protein	C/EBP gamma
2	100£ 10 at	טבטו מ	OE0E 10		

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1	A	В	اد		
_		1		CCR4-NOT transcription complex, subunit	
294	33861_at	CNOT2	Al123426	2	
_				CCR4-NOT transcription complex, subunit	
295		CNOT4	U71267		potential transcriptional repressor NO I 4Hp
296	34819_at	CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
297	34699 at	CD2AP	AL050105	CD2-associated protein	hypothetical protein
				CD36 antigen (collagen type I receptor,	
				thrombospondin receptor)-like 2	
298	33823 at	CD36L2	D12676	(lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
Γ				CD44 antigen (homing function and Indian	
299	2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
Γ				CD81 antigen (target of antiproliferative	
00	35282 r_at	CD81	M33680	antibody 1)	CD81 antigen
ဓ္ထ	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
Γ				CDC10 cell division cycle 10 homolog (S.	
302	32175_at	CDC10	S72008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	
304	31877_at	CDC23	AF053977	. (Bolomou	cell division cycle protein 23
305	40690 at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362 at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307	32833 at	CLK1	M59287	CDC-like kinase 1	
		CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
				CDP-diacylglycerol synthase	
309	41343_at	CDS2	Y16521	(phosphatidate cytidytyttransferase) 2	CDS2 protein
				CDP-diacy/glycerolinositol 3-	
				phosphatidyftransferase	
310	310 33397_at	CDIPT	AL050383	(phosphatidylinositol synthase)	
311	40591 at	CDC27	S78234	cell division cycle 27	H-NUC
				cell growth regulatory with ring finger	
312	450 g at	CGR19	U66469	domain	cell growth regulator CGR19
Ì				cell growth regulatory with ring finger	
313	313 36514_at	CGR19	U66469	domain	cell growth regulator CGR19

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T			,		cellular represent of E1A-etimulated genes
24.4	35311 01	000	AEOBAEOB	Cellular represents of E1A-etimulated general DEC	
		Ched	AFUGASES	כפווחומו ופחופיסטו חו בוע-סווווחומיםת חפונפס	Oneo
315 4	41333_at	CENTB2	D26069	centaurin, beta 2	centaurin, beta 2
	34676_at	CENTG2	AB029022	centaurin, gamma 2	KIAA1099 protein
317	38410_at	CETN2	X72964	centrin, EF-hand protein, 2	caltractin
				centrin, EF-hand protein, 3 (CDC31	
318	35232_f_at	CETN3	A1056696	homolog, yeast)	
319	31894_at	CENPC1	M95724	centromere protein C 1	centromere autoantigen C
	33805_at	CAP350	AB007949	centrosome-associated protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190_at	CDR2	M63256	(62kD)	major Yo paraneoplastic antigen
322	32262_at	CGI-01	AL049669	CGI-01 protein	hypothetical protein
323	323 40931_at	LOC50999	AL080084	CGI-100 protein	
324	38500_at	LOC51014	AB002450	CGI-109 protein	
325	325 34359_at	LOC51020	AA524058	CGI-130 protein	
326	38667_at	LOC51031	AA189161	CGI-150 protein	
327	327 41824_at	LOC51096	AI140114	CGI-48 protein	
328	34862_at	LOC51097	AA005018	CGI-49 protein	
329	37199_at	LOC51626	AI760932	CGI-60 protein	
	41411_at	LOC51103	AI566877	CGI-65 protein	
331	39814_s_at	LOC51635	AI052724	CGI-86 protein	
_				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759_at	CCT2	AF026166	(beta)	homolog
				chaperonin containing TCP1, subunit 3	
333	40774_at	CCT3	X74801	(gamma)	gamma subunit of CCT chaperonin
				chaperonin containing TCP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
				chaperonin containing TCP1, subunit 6A	
335	38416_at	CCT6A	L27706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CCT7	AF026292	(eta)	1, eta subunit
				chaperonin containing TCP1, subunit 8	chaperonin containing TCP1, subunit 8
337	39767_at	ССТВ	D13627	(theta)	(theta)
338	338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase

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340 38732_at 341 33891_at 342 32363_at 34112_g 343 381112_g 344 38111_at					
		_			
	732_at	CLNS1A	X91788	chloride channel, nucleotide-sensitive, 1A Icin protein	cln protein
	33891_at	CLIC4	AL080061	chloride intracellular channel 4	
	163_at	CH25H	AF059214		cholesterol 25-hydroxylase
				chondroitin sulfate proteoglycan 2	
	38112_g_at	CSPG2	X15998		chondroitin sulfate proteoglycan 2 (versican)
				n sulfate proteoglycan 2	
	111_at	CSPG2	X15998		chondroitin sulfate proteoglycan 2 (versican)
_				chondroitin sulfate proteoglycan 6	
345 347	34763_at	CSPG6	AF020043		chromosome-associated polypeptide
-				homolog 1 (HP1 beta homolog	
346 373	37304_at	CBX1	U35451		heterochromatin protein p25
			i	chromobox homolog 3 (HP1 gamma	
347 380	38085_at	CBX3	AI740522	homolog, Drosophila)	
_				chromobox homolog 3 (HP1 gamma	
348 380	38084_at	CBX3	AA648295	homolog, Drosophila)	
				chromodomain helicase DNA binding	
349 361	36137_at	CHD4	X86691	protein 4	Mi-2 protein
				chromodomain protein, Y chromosome-	
350 321	32111_at	CDYL	AL050164	like	hypothetical protein
351 399	39550_at	C1orf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
352 390	39033_at	C1orf8	278368	chromosome 1 open reading frame 8	
353 322	32217_at	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apotosis protein 12
354 406	40979_at	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
355 400	40045_g_at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
356 368	36860_at	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA1064 protein
357 343	34287_at	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
	33406_at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
329 33.	33778_at	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
360 41	41758_at	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
361 38	38690_at	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
362 36	36013_at	C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
363 36	36955_at	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
364 41	41375_at	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
365 41	41454_at	C6orf34	W27949	chromosome 6 open reading frame 34	
366 36139_at	139_at	Ceorf5	AL050289	chromosome 6 open reading frame 5	hypothetical protein

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_		٥) 	<u> </u>	
	35193_at	CHC1L	AF060219	Ì	RCC1-like G exchanging factor MLG
368	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
	41314_at	cs	AF047042		citrate synthase
370	41159_at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
					clathrin, light polypeptide A, isoform a;
371	38657_s_at	CLTA	M20471		clathrin, light polypeptide A, isoform b
				cleavage and polyadenylation specific	
372	35743_at	CPSF4	U79569	factor 4, 30kD subunit	no arches
				cleavage stimulation factor, 3' pre-RNA,	
373	32723_at	CSTF1	L02547	subunit 1, 50kD	cleavage stimulation factor
				cleavage stimulation factor, 3' pre-RNA,	
374	41183_at	CSTF3	U15782	subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017_at	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
				clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message repressed prostate message 2,	repressed prostate message 2,
377	36780_at	CLU	M25915	2, apolipoprotein J)	apolipoprotein J)
378	35180	LOC113251	AL050205	c-Mpl binding protein	
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
G	28052 at	E13A1	N114530	occupation factor XIII A1 polymentide	coagnistion factor XIII A1 subunit precursor
	1000	100140	00000	Congulation Company Profession	transmompton anatoin
5	36972_at	HNP24	X92098	coated vesicle membrane protein	transmembrane protein
382	34326_at	СОРВ	X82103	coatomer protein complex, subunit beta	beta-Coat protein
				coatomer protein complex, subunit beta 2	
383	36677_at	COPB2	X70476	(beta prime)	subunit of coatomer complex
384	35205_at	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
385	36648_at	CRSP9	AF031383	activation, subunit 9 (33kD)	hMed7
386	386 33659 at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	387 40879_at	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388	388 39864_at	CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
390	390 32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
391	32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392	392 32305 at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein



	A	۵	C	G	u
				collagen, type III, alpha 1 (Ehlers-Danlos	
393	32488_at	COL3A1	X14420	syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
394	36659_at	COL4A2	X05610	collagen, type IV, alpha 2	alpha (2) chain
395	38420_at	COLSA2	Y14690	collagen, type V, alpha 2	procollagen alpha 2(V)
968	38722_at	COL6A1	X15880	collagen, type VI, alpha 1	alpha-1 collagen VI (AA 574-1009)
397	38077_at	COLGA3	X52022	collagen, type VI, alpha 3	collagen type VI, alpha 3 chain
398	37459_at	COL8A1	X57527	collagen, type VIII, alpha 1	alpha 1(VIII) collagen
					alpha 1 type XI collagen, isoform A
					preproprotein; alpha 1 type XI collagen,
					isoform B preproprotein; alpha 1 type XI
399	37892_at	COL11A1	J04177	collagen, type XI, alpha 1	collagen, isoform C preproprotein
400	400 35168_f_at	COL16A1	M92642	collagen, type XVI, alpha 1	alpha-1 type XVI collagen
				complement component 1, q	complement component 1, q subcomponent
401	3/668_at	Clubr	M69039	supcomponent binging protein	pinding protein precuisor
				complement component 1, r	
402	39409_at	C1R	M14058	subcomponent	complement component 1, r subcomponent
				complement component 1, s	
403	403 40496_at	C1S	J04080	subcomponent	complement component 1, s subcomponent
404	404 36638_at	CTGF	X78947	connective tissue growth factor	connective tissue growth factor
				conserved gene amplified in	
405	41202_s_at	0S4	AF000152	osteosarcoma	OS-4 protein
				conserved helix-loop-helix ubiquitous	
406	33770_at	CHUK	AF009225	kinase	IKB kinase alpha subunit
				COP9 constitutive photomorphogenic	
407	1789_at	COPS5	U65928	homolog subunit 5 (Arabidopsis)	Jun activation domain binding protein
408	408 32539_at	COP9	U51205	COP9 homolog	COP9 signalosome subunit 1 CSN1
	9			polomod NEW Made and New Market Strain and N	24 KD a Model to mode
2	409 40138_at	MOV45-SAND	0/0/33	ON TO (BOIGHING TO ONL) O HINDRO BLOO	Social Food Park
4		CPNE1	U83246	copine i	copine i
411	39706_at	CPNE3	AB014536	copine III	KIAA0636 protein
				coproporphyrinogen oxidase	
412		CPO	D16611	(coproporphyria, harderoporphyria)	coproporphyrinogen oxidase
413	37026_at	COPEB	AF001461	core promoter element binding protein	Kruppel-like zinc finger protein 219
414	414 41175_at	CBFB	L20298	core-binding factor, beta subunit	transcription factor
415	32803_at	CNIL	AF104398	comichon-like	comichon



	A	a	C	Û	Ш
				COX11 homolog, cytochrome c oxidase	
416	416 34723_at	COX11	U79270	assembly protein (yeast)	COX11 homolog
1	- 20020 211		1101011	CpG island protein; Human nested gene	occupies factor VIII. accordated protein
4 6	417 37907 at	FBA, UASSZZE	M346//	protein gene, complete cus.	craniofacial development protein 1
	2000		ADM3200	CREB binding protein (Rubinstein-Taybi	
419	33831_at	CREBBP	U47741	syndrome)	CREB-binding protein
420	420 36948_at	CRI	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421	421 38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	37902_at	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
				CSE1 chromosome segregation 1-like	
454	424 38804_at	CSE1L	AF053641	(yeast)	cellular apoptosis susceptibility protein
425	425 1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426	426 41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	427 40780 at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	428 39723_at	CUL1	AF062536	cullin 1	cullin 1
429	429 40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
L				cut-like 1, CCAAT displacement protein	
430	31823_at	CUTL1	M74099	(Drosophila)	cut-like 1, CCAAT displacement protein
431		ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
				cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
432	432 41808_at	DMTF1	AF052102	factor 1	
				cyclin D1 (PRAD1: parathyroid	
433	433 38418_at	CCND1	X59798	adenomatosis 1)	cyclin
L				cyclin D1 (PRAD1: parathyroid	
\$	434 2020_at	CCND1	M73554	adenomatosis 1)	bcl-1
<u>表</u>	36650_at	CCND2	D13639	cyclin D2	cyclin D2
<u>융</u>	40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437	437 37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	438 1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439	1924_at	CCNH	U11791	cyclin H	cyclin H
440	440 1836_at	CCNI	D50310	cyclin 1	cyclin I
44	441 1792 g at	CDK2	M68520.	cyclin-dependent kinase 2	cdc2-related protein kinase

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CDK7 L20320 CDK7 X77743 CDK8 R59697 CDKN1A U03106 CDKN1B A1304854 CDKN2C AF041248 CSRP1 M33146 CSRP2 U57646 COXRAH D86324 COXBB A1526089 COXFB A152608 COXFB A1708889			-	Č		
33317_at CDK7 L20320 1969_s_at CDK7 X77743 35140_at CDK8 R59697 2031_s_at CDKN1A U03106 33847_s_at CDKN1B AI304854 3800_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 AI651806 3872_at CYR61 Y11307 40408_at CARS L06845 39317_at CARS D00265 39317_at COX6A1 AI526089 41206_r_at COX6A1 AI526089 41206_r_at COX7A2 AA978033 34330_at COX7A2L AB007618	7		В)	ח	IJ
33317_at CDK7 L20320 1969_s_at CDK8 R59697 2031_s_at CDKN1A U03106 2031_s_at CDKN1B R59697 33847_s_at CDKN1B AI304854 39700_at CSRP1 M33146 41401_at CSRP2 U57646 40408_at CSRP1 M33146 40408_at CARS L06845 39317_at CMAH D86324 39317_at COXEB AI526089 41206_r_at COXEB AI526089 39921_at COXEB AI526089 39031_at COXTA2 AA978033 34330_at COXTA2 AB007618					cyclin-dependent kinase 7 (MO15	
33317_at CDK7 L20320 1969_s_at CDK8 R59697 2031_s_at CDKN1A U03106 2031_s_at CDKN1B R59697 30053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CYR61 Y11307 40408_at CYR5-M AA173896 39317_at CYR5-M AA173896 39921_at COX6A1 Al526089 41206_r_at COX6A1 Al526089 39031_at COX7A2 AA978033 34330_at COX7A2L AB007618					homolog, Xenopus laevis, cdk-activating	
1969_s_at CDK7 X77743 35140_at CDK8 R59697 2031_s_at CDKN1A U03106 33847_s_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRM1 Ale51806 39772_at CYR61 Y11307 40408_at CARS L06845 39317_at CMAH D86324 39317_at CCX6B Ale56089 41206_r_at COX6A1 Ale52608 36165_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AA978033	442	33317_at	CDK7	L20320	kinase)	protein serine/threonine kinase
1969_s_at CDK7 X77743 35140_at CDK8 R59697 2031_s_at CDKN1A U03106 33847_s_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40408_at CRIM1 AI651806 38772_at CYR61 Y11307 40408_at CARS L06845 40408_at CARS L06845 39317_at CMAH D86324 39317_at COXBS AA173896 35818_at HCS D00265 39921_at COX6A1 AI526089 41706_r_at COX6C W51774 39031_at COX7A2 AA978033 34330_at COX7A2 AA978033 34331_at COX7A2 AA978899					cyclin-dependent kinase 7 (MO15	
1969_s_at CDK7 X77743 35140_at CDK8 R59697 2031_s_at CDKN1B AI304854 3847_s_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 AI651806 38772_at CYR61 Y11307 40408_at CARS L06845 40408_at CARS L06845 40408_at CARS L06845 40408_at COX AA173896 39317_at COX56 AA173896 35818_at COX66 M51774 39921_at COX66 W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AA978899	_				homolog, Xenopus laevis, cdk-activating	
35140_at CDK8 R59697 2031_s_at CDKN1A U03106 33847_s_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CARS L06845 39317_at CMAH D86324 39317_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AA978033	443	1969_s_		X77743	kinase)	CDK activating kinase
2031_s_at CDKN1A U03106 33847_s_at CDKN1B AI304854 36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CYR61 V11307 40408_at CYR61 V11307 40408_at CYR5-M AA651806 38772_at CYR5-M AA173896 34340_at CYR5-M AA173896 35818_at COX5B AI526089 41206_r_at COX6A1 AI526089 41760_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AA978889	444	35140_at		R59697	cyclin-dependent kinase 8	•
2031_S_at CDKN1B U03106 33847_S_at CDKN2C AF041248 36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CYR61 V11307 40408_at CYR61 V11307 40408_at CARS L06845 39317_at CMAH D86324 39317_at CMAH D86324 39921_at COX5B AA173896 39921_at COX6B AI526089 41206_r_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AA978899					cyclin-dependent kinase inhibitor 1A (p21,	
3847_s_at CDKN1B AI304854 36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 AI651806 38772_at CYR61 Y11307 40408_at CARS L06845 39317_at CARS D00265 39921_at COX5B AI526089 41206_r_at COX6A1 AI540925 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618	445	2031_s_at	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
3847_s_at CDKN1B Al304854 36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 440936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CARS L06845 39317_at CARS L06845 39317_at CARS Al526089 34340_at CYR5-M AA173896 35818_at COX5B Al526089 41206_r_at COX6A1 Al540925 36165_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618					cyclin-dependent kinase inhibitor 1B (p27,	
36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CARS L06845 39317_at CARS L06845 39921_at COX5B A8173896 39921_at COX6A1 A81540925 36165_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618	446	33847_s_at	CDKN1B	Al304854	Kip1)	
36053_at CDKN2C AF041248 38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CYR61 Y11307 40408_at CYR5-M D86324 39317_at CYR5-M D86324 39321_at COX5B A1526089 36165_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618					cyclin-dependent kinase inhibitor 2C (p18,	
38700_at CSRP1 M33146 41401_at CSRP2 U57646 40936_at CRIM1 Al651806 38772_at CYR61 Y11307 40408_at CYR61 Y11307 40408_at CARS L06845 CARS L06845 CARS L06845 COKB4 D86324 34340_at CYB5-M AA173896 35818_at COX68 Al526089 341206_r_at COX6A1 Al540925 36165_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618	447	36053_at	CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent kinase inhibitor
41401_at CSRP2 U57646 40936_at CRIM1 AI651806 38772_at CYR61 Y11307 40408_at CARS L06845 24340_at CARS L06845 39317_at CMAH D86324 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618 34381_at COX7AC AI708889	448		CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
40936_at CRIM1 AI651806 38772_at CYR61 Y11307 40408_at CARS L06845 39317_at CMAH D86324 34340_at CYB5·M AA173896 39921_at COX5B AB26089 41206_r_at COX6B AI526089 39031_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618 34381_at COX7AC AI708889	449	41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
38772_at CYR61 Y11307 40408_at CARS L06845 40408_at CARS L06845 39317_at CMAH D86324 34340_at CYB5·M AA173896 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2 AB007618 34381_at COX7C AI708889	450	40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
40408_at CARS L06845 39317_at CMAH D86324 34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2L AB007618 34381_at COX7C AI708889		38772_at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
39317_at CMAH D86324 34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX6A1 AI526089 41206_r_at COX6A1 AI540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033	452	40408_at	CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
39317_at CMAH D86324 34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6A1 AI540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033						
39317_at CMAH D86324 34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B A1526089 41206_r_at COX6A1 A1540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033					cytidine monophosphate-N-	
39317_at CMAH D86324 34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B A1526089 41206_r_at COX6A1 A1540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033					acetylneuraminic acid hydroxylase (CMP-	
34340_at CYB5-M AA173896 35818_at HCS D00265 39921_at COX5B A1526089 41206_r_at COX6A1 A1540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033 34330_at COX7A2 AB007618	453		СМАН	D86324	N-acetylneuraminate monooxygenase)	CMP-N-acetylneuraminic acid hydroxylase
34340_at CYB5.M AA173896 35818_at HCS D00265 39921_at COX5B AI526089 41206_r_at COX6A1 AI540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 34330_at COX7A2 AA978033 34330_at COX7A2 AB007618					cytochrome b5 outer mitochondrial	
35818_at HCS D00265 39921_at COX5B Al526089 41206_r_at COX6A1 Al540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2L AB007618	454	34340_at	CYB5-M	AA173896	membrane precursor	
39921_at	455	35818_at	HCS	D00265	сутостгот с	cytochrome c
41206_r_at COX6A1 Al540925 36165_at COX6C W51774 39031_at COX7A1 AA152406 41760_at COX7A2 AA978033 34330_at COX7A2L AB007618 34381_at COX7A2 A1708889	456	39921_at	сохев	AI526089	cytochrome c oxidase subunit Vb	
41206_r_at					cytochrome c oxidase subunit Vla	
39031_at	457	41206_r_at	COX6A1	AI540925	polypeptide 1	
39031_at	458	36165_at	coxec	W51774	cytochrome c oxidase subunit VIc	
39031_at					cytochrome c oxidase subunit VIIa	
41760_at COX7A2 AA978033 34330_at COX7A2L AB007618	459		COX7A1	AA152406	polypeptide 1 (muscle)	
41760_at					cytochrome c oxidase subunit VIIa	
34330_at COX7A2L AB007618	94	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
34330_at	- 3				cytochrome c oxidase subunit VIIa	
PALYORNA CONTRACT	9	9435 OS	COX/AZL	AB00/618	polypeptide Z like	14/YO
	462	34381_at	COX7C	AI708889	cytochrome c oxidase subunit VIIc	

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463	38080_at		33	cytochrome c oxidase subunit VIII	
464	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
				cytochrome P450, 51 (lanosterol 14-alpha-	
465	33389_at	CYP51	U23942	demethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
466	859 at	CVP1B1	Позева	Inducible), polypepilde i (gladcoma s, primary infantila)	cytochrome P450
	15-500		20000	cytochrome P450 subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
467	40071_at	CYP1B1	U03688	primary infantile)	cytochrome P450
468	37509_at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469	37306_at	KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
				cytoplasmic; Human Ser/Thr protein	
470	1706_at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	34338_at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	40282_s_at	DF PF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877_s_at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	1243_at	DDB2	U18300	(48kD)	008b p48
476		DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
477	37663_at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent RNA helicase #46
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
479	479 40490_at	DDX21	U41387	polypeptide 21	Gu protein
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, X isoform
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDX5	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
				polypeptide 9 (RNA helicase A, nuclear	
482	36153_at	6XQQ	L13848	DNA helicase II; leukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

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					ionizing radiation resistance conferring
	DAP3	5	U18321	death associated protein 3	protein
	DEPP	AB	AB022718	decidual protein induced by progesterone	ОЕРР
	DOCK1	DS	D50857		DOCK180 protein
	DAD1	01	D15057	ath 1	DAD-1
				deficient in late-infantile neuronal ceroid	
				lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2)	
	CLN2	AF.	AF039704		lysosomal pepstatin insensitive protease
				atocyte homolog, lipid	
	DEGS	AA	AF002668		MLD
ŀ	DEK	9X	X64229	DEK oncogene (DNA binding)	putative oncogene
	DLC1	AF	AF035119		deleted in liver cancer-1
	DLEU1	X	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
	DSS1	5 <u>N</u>	N95406	Deleted in split-hand/split-foot 1 region	
				detta sleep inducing peptide,	
	DSIPI	¥	AI635895	immunoreactor	
	GA17	AF	AF064603	dendritic cell protein	GA17 protein
	DSTN	S	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
				development and differentiation enhancing	development and differentiation enhancing development- and differentiation-enhancing
	DDEF2		AB007860	factor 2	factor 2
498 39044 s at	DGKD		D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499 38003 s at	DGKZ		U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
	DIAPH1		AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
				diazepam binding inhibitor (GABA	
ø				receptor modulator, acyl-Coenzyme A	
	DBI	<u>₹</u>	AI557240	binding protein)	
				dihydrolipoamide S-acetyftransferase (E2	•
				component of pyruvate dehydrogenase	
	DLAT	<u>></u>	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
	DPYSL2		U97105	dihydropyrimidinase-like 2	N2A3
	DPYSL3		D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
505 39503 s at	DPYSL4		AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
	DPYD		U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507 40485 at	HSA249128		AA176780	DIPB protein	
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disabled homolog 2, mitogen-responsive obosphoprotein (Drosophila)
discoidin domain receptor family, member
discs, large (Drosophila) homolog 5
dishevelled associated activator of
morphogenesis 1
disrupter of silencing 10
dJ635G19.1 (LAMR1 (Laminin Receptor
(67kD) (RPSA, 40S Ribosomal Protein
SA, P40)) pseudogene); match: cDNAs:
Em:X15005 Em:J03799 Em:X61156
Em:M64923 Em:X06406 Em:AF140348
Em:J02870 Em:L16589 Em:Z22749
Em:D25224 Em:M14199 Em:M27798;
match: ESTs: Em:AA642
dJ734P14.1 (KRAB box and C2H2 Zinc
finger domain protein pseudogene) match:
cDNAs: Em:M27878 Em:M29580
Em:U27186 Em:D31763 Em:AB007872
Em:U09366 Em:U09413 Em:X17617
Em:AF011573 Em:AF020591 Em:X78925
match: proteins: Sw:P52736 Sw:Q06730
Sw.P51523 Tr:Q14585 Sw.P15620
Sw.Q02386 Sw:P51786 Sw:Q99676
Tr:O60792 Sw:Q03923 Sw:O75820
Tr:O61116 Tr:O64247

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515	38455_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q03923 Sw:Q099676 Tr:Q60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear
516	516 35809_g_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
518	518 32433 at	dJ90L6.1	297353	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O77445 Sw:P54780 Sw:O23515 Sw:O17445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P65818 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O65082 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	·

Fig 21

	Δ	α	[c		ш
519	34183 at	4C171		q	hypothetical protein
-	40801_at	. 2			
	38400_at	35		c	
	33392_at	DKFZP434J154			hypothetical protein
523	39411_at	DKFZP434J214	AL080156		hypothetical protein
524	40564_at		N42007		
525	37000_at	DKFZP564B167	AL035304		hypothetical protein
526	33433_at	DKFZP564F0522	AL049943		hypothetical protein
527	41437_at	DKFZP564F1123	AL080178		hypothetical protein
528	39442_at	DKFZP564G0222 AL080115			hypothetical protein
529	40437_at	DKFZP564G2022 AL049944		DKFZP564G2022 protein	hypothetical protein
530	36456_at	DKFZP5641052			hypothetical protein
531	38033_at	DKFZP564M1416	16 AL049934	DKFZP564M1416 protein	hypothetical protein
532	36078_at	DKFZP56400423 AL080120	0.	u u	hypothetical protein
533	533 38256_s_at	DKFZP5640092 W21827		DKFZP5640092 protein	
534	39034_at	DKFZP5640123 AL080122		DKFZP564O123 protein	hypothetical protein
535	535 41662_at	DKFZP566B183		DKFZP566B183 protein	hypothetical protein
536	536 32807_at	DKFZP566C134		DKFZP566C134 protein	
537	537 38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
538	538 33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	539 41335_at	DC8	AL050084	DKFZP56601646 protein	hypothetical protein
540	540 36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	38717_at	DKFZP586A0522 AL050159	AL050159	DKFZP586A0522 protein	hypothetical protein
542	542 40831_at	DKFZP586B0923 AL050190	AL050190	DKFZP586B0923 protein	hypothetical protein
543	34821_at	DKFZP586D0623 AL050197	AL050197	DKFZP586D0623 protein	hypothetical protein
544	544 39986_at	DKFZP586D0919 AL050100	AL050100	DKFZP586D0919 protein	hypothetical protein
545	34269_at	DKFZp586F1019 AL050102	AL050102	DKFZp586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918	118 AL050091	DKFZP586F1918 protein	hypothetical protein
547	40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	548 36007 at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	549 34833 at	DKFZP58600120	120 AL050157	DKFZP58600120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5-)-methyltransferase 1	DNA (cytosine-5-)-methyttransferase
				DNA segment on chromosome X (unique)	
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
				DNA segment on chromosome X and Y	DNA segment on chromosome X and Y
552	552 34215_at	DXYS155E	L03426	(unique) 155 expressed sequence	(unique) 155 expressed sequence

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				DNA segment, single copy probe LNS-	
553	1252_at	D5S346	M73547	CAI/LNS-CAII (deleted in polyposis	polyposis locus-encoded protein
				DNA segment, single copy, probe pH4	DNA segment, single copy, probe pH4
554	37162_at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
				DnaJ (Hsp40) homolog, subtamily A,	
555	39118_at	DNAJA1.	690807	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily A,	
556	276_at	DNAJA1	690807	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
557	41233_at	DNAJBe	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	
559	36166_at	DNAJC8	AF083190	member 8	SPF31
	-			docking protein 1, 62kD (downstream of	
560	816_g_at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
				docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
0	24070	7700	A E007076	dolicinyi-phosphate mannosymansierase	dolichol monoposphate mannose svnthase
200	2407	באונו	Arw/6/3	polypopulae 1, catalytic subulin	
563	563 38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecoriin and Cam Kinase-IIKe I
564	564 32168_s_at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
292	36088_at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
999	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
267		DR1	M97388	binding (negative cofactor 2)	phosphoprotein
568	37981_at	DBN1	D17530	drebrin 1	drebrin E
				dual specific protein; Homo sapiens	
				tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570		DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
573	579 41225 at	N SP3	A! 049417	dual specificity phosphatase 3 (vaccinia vinis phosphatase VH1-related)	
7/6	41223 al	Jour 3	OLOHOT I		

573 41193_at 574 36946_at 575 1512_at 576 760_at 577 39931_at 577 39931_at 579 38475_at 579 38475_at 580 34891_at 580 34891_at 580 34829_at	B DUSP6 DYRK1A DYRK2 DYRK3 DOTN2 PIN	C AB013382 D86550 D86550	9 6	DUSP6
	DVRK1A DYRK1A DYRK2 DYRK3 DVRK3 DOT DOT NO	AB013382 D86550 D86550		DUSP6
	DYRK1A DYRK1A DYRK2 DYRK3 DOT DCTN2 PIN	D86550 D86550		
	DYRK1A DYRK2 DYRK3 DOT DOT PIN	D86550		
	DYRK1A DYRK2 DYRK3 DUT DCTN2 PIN	D86550	inase 1A	serine/threonine protein Kinase
	DYRK2 DYRK3 DUT DCTN2 PIN	000000		serine/hreonine protein kinase
	DYRK2 DYRK3 DUT DCTN2 PIN		prospriory ration 1 oguiated milaso 12	
	DYRK3 DYRK3 DCTN2 PIN	_	dual-specificity tyrosing-(Y)-	dual-specificity tyrosine-(Y)-phosphorylation
	DYRK3 DUT DCTN2 PIN	Y09216	inase 2	regulated kinase 2 isoform 1
	DYRK3 DUT DCTN2 PIN			
	DUT DCTN2 PIN	Y12735	d kinase 3	Dyrk3 protein
	DCTN2 PIN	U31930	phatase	deoxyuridine nucleotidohydrolase
	NIG	U50733		dynamitin
		AI540958	dynein, cytoplasmic, light polypeptide	
	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
			dystonia 1, torsion (autosomal dominant;	
	DYT1	AF007871	torsin A)	torsinA
_			dystroglycan 1 (dystrophin-associated	
583 36989_at	DAG1	L19711	glycoprotein 1)	dystroglycan
			dystrophin (muscular dystrophy,	
584 40488_at	DWD	M18533	Duchenne and Becker types)	dystrophin
585 40106 at	E18-AP5	AJ007509	E1B-55kDa-associated protein 5	E1B-55kDa-associated protein
586 33354 at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587 40375 at	EGR3	X63741	early growth response 3	transcription factor
588 36135 at	EBNA18P2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589 37730 at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
	. EVI5	AF008915	ecotropic viral integration site 5	EVI-5 homolog
			ectodermal-neural cortex (with BTB-like	!!
591 39542_at	ENC1	AF059611	(domain)	nuclear matrix protein NRP/B
			ectonucleotide	
			pyrophosphatase/phosphodiesterase 2	•
592 41124_r_at	at ENPP2	L35594	(autotaxin)	autotaxin
			ectonucleotide	
593 41123 s at	ENPP2	1.35594	(autotaxin)	autotaxin
			EGF-containing fibulin-like extracellular	
594 32551_at	EFEMP1	U03877	matrix protein 1	extracellular protein

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595	36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
				Ipha	electron transfer flavoprotein, alpha
296	40509_at	ETFA	J04058	polypeptide (glutaric aciduria II)	polypeptide
				electron-transfer-flavoprotein, beta	
265	36881_at	ЕТЕВ	X71129	polypeptide	electron transfer flavoprotein beta subunit
				elongation factor EF-1-alpha; Human	
				elongation factor EF-1-alpha gene,	eukaryotic translation elongation factor 1
598	598 1288_s_at	EEF1A	J04617	complete cds.	alpha 1
599	599 31853_at	EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
				squamous cell carcinoma-associated	
8	39861_at	EMS1	M98343	(p80/85 src substrate)	amplaxin
				end of last exon based on GENSCAN	
				prediction presumably this gene and	
				dJ477H23.2 are part of the same gene	
601	41478_at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	39010_at	ENSA	A1658639	endosultine alpha	
Γ				endothelial differentiation,	
				lysophosphatidic acid G-protein-coupled	
605	40387_at	EDG2	U80811	receptor, 2	lysophosphatidic acid receptor homolog
909	40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
				enhancer of rudimentary homolog	human protein homologous to DROER
607	39079_at	EBH	D85758	(Drosophila)	protein
88	608 2035_s_at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609	34335_at	EFNB2	AI765533	ephrin-82	
				epidermal growth factor receptor pathway	epidermal growth factor receptor pathway
610	37731_at	EPS15	Z29064	substrate 15	substrate 15
				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
611	611 1467_at	EPS8	U12535	substrate 8	substrate
612	612 37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	613 39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

F13 21

	A	8	၁	Q	ш
				EPM1 disease gene; cysteine protease	
7	10 30		1148800	inhibitor; Human cystatin B gene,	cystatin B
7	33010_ai	cystatili D	760040	embrane protein band 4.1-	
615	32585 at	EPB41[2	AF027299		protein 4:1-G
616	616 38375 at		AF112219	esterase D/formylglutathione hydrolase	esterase D
				estrogen receptor binding site associated,	
617	617 38283_at	EBAG9	AB007619	antigen, 9	EBAG9
618	618 37161 at		W28948	ESTs	
619	619 40885_s_at		N30151	ESTs	
029	620 33328 at	C1S	W28612	ESTs	
621	33453 at	ATP6S1	AI400326	ESTs	
622	622 31801 at		AI808712	ESTs	
533	623 41598 at		AA890010	ESTs	
				ESTs, Highly similar to RS21_HUMAN	
				40S RIBOSOMAL PROTEIN S21	
624	32744 at	RPS21	AI526078	[H.sapiens]	
				ESTs, Moderately similar to	
				ALUB HUMAN ALU SUBFAMILY SX	
				SEQUENCE CONTAMINATION	
625	39750 at		W61005	WARNING ENTRY [H.sapiens]	
				ESTs, Moderately similar to	
		-		GLK5_HUMAN GLUTAMATE	
				RECEPTOR, IONOTROPIC KAINATE 5	
626	34906 o at		AA977136	PRECURSOR [H.sapiens]	
	<u> </u>			ESTs, Moderately similar to T46365	
				hypothetical protein DKFZp434A1518.1	
627	35787 at		A1986201	[H.sapiens]	
	-			ESTs, Weakly similar to 0903209A	
628	41463 at		AL042729	peptide PD,basic Pro rich [H.sapiens]	
				ESTs, Weakly similar to N-WASP	
629	41273_at		AL046940	[H.sapiens]	
88		PIG8	AF010313	etoposide-induced mRNA	Pig8
3	1 7 00007	4 4 4 0	W28170	eukaryotic translation elongation factor 1	
3	631 40888 T at	EEFIAI	W20170	alphia	

HS 21

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	τ	۵	נ	D	
				eukaryotic translation elongation factor 1	
632	35175_f_at	EEF1A2	X70940	aipha 2	elongation factor 1 alpha-2
000		i i		eukaryotic translation elongation factor 1	4
3	35/48_at	EEF182	X60489	Deta 2	elongation ractor- I-Deta
				eukaryotic translation elongation factor 1	
634	41256 at	EEF1D	Z21507	delia (guarinio indepondo excitatigo protein)	human elongation factor-1-delta
	1			eukaryotic translation elongation factor 1	
635	1676_s_at	EEF1G	M55409	gamma	pancreatic tumor-related protein
969	36587_at	EEF2	Z11692	eukaryotic translation elongation factor 2	human elongation factor 2
			7,0000	V F = 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
3	oos al	EIFIA	L18960	eukaryone translation miliation lactor 1A	אוווופטוס ומכנסו
638	638 34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
063	1154 00	EIESE	100646	eukaryotic translation initiation factor 2,	eukaryotic translation initiation factor 2,
2	104-01	E17231	202043	Subulli (alpila, CARD)	subdim ((applie, conc)
9	640 40515_at	EIF2B2	AF035280	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)	eukaryotic translation initiation factor 28, subunit 2 (beta, 39kD)
				eukaryotic translation initiation factor 3,	
641	1644_at	EIF3S2	U36764	subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
				eukaryotic translation initiation factor 3,	
642	35327_at	EIF3S3	U54559	subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
				eukaryotic translation initiation factor 3,	4
3	32576_al	EFSSS	094855	Subunit 3 (epsilon, 47kD)	mining mammapy frimor integration site 6
644	38681 at	EIF3S6	U62962	subunit 6 (48kD)	(oncogene homolog)
				eukaryotic translation initiation factor 3,	
645	35298_at	EIF3S7	U54558	subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
	000	L	L C	eukaryotic translation initiation factor 3,	
8 0	33323_at	EIF339	078525	Subutility (eta., 110hD)	פתאמו לכוום וופווסון ווווומווסון ומכנסו
				eukaryotic translation initiation factor 4	
647	41785_at	EIF4G2	U73824	gamma, 2	p97
648	648 33907 at	FIEAG3	AE012072	eukaryotic translation initiation factor 4	e E4G
3	33307 at	E17+03	ALDIEU/E	games, o	

	A	89	ပ	O	u
				translation initiation factor 4A,	11 44 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
649	1420_s_at	EIF4A2	D30655	isoform 2	eukaryotic initiation factor 4Aii
			1		sichter auf
650	37752_at	EIF4E	M15353	T	cap-pilianig protein
				eukaryotic translation inflation factor 4E	
	35263_at	EIF4EBP2	N73769	binding protein 2	
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318 at	FTE	X81625	eukarvotic translation termination factor 1	C11 protein
3	5			excision renair cross-complementing	excision repair cross-complementing rodent
				rodent repair deficiency, complementation	rodent repair deficiency, complementation repair deficiency, complementation group 3
				group 3 (xeroderma pigmentosum group	(xeroderma pigmentosum group B
654	654 1885 at	FBCC3	M31899		complementing)
				excision repair cross-complementing	
			,	rodent repair deficiency, complementation	-
				group 5 (xeroderma pigmentosum,	-
				complementation group G (Cockayne	
655	2063 at	ERCCS	120046	syndrome))	excision repair protein
				exons 1-4 beyond this clone; match:	
929	656 33734_at	HSD11B1	AL022398	proteins P28845 P50172 P51975 Q29608	
657	657 222_at	EXT1	S79639	exostoses (multiple) 1	exostoses (multiple) 1
658	658 36526 at	EXTL2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
629	659 38809_s_at	EXTL3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
8	660 37729_at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
			*	exportin, tRNA (nuclear export receptor for	
661	38753_at	XPOT	AF039022	(tRNAs)	exportin t
				extracellular matrix protein 2, female	
662	39673 i at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
				extracellular matrix protein 2, female	
	663 39674 r at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
964	35226 at	EYA2	U71207	eyes absent homotog 2 (Drosophila)	Eab1
				family with sequence similarity 8, member	
965	38318_at	FAM8A1	AL050128	A1	
		i	107001	far upstream element (FUSE) binding	ELISE hinding protein 3
999	666 31879_at	FUBP3	U69127	protein 3	I con primarile process

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			_	ase (famesyl	farnesyl diphosphate synthase (tarnesyl
					pyrophosphate synthetase,
•				rase,	dimethylallyltranstransferase,
299	37325_at	FDPS	D14697	\neg	geranyftranstransferase)
				nesyttransferase	
899	34848_at	FDFT1	X69141		farnesyl-diphosphate farnesyltransferase
699	669 1499_at	FNTA	L10413		farnesyl-protein transferase alpha-subunit
				Fas (TNFRSF6)-associated via death	
670	38755_at	FADD	X84709	domain	mediator of receptor induced toxicity
				fasciculation and elongation protein zeta 1	
671	37743_at	FEZ1	09009N	(zygin I)	FEZ1
				fasciculation and elongation protein zeta 2	
672	38651_at	FEZ2	U60061	(zygin li)	FEZ2
				FAT tumor suppressor homolog 1	
673	40454_at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
				fatty-acid-Coenzyme A ligase, long-chain	
674	40082_at	FACL2	D10040	2	long-chain acyl-CoA synthetase
	- 00000	0 0		fatty-acid-Coenzyme A ligase, long-chain	Aryl-CoA symthetese 3
0/2	3388U_at	FACL3	U89053	2	Constitution of the Consti
			•	fatty-acid-Coenzyme A ligase, long-chain	
676	33881_at	FACL3	AA977580	3	
677	33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	37205_at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
679	679 32854_at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
889	32169 at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBX07	AL050254	F-box only protein 7	hypothetical protein
				de formación modia amondo actorio de la constanta de la consta	
				FBRINF; neterogeneous inconduceoptotem homolog: This sequence comes from Eig	
				nomong, this sequence comes month ig.	
Cas	G82 33817 at	0108109	S63912	9, 0.190,102=1 01 mm [mmmm; com com; mmmm] mRNA, 3043 nt].	FBRNP
683	1877 g at	nith	HG1103-HT1103		dinitrogenase reductase
884	684 34678 at	FFR113	AI 096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
3	in Color				
	9 9 9	I	1	FERM, RhoGEF (ARHGEF) and pleckstrin	
685	685 32148_at	FAHP1	AI/U1049	domain protein i (כווטווטוסיטים שפוואפט)	

F1.9 Z)

Ш	ain	antigen		ion protein	wth factor	fibroblast growth factor receptor 1, isoform 1 precursor, fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth	factor receptor 1, isoform 3 precursor;	ilbrobiast growth factor receptor 1, isoloffit 4	precursor, libropiast grown lactor receptor 1. isoform 5 precursor: fibroblast growth	factor receptor 1, isoform 6 precursor;	fibroblast growth factor receptor 1, isoform 7	precursor; fibroblast growth factor receptor	cursor; fibroblast growth	actor receptor 1, isoform 9 precursor	ibronectin 1, isoform 1 preproprotein;	fibronectin 1, isoform 2 preproprotein	ursor	fibronectin leucine rich transmembrane								follistatin isoform FST317 precursor;	
	ferritin heavy chain	fetal Alzheimer antigen	fibrillin	fibroblast activation protein	keratinocyte growth factor	fibroblast growth precursor; fibrob 1, isoform 2 pre	factor receptor	ribroblast grown	precursor, libror	factor receptor	fibroblast growth	precursor; fibrol	1, isoform 8 pre	factor receptor	fibronectin 1, is	fibronectin 1, iso	fibronectin precursor	fibronectin leuc	protein 2	fibulin-1D	UP50	beta-filamin		flavoprotein	Fln29	follistatin isofor	
Q	ferritin, heavy polypeptide 1	fetal Alzheimer antigen	fibrillin 1 (Marfan syndrome)	fibroblast activation protein, alpha	fibroblast growth factor 7 (keratinocyte growth factor)							fibroblast growth factor receptor 1 (fms-	related tyrosine kinase 2, Pfeiffer	syndrome)		fibronectin 1	fibronectin 1	fibronectin leucine rich transmembrane	protein 2	fibulin 1	fibulin 5	filamin B, beta (actin binding protein 278)	FK506 binding protein 9 (63 kD)	flavin containing monooxygenase 3	FLN29 gene product	follistatin precursor; Human follistatin	
C	120941	U05237	X63556	U09278	M60828									M34641		M10905	X02761		AB007865	U01244	AF093118	AF042166	AA487755	M83772	AB007447		
8	FTH1	FALZ	FBN1	FAP	FGF7									FGFR1		FN1	FN1		FLRT2	FBLN1	FBLN5	FLNB	FKBP9	FMO3	FLN29	-	
A	33943 at				1380_at									691 2057_g_at		31720_s_at	31719_at		694 34853_at	695 38026_at	696 39038_at	38078_at	698 38761_s_at	699 40665 at	700 35254 at		
T	989	687	688	689	069									691		692	693		694	695	969	269	698	669	700		

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Total 1927_at FKHL7 AF078096 Honosophial)-like 7; FREAG3; Honosophial Honosophia						
41027_at FKHL7 AF078096 th 36319_at FOXF2 U13220 ft 40570_at FOXO1A AF032885 ft 32542_at FHL1 AF03202 ft 38422_s_at FHL2 U29332 ft 41649_at FHL2 U29332 ft 38422_s_at FHL2 U43318 ft 34997_r_at FZD5 U43318 ft 34472_at FAD5 AB012911 ft 34997_r_at FAD5 AB012911 ft 34472_at FAD5 AB012911 ft 34472_at FAD5 AB012911 ft 40922_at FAG1 L76159 ft 38139_at FAG1 M29877 ft 40480_s_at FW M14333 ft 40480_s_at FYN M14333 gt 2039_s_at FYN M14333 gt 3729g_at GABARAPL AF044671 gt		A	В	3	O	ש
41027_at FKHL7 AF078096 of 36319_at FOXF2 U13220 ff 40570_at FOXO1A AF032885 ff 32542_at FHL1 AF08332 ff 41649_at FHL2 U29332 ff 41814_at FLD5 AB017365 ff 53622_at FRG1 L76159 ff 40022_at FRG1 L76159 ff 40022_at FRMD AB003286 ff 40022_at FRMD AB003286 ff 40022_at FRMD AB003286 ff 40022_at FRMD AB003286 ff 40039_s_at FRMD AB00338 ff 40039_s_at FYN M14333 ff 40039_s_at FYN M14333 ff 60039_s_at GABARAPL AF044671 ff 40039_at GABARAPL AF044671 ff 400329_at GABARAPL AF044671 ff 4003742_at GABARAPL AF044671					forkhead (Drosophila)-like 7; FREAC3;	
41027_at FKHL7 AF078096 th 36319_at FOXF2 U13220 ft 40570_at FOXO3A AF032885 ft 34740_at FOXO3A AF032886 ft 34740_at FOXO3A AF032886 ft 34740_at FOXO3A AF032886 ft 38422_s_at FHL1 AF03318 ft 38422_s_at FHL2 U29332 ft 41649_at FHX AF03117 ft 38472_at FAD5 AB012911 ft 38139_at FRG1 L76159 ft 40022_at FCMD AB012911 ft 40022_at FCMD AB008226 ft 36145_at FH U59309 ft 40480_s_at FYN M14333 ft 3728_at FYN M14333 ft 3728_at GABARAPL1 W28281 ft 3728_at GABARAPL2 AI565760 ft					×-iike	1
41027_at FKHL7 AF078096 6 36319_at FOXF2 U13220 f 40570_at FOXO3A AF032885 f 34740_at FOXO3A AF032886 f 34740_at FOXO3A AF032886 f 34740_at FML1 AF032886 f 38422_s_at FHL2 U29332 f 41649_at FHX AF03117 f 38422_s_at FMX AB012911 f 38222_at FZD5 U43318 f 38139_at FRG1 L76159 f 38139_at FCMD AB017365 f 40022_at FCMD AB008226 f 36145_at FH U59309 f 36145_at FYN M14333 f 32546_at FYN M14333 f 3258_at FYN M14333 f 37298_at GABARAPL1 W28281 f 35785_at						torkhead/winged helix-like transcription
36319_at FOXF2 U13220 If 40570_at FOXO1A AF032885 If 34740_at FOXO3A AF032885 If 34740_at FOXO3A AF0328177 If 38422_s_at FHL2 U28332 If 41649_at FHX AF038177 If 34997_r_at FZD5 U43318 If 34472_at FZD6 AB012911 If 34472_at FZD6 AB017365 If 38923_at FRG1 L76159 If 40022_at FCMD AB008226 If 40480_s_at FW U59309 If 40480_s_at FYN M14333 If 2039_s_at FYN M14333 If 37308_at GABARAPL1 W28281 If 37298_at GABARAPL1 W28281 If 36767_at GALK2 M84443 If 37742_at GALB1 M34423	702	41027_at	FKHL7	AF078096		actor 7
40570_at FOXO1A AF032885 f 324740_at FOXO3A AF032885 f 32542_at FHL1 AF063002 f 38422_s_at FHL2 U29332 f 41649_at FHX AF038177 f 34472_at FZD5 U43318 f 34472_at FZD6 AB012911 f 38923_at FAD5 AB012911 f 38923_at FRG1 L76159 f 40022_at FCMD AB008226 f 40480_s_at FH U59309 f 40480_s_at FYN M14333 f 2039_s_at FYN M14333 g 37308_at GABARAPL M14333 g 37298_at GABARAPL W28281 g 35785_at GABARAPL M84443 g 37742_at GALR M84443 g		36319_at	FOXF2	U13220		forkhead protein FREAC-2
40370_at FOXO3A AF032886 f 34740_at FOXO3A AF032886 f 32542_at FHL1 U29332 f 41649_at FHX AF038177 f 34472_at FZD5 U43318 f 34472_at FZD6 AB012911 f 38923_at FRG1 L76159 f 38139_at FPGT AF017445 f 40022_at FCMD AB008226 f 32546_at FH U59309 f 40480_s_at FYN M14333 f 2039_s_at FYN M14333 f 3720B_at GABARAPL U67784 f 3720B_at GABARAPL W28281 f 35765_at GABARAPL M84443 g 37742_at GALB M84443 g	70.4	40570 01	EOVO4 &	98866034		forkhead protein
25542 at FHL1 AF063002 f 32542 at FHL1 AF063002 f 38422 s. at FHL2 U29332 f 41649 at FHX AF038177 f 3472 at FZD5 U43318 f 38923 at FZD7 AB012911 f 40022 at FZD7 AB017365 f 40022 at FCMD AB017445 f 40480 s. at FCMD AB008226 f 2039 s. at FCMD AB00826 f 37308 at FVN M14333 f 37308 at GPR107 AI888084 f 37298 at GABARAPL1 W28281 g 35785 at GABARAPL1 W28281 g 35785 at GABARAPL2 AI565760 g 37729 at GABARAPL2 AI565760 g 3772 at GAL81 GALB1 M34423	300	34740 04	EOXO3A	A Engage		forkhead protein
32242_at FHL2 U29332 f 38422_s_at FHL2 U29332 f 41649_at FHX AF038177 f 34997_r_at FZD5 U43318 f 34472_at FZD6 AB012911 f 33222_at FZD7 AB017365 f 38923_at FZD7 AF017445 f 41814_at FDGT AF017445 f 40022_at FCMD AB008226 f 32546_at FYN M14333 f 32546_at GABARAPL1 W28281 f 35788_at GABARAPL1 W28281 f 35785_at GABARAPL1 W28281 f 35767_at GABARAPL2 AI565760 f 37742_at GALB1 M34423		205.40	- COVO	00000 V	-	I IM protein SI IMMER
2692_ s. at FRICK Oceanor 41649_ at FHX AF038177 43997_r. at FZD5 U43318 3472_ at FZD6 AB012911 33222_ at FZD7 AB017365 38923_ at FRG1 L76159 38139_ at FPGT AF017445 40022_ at FUCA1 M29877 40022_ at FCMD AB008226 32546_ at FH U59309 40480_ s. at FYN M14333 2039_ s. at FYN M14333 37308_ at GABARAP U67784 37308_ at GABARAP AF044671 35785_ at GABARAP AF044671	3 3	32342 BI		AFOOSOOZ	four and a balf I'M domains 9	heart protein
41649_at FHA AFU36177 41649_at FZD5 U43318 FZD6 AB012911 FZD6 AB012911 FZD6 AB017365 S3222_at FZD7 AFG1 L76159 FPGT AF017445 FPGT AF01745 FPGT AF01745 FPGT AF01745 FPGT AF01745 FPGT AF01742 FPGT AF044671 FPK AF04443 FPK FPK	2	38422 S at	בובו	029332	FOVE SINGLE LINE COLISINS &	
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It FZD6 AB012911 f It FZD7 AB017365 f It FRG1 L76159 f It FPGT AF017445 f It FPGT AF017445 f It FCM1 M29877 f It FCMD AB008226 f It FCMD AB008226 f It FM U51586 f It FYN M14333 f It RDC1 U67784 f It GABARAP AF044671 f It GABARAP AF044671 f It GABARAPL W28281 f It GALK2 M84443 f It GLB1 M34423 f	709	34997_r_at	FZD5	U43318	frizzled'homolog 5 (Drosophila)	transmembrane receptor
at FZD7 AB017365 if FRG1 L76159 it FRG1 L76159 it FPGT AF017445 it FPGT AF017445 it FPGT AB008226 at FYN M14333 at FYN M14333 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GABI	710	34472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
at FRG1 L76159 II II FPGT AF017445 II II FUCA1 M29877 II II FCMD AB008226 II FH U59309 II FH U59309 II FH U59309 II FYN M14333 II FYN M14333 II GABARAP AF044671 II GABARAPL AF044671	711	33222 at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
at FPGT AF017445 is FUCA1 M29877 is FUCA1 M29877 is FUCA1 M29877 is FUCA1 M29877 is FUCA1 L59309 is FYN M14333 at FYN M14333 at FYN M14333 at GABARAP AF044671 at GABARAPL W28281 at GABARAPL M28281 at GABARAPL M28281 at GABARAPL M28281 at GABARAPL M28281 at GABARAPL M34433 at GALK2 M84443	712	38923 at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
at FUCA1 M29877 i at FCMD AB008226 at FH U59309 at SIAHBP1 U51586 at FYN M14333 at FYN M14333 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GALR1 M34423	713	38139 at	FPGT	AF017445	fucose-1-phosphate guanylyttransferase	GDP-L-fucose pyrophosphorylase
at FCMD AB008226 at FH U59309 at SIAHBP1 U51586 at SIAHBP1 U51586 at FYN M14333 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GALB1	714	41814 at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
at FCMD AB008226 at FH U59309 at SIAHBP1 U51586 at FYN M14333 at GPR107 AI88084 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GALK2					Fukuyama type congenital muscular	
at FH U59309 at SIAHBP1 U51586 at FYN M14333 at FYN M14333 at GPR107 AI88084 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GALB1	715	40022_at	FCMD	AB008226	dystrophy (fukutin)	fukutin
at SIAHBP1 U51586 at FYN M14333 at FYN M14333 at GPR107 AI888084 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GABARAPL2 M84443 at GALK2 M84443	716	32546_at	표	U59309	fumarate hydratase	fumarase precursor
at FYN M14333 at FYN M14333 at RDC1 U67784 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 Al565760 at GALK2 M84443 at GALB1 M34423	747	25145 04	SIAURD1	1151586	fuse-hinding protein-interacting repressor	siah bindina protein 1
at FYN M14333 at FYN M14333 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 Al565760 at GABK2 M84443 at GALK2 M34443		30145	I JOUNIO	200100	and the firm and the state of t	
at FYN M14333 at RDC1 U67784 at GPR107 AI888084 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GLB1 M34423	718	40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
at RDC1 U67784 at GPR107 AI888084 at GABARAP AF044671 at GABARAPL1 W28281 at GABARAPL2 AI565760 at GALK2 M84443 at GLB1 M34423	719	2039 s. at	Į.	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
at GPR107 AI888084 G protein-coupled receptor 107 at GABARAP AF044671 GABA(A) receptor-associated protein like at GABARAPL1 W28281 1 at GABARAPL2 AI565760 2 at GALK2 M84443 galactokinase 2 at GLB1 M34423 galactosidase, beta 1	720	34288 at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
at GABARAP AF044671 GABA(A) receptor-associated protein like at GABARAPL1 W28281 1 at GABARAPL2 A1565760 2 at GALK2 M84443 galactokinase 2 at GLB1 M34423 galactosidase, beta 1	721	37308 at	GPR107	AI888084	G protein-coupled receptor 107	
at GABARAPL1 W28281 1 at GABARAPL2 A1565760 2 at GALK2 M84443 galactokinase 2 at GLB1 M34423 galactosidase, beta 1	722	37298 at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
GABARAPL1 W28281 1 GABARAPL2 Al565760 2 GALK2 M84443 galactokinase 2 GLB1 M34423 galactosidase, beta 1					GABA(A) receptor-associated protein like	
GABARAPL2 Al565760 2 GALK2 M84443 galactokinase 2 GLB1 M34423 galactosidase, beta 1	723		GABARAPL1	W28281	1	
GABARAPI.2 Al565760 2 GALK2 M84443 galactokinase 2 GLB1 M34423 galactosidase, beta 1					GABA(A) receptor-associated protein-like	
GALK2 M84443 galactokinase 2 GLB1 M34423 galactosidase, beta 1	724	35767_at	GABARAPL2	AI565760	2	
GLB1 M34423 galactosidase, beta 1	725	37825_at	GALK2	M84443	galactokinase 2	galactokinase
	726	37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

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				ase,	
727	37263_at	GGH	U55206		human gamma-glutamyi hydrolase
				rotein, alpha 1, 43kD	
728	32531_at	GJA1	X52947		connexin 43
				GCN1 general control of amino-acid	
729	36603_at	GCN1L1	D86973	synthesis 1-like 1 (yeast)	
730	35307_at	GDI2	Y13286	1.2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811		coding sequence
				gene with multiple splice variants near HD	gene with multiple splice variants near HD
732	32180 s at	RES4-22	AB000461		locus on 4p16.3
					Bruton's tyrosine kinase-associated protein-
733	466 at	GTF2	U77948	general transcription factor II, i	135
734	734 35450 s at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010_at	GTF2A2	AI203737	subunit)	
				general transcription factor IIA, 2 (12kD	
736	869 at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kD)	TFIIE-alpha
				general transcription factor IIE,	
738	37295_at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kD)	TFIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
			*	general transcription factor IIH,	
740	740 40754 at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 KD subunit
741	36188 at	GTE3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742	35296 at	GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	763 at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
4		GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	or the state of th
745	745 32643_at	GBE1	L07956	(All	1,4-alpha-glucari Dranciniig enzyme
746	746 34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

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				glucosaminyl (N-acetyl) transferase 1,	
				COIR Z (DBIB-1,0-IV-	heta-1 6-N-acetydolycosaminyltransferase
/4/		GCNII		acetylgiucosarfilliyirialisterase/	Dolla-1,0-14-acetylgidocetimiymaricion
748		GPI	K03515	glucose phosphate isomerase	neuroleukin
749		GRP58	Z49835	glucose regulated protein, 58kD	protein disultide isomerase
750	38042 at	GePD	X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751	33308 at	GUSB	M15182	glucuronidase, beta	glucuronidase, beta
752		GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753		GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
				glutamate-ammonia ligase (glutamine	;
754	40522_at	GLUL	X59834	synthase)	glutamateammonia ligase
				glutamate-cysteine ligase, catalytic	
755	31850_at	GCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
				glutamic-oxaloacetic transaminase 1,	
757	35343_at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
				glutamic-oxaloacetic transaminase 2,	
				mitochondrial (aspartate aminotransferase	_
758	758 40764_at	GOT2	M22632	2)	_
759	34719_at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
760	32626_at	GFPT1	M90516	transaminase 1	amidotransferase
				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640_at	GFPT2	AB016789	transaminase 2	amidotransferase
762	762 35300_at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutaminyl-tRNA synthetase
763	763 34311_at	GLRX	X76648	glutaredoxin (thiottransferase)	glutaredoxin
764	764 37033 s at	GPX1	X13710	glutathione peroxidase 1	
765	765 40508 at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
766	38386 r at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824_at	GSTTLp28	U90313	transferase omega	glutathione-S-transferase homolog
				glyceraldehyde-3-phosphate	
768	AFFX-HUMGAP(GAPD	(GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
760	3500% c at	CAPD	1134995	głyceraldehyde-3-phosphate dehydrogenase	
3	133303 S C	0	20000		

1						
•	∢	60	ပ	Q	'n	
130	770 AFFX-HUMGAP(GAPD		M33197	głyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase	
11	39392 at	GNPAT	AJ002190	glyceronephosphate O-acyltransferase	dihydroxyacetone phosphate acytransferase	
				glycine cleavage system protein H	glycine cleavage system protein H	
772	37357_at	ВСЅН	D00723	(aminomethyl carrier)	(aminomethyl carrier)	
73	773 39665 at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit	
774	74 40645 at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase	
775		GYG	U31525	glycogenin	glycogenin	
776	1	GYG2	U94362	glycogenin 2	glycogenin-2 alpha	
111	1	GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb	
778	37251_s_at	GPM6B	AF016004	glycoprotein M6B		
779	33126_at	AD-017	L13435	glycosytransferase AD-017		
780	780 36582 g at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase	
78	36581 at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase	
782	782 36201 at	GL01	D13315	głyoxalase I	lactoyl glutathione lyase	
				glyoxylate reductase/hydroxypyruvate		
783	40133 s at	GRHPR	W28944	reductase		
					guanine nucleotide binding protein (G	
					protein), alpha stimulating activity	
					polypeptide 1, isoform alpha-s-2;	
					neuroendocrine secretory protein 55;	
					guanine nucleotide binding protein (G	
					protein), alpha stimulating activity	
					polypeptide 1, isoform XL-alpha-s; guanine	
					nucleotide binding protein (G protein), alpha	
					stimulating activity polypeptide 1, isoform	
784	784 37449 i at	GNAS	X04409	GNAS complex locus	alpha-s-1	
785	785 37448 s at	GNAS	X56009	GNAS complex locus	alpha subunit of GsGTP binding protein	

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					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
			•		polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					quanine nucleotide binding protein (G
		-			protein), alpha stimulating activity
					nother still a softem VI slabers allenine
					polypeptide 1, Isoloitii AL-aipila-s, guainile
					nucleotide binding protein (G protein), alpha
					stimulating activity polypeptide 1, isoform
786	37450 r at	GNAS	X04409	GNAS complex locus	alpha-s-1
					ADP-ribosylation factor binding protein 3,
				golgi associated, gamma adaptin ear	isoform short; ADP-ribosylation factor
787	37959 at	GGA3	De3876		binding protein 3, isoform long
788	788 32713 at	GOLGA1	U51587	y a, 1	Golgi complex autoantigen golgin-97
789	32150 at	GOLGA4	X82834	golgi autoantigen, golgin subfamily a, 4	256 kD golgin
790	36827	GOLPH1	62	golgi phosphoprotein 1	unknown protein
791	38620 at	GOSBo	44905543	noloi SNAP recentor complex member 2	
				20.00	putative 13 S Golgi transport complex 90kD
792	34737_at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	subunit brain-specific isoform
793	41767_r_at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950_at	HSGP25L2G	X90872	gp25L2 protein	
				GPAA1P anchor attachment protein 1	glycosylphosphatidylinositol anchor
795	36035_at	GPAA1	AB002135	homolog (yeast)	attachment 1 (GPAA1)
962	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
				growth arrest and DNA-damage-inducible,	growth arrest and DNA-damage-inducible, growth arrest and DNA-damage-inducible
797	39822_s_at	GADD45B	AF078077	beta	protein GADD45beta
				growth arrest and DNA-damage-inducible,	
798	798 39821_s_at	GADD45B	N95168	beta	_
799	799 661_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
န္ထ	800 41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801	37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802	802 1598 g at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
				growth hormone inducible transmembrane	
8	804 41752 at	GHITM	W28190	protein	

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	∢	80	ပ	D	
88	160030 at	GHR	X06562	growth hormone receptor	growth hormone receptor
	40113 at	55	D87119		GS3955
				stein overexpressed in	
807	37279_at	GEM	U10550		Gem
				guanine nucleotide binding protein (G	
				a inhibiting activity	
808	33809_at	GNA11	AL049933		hypothetical protein
				ein (G	guanine nucleotide binding protein (G
					protein), alpha inhibiting activity polypeptide
808	37307_at	GNAI2	X04828		2
				<u>၅</u>	
810	34608_at	GNB2L1	M24194		MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	35272_at		AI541042	protein), gamma 5	
812		GNG10	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	35735_at	GBP1	M55542	inducible, 67kD	guanylate binding protein isoform l
814	814 905 at		L76200	guanylate kinase 1	guanylate kinase
815	32249 at		M65292	H factor (complement)-like 1	factor H homologue
816	32250 at		X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	31673_s_at	S	n regu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
910		CD63: MI A1: ME	I: ME4X62654	H sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
2			2000		ATP synthase, H+ transporting,
				H.sapiens gene for mitochondrial ATP	mitochondrial F0 complex, subunit c (subunit
820	820 38076_at	P1 gene for c subt	c sub(X69907	synthase c subunit (P1 form).	9), isoform 1
3	0.00	33 - 1	V67300	H ceniene den for ribosomal protein S6	ribosomal protein S6
8	30120 at	00 dill	200700	יויימקונונים אתוכן נכו נוסיבונים בייניים ביינים ביינים בייניים בייניים ביינים ביינים ביינים ביינים ביינים ביינים בייניים ביינים ביינים ביינים ביינים ביינים ביינים ביינים ביינים בייניים ביינים ביינים ביינים ביינים ביינים ביינים ביינים ביינים בייניים ביינים ביינים ביינים ביינים ביינים ביינים ביינים ביינים בייני	
822	34646_at	rpS7	225749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
S	24540 0 04	200	748950	H seniens hH3 3B gene for histone H3 3	histone H3.3
823	823 31510 S BI	การ.วธ	008047	I I. Sapieira III 10: OD general mesene i co.c.	

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	A	В	၁	O	ш
				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	B esenencypydeb esenen
824	33820_g_at	dub	X13/94	cus).	laciale deliyalogellase D
				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	
825	33819_at	IdhB	X13794	CDS).	actate dehydrogenase B
		ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
				H.sapiens mRNA for PIBF1 protein,	
827	36012_at	PIBF1	Y09631	complete.	PIBF1 protein
				H.sapiens mRNA for tre oncogene (clone	
828	31526_f_at	tre	X63547	213).	oncogene
829	829 40471_at	PXF	Y09048	H.sapiens PxF gene.	PxF protein
				H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
830	37038_at	PXMP1	X83467	joined CDS).	protein
				H.sapiens rpS8 gene for ribosomal protein	
831	31583_at	rpS8	X67247	S8.	ribosomal protein S8
				H.sapiens SPHAR gene for cyclin-related	
832	1685_at	SPHAR	X82554	protein.	S-phase response (cyclin-related)
000	20107 01	t accopano	248100	Heaniene syndecap-1 gene (exons 2-5)	syndecan 1
3 8	834 37310 at	JIIDA	X02419	H sapiens uPA dene.	urokinase-plasminogen activator
3 8	03E 37300 at	10 V CT	1 19055-1	H2A histone family member L	histone 2A-like protein
38	39337 at	H2AF7	M37583	H2A histone family, member Z	H2A histone family, member Z
32	33458 r at	H2BFL	AI688098	H2B histone family, member L	
838	40818 at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839	839 254 at	H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
8	840 39969 at	H4FG	AA255502	H4 histone family, member G	
2	32591 at	HCDI	AI494623	HCDI protein	
842	35215	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
				heat shock 10kD protein 1 (chaperonin	
843	843 39353_at	HSPE1	AI912041	10)	
\$	844 37720 at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
				heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
845	36614_at	HSPA5	X87949	regulated protein, 78kD)	regulated protein, 78kD)
978	846 41510 c at	HSPA9B	115189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
3	200	200			



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847	32316_s_at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
848	33984_at	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906 at	HSBP1	AF068754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
					turnor necrosis factor type 1 receptor
850	1468_at	TRAP1	U12595	heat shock protein 75	associated protein
851	38054_at	HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
				hepatoma-derived growth factor (high-	
852	38779_r_at	HDGF	D16431	mobility group protein 1-like)	hepatoma-derived GF
853	35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
				heterogeneous nuclear ribonucleoprotein	
854	38094_at	HNRPAB	M65028	A/B	hnRNP type A/B protein
				heterogeneous nuclear ribonucleoprotein	
855	37334_at	HNRPAO	U23803	A0	heterogeneous ribonucleoprotein A0
				heterogeneous nuclear ribonucleoprotein	
856	34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
				heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857	36654_s_at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
					heterogeneous nuclear ribonucleoprotein C,
			!	heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
858	33666_at	HNRPC	M16342	C (C1/C2)	ribonucieoprotein C, isotorm a
				heterogeneous nuclear ribonucleoprotein	
				D (AU-rich element RNA binding protein 1,	
829	38016_at	HNRPD	M94630	37kD)	DNA-binding protein
			-	heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
L				heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
					heterogeneous nuclear ribonucleoprotein
862	41283 at	HOUNH	AF052131	neterogeneous nuclear ribonucleoprotein H3 (2H9)	rischen a. neterogeneous mucean ribonucleoprotein H3. isoform b
	in			heterodeneous nuclear ribonucleoprotein	
863	863 40836_s_at	HNRPH3	W26677	H3 (2H9)	

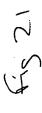
H3 21

	V	ω	ပ	D	
				eterogeneous nuclear ribonucleoprotein	
864	39415_at	HNRPK	X72727		transformation upregulated nuclear protein
3	, 0000			heterogeneous nuclear ribonucleoprotein	
ğ	35201_at	HNHPL	X16135		neterogeneous fluctear fiboliucieopioteiii c
866	37717 at	HNRPM	L03532	neterogeneous nuclear ribonucleoprotein M	M4 protein
867	39792	HNRPR	AF000364	heterogeneous nuclear ribonucleoprotein R	heterogeneous nuclear ribonucleoprotein R
			007	heterogeneous nuclear ribonucleoprotein	ha BND II arotain
869	32818 at	HXB	X78565	hexabrachion (tenascin C, cytotactin)	human tenascin-C
870	39827	RTP801	AA522530	HIF-1 responsive RTP801	
871	31504	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	high density lipoprotein binding protein
872	872 32220_at	HMG1	D63874	high-mobility group (nonhistone chromosomal) protein 1	HMG-1
873	306 s at	HMG14	J02621	high-mobility group (nonhistone chromosomal) protein 14	high-mobility group (nonhistone chromosomal) protein 14
874		HMG17L3	Al347088	high-mobility group (nonhistone chromosomal) protein 17-like 3	
1		OND	Xenen 4	high-mobility group (nonhistone	high-mobility group (nonhistone
0/0 876	38843 at	HMG211	A1 079310	high-mobility group protein 2-like 1	hypothetical protein
877		HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009 at	HINT.	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	3423	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
88	41855	HAT1	AF030424	histone acetyftransferase 1	histone acetyltransferase 1
881	38771	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	34368	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
88 83	38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
88	1 39046_at	H2AV	AL049324	histone H2A.F/Z variant	
88	39092_at	H2AV	AW007731	histone H2A.F/Z variant	
988	38824_at	HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	7 40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein
				(

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888	39809_at	HBP1	AF019214		HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWVSNF-related	
				BAF complexes; contains a proline-rich N-	
				terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
				sapiens BAF57 (BAF57) gene, complete	
889	33828_at	BAF57	AF035262	cds.	BAF57
				HMT1 hnRNP methyltransferase-like 1 (S.	
890	39348_at	HRMT1L1	X99209		arginine methyltransferase
				NP methyltransferase-like 2 (S.	
891	32825_at	HRMT1L2	Y10805	cerevisíae)	arginine methyttransferase
				HNRNP Core Protein A1 LIKE	
		-		pseudogene; match: proteins P04256	
				Q28521 P49312 P09651 P51991 P51992	
892	31463_s_at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787		holocytochrome c-type synthetase
894	39610_at	HOXB2	X16665		hотео box B2
895	40674 s at	HOXCe	S82986	homeo box C6	homeo box C6
				4	
988	896 38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3 homer-3	nomer-3
_			-	Homo sapiens (clone f17252) ubiquinol	
				cytochrome c reductase Rieske iron-	
897	897 34401_at	UQCRFS1	L32977	sulphur protein (UQCRFS1) gene, exon 2. Rieske Fe-S protein	Rieske Fe-S protein
				Homo sapiens (clone FFE-7) type II	
				inosine monophosphate dehydrogenase	
				(IMPDH2) gene, exons 1-13, complete	inosine monophosphate denydrogenase type
888	36624_at	IMPDH2	L33842	cds.	
				Homo sapiens aldehyde oxidase (AOX1)	
899	37599_at	AOX1	AF017060	gene, exon 35 and complete cds.	aldehyde oxidase
[8	001400	V (414	A EOE 4197	Homo sapiens alpha NAC mRNA,	alpha NAC
3	900 39740_g_at	NACA	APU3410/	icompiere cas.	

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	Α	В	ပ	U	1
901	39739 at	NACA	AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
T					•
905	902 41154 r at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903	903 41153 f at	CTNNA1	AF102803	Homo sapiens alphat-catenin (CTNNA1) gene. exon 18 and complete cds.	alphaE-catenin
	i.				
				Homo sapiens cDNA FLJ10784 fis, clone	
				NT2RP4000448, highly similar to Homo	
904	39324_at		AL050078	sapiens mRNA; cDNA DKFZp566G0746	
				Homo sapiens cDNA FLJ13267 fis, clone	
905	35310_at		D45288	OVARC1000964	
				Homo sapiens cDNA FLJ13553 fis, clone	
906	35754_at		L40391	PLACE1007454	
				Homo sapiens cDNA FLJ14821 fis, clone	
				OVARC1000556, highly similar to	
				RIBOSOMAL PROTEIN S6 KINASE II	
907	33325_at		W26667	ALPHA 2 (EC 2.7.1)	
				Homo sapiens cDNA FLJ25016 fis, clone	
908	38102_at		W28575	CBL01574	
9	44050 0 04		A1082043	Homo sapiens cDNA FLJ30436 fis, clone	
200	41533 3 9		CLOCOEL V	Homo saniens CDNA FI J30544 fis. clone	
910	39162 at		AA156987	BRAWH2001412	
				Homo sapiens cDNA FLJ31959 fis, clone	
911	41807_at		AL040137	NT2RP7007422	•
				Homo sapiens cDNA FLJ33151 fis, clone	
912	38643_at		W87466	UTERU2000263	
				Homo sapiens cDNA: FLJ21175 fis, clone	
913	34246_at		AA418437	CAS11071	
914	914 40813 at		A1768188	Homo sapiens cDNA: FLJ21243 fis, clone COL01164	



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				Homo sapiens cDNA: FLJ21449 fis, clone COL04483, highly similar to AF010235 Homo sapiens mRNA from chromosome	
915	915 40923_at		AA290994	5q31-33 region	
916	38993 r at		W27522	Homo sapiens cDNA: FLJ21904 fts, clone HFP03585	
3	15 - COOO		11 51 055		
				Homo sapiens cDNA: FLJ21927 fis, clone	
	•			HEP04178, highly similar to HSU90909	
917	38093_at		08060 0	Human clone 23722 mRNA sequence	
				Homo sapiens cDNA: FLJ22642 fis, clone	
918	918 34840_at		AI700633	HSI06970	
				Homo sapiens cDNA: FLJ23324 fis, clone	
				HEP12482, highly similar to	
				HUMMYOHCB Human nonmuscle myosin smooth muscle myosin heavy chain isoform	nooth muscle myosin heavy chain isoform
919	919 32838_at	smooth muscle m	m\S67247	heavy chain-B (MYH10) mRNA	SMemb
				Homo sapiens cervical cancer suppressor-	
920	920 33737 f. at		AI871359	1 mRNA, complete cds	
				Homo sapiens clone 23570 mRNA	
921	921 41663_at	_	AF038202	sednence	
				Homo sapiens clone 23700 mRNA	
922	922 36815_at		AF038185	sequence	
				Homo sapiens clone 23718 mRNA	
923	923 41841_at		AF052138	sednence	
				Homo sapiens clone 23903 mRNA	
924	37794_at		AF035281	sednence	
				Homo sapiens clone 23938 mRNA	
925	38764_at		AF007142	sednence	
				Homo sapiens clone 24416 mRNA	
956	35342_at		AF052159	sednence	
				Homo sapiens clone 24630 mRNA	
927	31867_at		AF052174	sequence	
				Homo sapiens clone 24674 mRNA	
928	928 36758_at		AF070578	sednence	
				Homo sapiens clone 24790 mRNA	
929	929 41864_at		AF052181	sednence	

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				Homo sapiens clone FBD3 Cri-du-chat	
930	38070_at		AL080234	critical region mRNA	
				Homo sapiens cofactor A protein mRNA,	
931	34773_at	TBCA /	AF038952	complete cds.	cofactor A protein
				Homo sapiens cytochrome c oxidase	
				subunit IV precursor (COX4) gene,	
				nuclear gene encoding mitochondrial	
932	932 39027 at	COX4	AF017115		cytochrome c oxidase subunit IV precursor
				pseudogene, S4	
933	40878_f_at	D15F37	AF041081	allele, mRNA sequence.	
				Homo sapiens deoxycytidylate deaminase	
934	631_g_at	DCTD	L39874	$\overline{}$	deóxycytidylate deaminase
				Homo sapiens deoxycytidylate deaminase	
935	935 630_at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
				Homo sapiens DNA for	
				galactocerebrosidase, exon 17 and	
936	33936_at	GALC	D86181		galactocerebrosidase
				Homo sapiens F1Fo-ATPase synthase f	
937	40134_at	ATP5J2; ATP5JL; AF047436	AF047436	subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
				Homo sapiens gene for LD78 alpha	
938	938 36103_at	SCYA3; LD78ALP	ALP D90144	precursor, complete cds.	LD78 alpha precursor
				Homo sapiens GOS28/P28 protein	
939	939 40725_at	GOSR1; P28; GS2	GS2AF047438	mRNA, complete cds.	GOS28/P28 protein
				Homo sapiens GTP binding protein	
940	38708_at	RAN; TC4; ARA24	RA24AF054183	mRNA, complete cds.	GTP binding protein
				Homo sapiens H beta 58 homolog mRNA,	
941	35790_at	VPS26; HB58; HB AF054179	AF054179	complete cds.	H beta 58 homolog
				Homo sapiens histone macroH2A1.2	
942	942 36576 at	H2AFY; H2A.y; H2	.y; H2AF054174	mRNA, complete cds.	histone macroH2A1.2
				Homo sapiens insulin induced protein 1	
943	35303_at	INSIG1	U96876	(INSIG1) gene, complete cds.	insulin induced protein 1
				Homo sapiens interferon-gamma receptor	
			!	alpha chain gene, exon / and complete	richo chalo actuados comuntos actual de la comunicación de la comunica
9 4	944 1038_s_at	interferon-gamma U19247	U19247	cds.	interreron-gamma receptor aipina citatii

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945	895_at	- JIW	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. macrophage migration inhibitory factor	macrophage migration inhibitory factor
				Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene	
				encoding mitochondrial protein, complete	
946	38967_at	C14orf2; MP68; P	8; P(AF054175	cds.	mitochondrial proteolipid 68MP homolog
7,7	17 10010			Homo sapiens mRNA for Hmob33 protein, 2' udenciated region	
947	31881_at	11139	55	Homo sapiens mRNA for TL132	TL132 protein
2	-1-ai	70111		Long confere mONA full lands incort	
949	38786_at		AL079279	Homo sapiens melva lui lengin inseri cDNA clone EUROIMAGE 248114	
				Homo sapiens mRNA; cDNA	
				DKFZp434A012 (from clone	
950	950 33418_at		AL096752	DKFZp434A012)	
				Homo sapiens mRNA; cDNA	
				DKFZp434B102 (from clone	
951	38630_at		AL080192	DKFZp434B102)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M162 (from clone	
952	952 41529 g at		W72239	DKFZp434M162)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M245 (from clone	
953	36451_at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
	<u>.</u>			DKFZp564A026 (from clone	
954	36821_at	DKFZp564A026	AL050367	DKFZp564A026)	hypothetical protein
				Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366_at		AL049969	DKFZp564A072)	
L				Homo sapiens mRNA; cDNA	
				DKFZp564B222 (from clone	
926	39506_at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564D016 (from clone	
957	957 39748 at		AL050021	DKF2p364U016)	

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				Homo sapiens mRNA; cDNA	
				DKFZp564D156 (from clone	
958	958 38357_at		AL049321	DKFZp564D156)	
				Homo sapiens mRNA; cDNA	
				DKFZp564E122 (from clone	
959	959 33716_at		N95443	DKFZp564E122)	
		٠		Homo sapiens mRNA; cDNA	
7,70				DKFZp564E2222 (from clone	
960	960 35301_at		AL049941	DKFZp564E2222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564F053 (from clone	
961	961 35842 at		AL049265	DKFZp564F053)	
				Homo sapiens mRNA; cDNA	
				DKFZp564F112 (from clone	
962	40552 s at		AL049987	DKFZp564F112)	
				Homo sapiens mRNA; cDNA	
				DKFZp564J0323 (from clone	
963	39170_at		AL049957	DKFZp564J0323)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L0822 (from clone	
964	34303_at		AL049949	DKFZp564L0822)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L222 (from clone	
965	36509_at		AL049998	DKFZp564L222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564P0823 (from clone	
996	966 40353_at		AL049962	DKFZp564P0823)	
				Homo sapiens mRNA; cDNA	
				DKFZp566J2146 (from clone	
296	35290_at		AL050081	DKFZp566J2146)	
				Homo sapiens mRNA; cDNA	
				DKFZp586B0918 (from clone	
896	38079_at		AL049367	DKFZp586B0918)	
				Homo sapiens mRNA; cDNA	
				DKFZp586B1922 (from clone	
696	969 32195_at		AL049450	DKFZp586B1922)	

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				Homo sapiens mRNA; cDNA	
				DKFZp586C1019 (from clone	
970	39379_at		AL049397	DKFZp586C1019)	
				Homo sapiens mRNA; cDNA	
				DKFZp586C1723 (from clone	
971	37575_at		AL050192	DKFZp586C1723)	
				Homo sapiens mRNA; cDNA	
				DKFZp586F071 (from clone	
972	34283_at		AL050125	DKFZp586F071)	
				Homo sapiens mRNA; cDNA	
				DKFZp586G1922 (from clone	
973	39600_at		AL080110	DKFZp586G1922)	
				Homo sapiens mRNA; cDNA	
				DKFZp586G2222 (from clone	
974	974 34752_at		AL080111	DKFZp586G2222)	
				Homo sapiens mRNA; cDNA	
				DKFZp586l0523 (from clone	
975	39103_s_at		H98552	DKFZp586l0523)	
				Homo sapiens mRNA; cDNA	
				DKFZp58611823 (from clone	
926	36092_at		AL080213	DKFZp586l1823)	
				Homo sapiens mRNA; cDNA	
-				DKFZp586K1123 (from clone	
977	35187_at		AL080216	DKFZp586K1123)	
				Homo sapiens mRNA; cDNA	
				DKFZp586K2322 (from clone	
978	35363_at	DDX17	AL080113	DKFZp586K2322)	
L				Homo sapiens mRNA; cDNA	
				DKFZp586M2022 (from clone	
979	41013 at	-	AL080114	DKFZp586M2022)	
				Homo sapiens mRNA; cDNA	
				DKFZp586N012 (from clone	
980	41690_at		AL049471	DKFZp586N012)	
				Homo sapiens mRNA; cDNA	
				DKFZp586N1720 (from clone	
981	981 40349_at		AL049442	DKFZp586N1720)	

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Γ				Homo sapiens mRNA; cDNA	
				DKFZp586N1918 (from clone	
982	32672_at		AL049387	DKFZp586N1918)	
				me b5	
983	36668_at	DIA1	M28713	reductase (b5R) gene, exon 9.	NADH-cytochrome b5 reductase
				Homo sapiens nucleophosmin	
				phosphoprotein (NPM) gene, 3' flanking	
984	38542 at		U89322	sequence.	
				Homo sapiens p18 protein mRNA,	
985	40587 s at	EEF1E1; P18	AF054186	complete cds.	p18 protein
				Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	41448_at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
				Homo sapiens prion protein (PrP) gene,	•
987	36159_s_at	PrP	U29185	complete cds.	prion protein
				Homo sapiens putative dienoyl-CoA	
			-	isomerase (ECH1) gene, exons 7-10, and	
988	988 32756_at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
989	35824_at	RP58	AJ223321	CDS.	RP58 protein
				Homo sapiens Sec61 gamma mRNA,	
990	39169_at	SEC61G	AF054184	complete cds.	Sec61 gamma
				eue,	signal transducer and activator of
991	991 41222_at	STAT6	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	
992	38817_at	SPAG7; ACRP; F\$AF047437	AF047437	mRNA, complete cds.	sperm acrosomal protein
				Homo sapiens splicing factor,	
				arginine/serine-rich 12 (SFRS12) mRNA,	
993	36033_at		AL049309	complete cds	
				Homo sapiens thymosin beta-10 gene,	
994	31481_s_at	TMSB10	M92383	3'end.	thymosin beta-10
				Homo sapiens TIMP gene for tissue	
995	995 1693 s at	TIMP	D11139	inhibitor of metalloproteinases, partial cds. itissue inhibitor of metalloproteinases	tissue inhibitor of metalloproteinases

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				Homo sapiens transaldolase-related	
				protein gene, exons 3-8 and complete	
966	996 37311_at	TALDO1; TAL-H; AF010400		cds.	transaldolase-related protein
				Homo sapiens translation initiation factor	
997	32229 at	EIF4EL3: 4EHP: 4	HP: 4 AF038957	4e mRNA, complete cds.	translation initiation factor 4e
		UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
	32153 s at	UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
8	38372 at		U66042	Homo sapiens unknown mRNA	
				Homo sapiens vacuolar H(+)-ATPase	
1001	1001 38814_at	ATP6V1G1; ATP6	ATP6AF038954	subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
				Homo sapiens vesicle trafficking protein	
1002	1002 41597_s_at	SEC22L1; SEC22	EC22 AF047442	sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003	1003 34957_at	XSL	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662 at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312 at		AL050002	mRNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388 at		AL080223	mRNA, partial cds	
	ı			Homo sapiens, clone IMAGE:4132509,	
1007	1007 38676 at	*	AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
108	1008 40238 at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
100	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
1010	1010 38650 at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4183312,	
101	1011 1396 at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	
101	1012 40432 at		AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	
				related protein, clone MGC:9246	
101	1013 36130_f_at	MT1E	R92331	IMAGE:3892441, mHNA, complete cds	

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				Homo sapiens, Similar to serine (or	i
				cysteine) proteinase inhibitor, clade E	
	•			(nexin, plasminogen activator inhibitor	
				type 1), member 2, clone MGC:23129	
1014	1014 41246_at		AI743134	IMAGE:4578406, mRNA, complete cds	
				Homo sapiens, similar to unknown, clone	
				MGC:39325 IMAGE:5440447, mRNA,	
1015	1015 41533 at		U79298		
				-inducible, endoplasmic	homocysteine-inducible, endoplasmic
				0	reticulum stress-inducible, ubiquitin-like
1016	1016 39733_at	HERPUD1	AF055001		domain member 1
				homolog of yeast mutL gene; Human	
				<u>.</u>	
1017	1017 525 g at	hPMS1	U13695		postmeiotic segregation 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1018	1018 32545_r_at	HSU-1	L12535		ras suppressor protein 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1019	1019 32544 s_at	RSU-1	L12535	cds.	ras suppressor protein 1
1020	1020 39800 s at	HAX1	U68566	HS1 binding protein	HAX-1
				Human 2,4-dienoyl-CoA reductase gene,	
1021	1021 38104_at	DECR1; NADPH	U78302		2,4-dienoyl-CoA reductase
L				Human alcohol dehydrogenase chi	
			7.	polypeptide (ADH5) gene exons 8-9,	
1022	1022 37708 r at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
1023	1023 37707 i at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alpha-1 collagen type IV gene,	
1024	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collagen
,	20447 -4	AMBDA	Motoro	HIMPO (AMPD) mBNA	Human AMP desminase (AMPD2) mBNA AMP desminase isoform L solicing variant
301	1023 304 17 at	Aivir US	1413 1023		
1026	1026 37747 at	ANX5	U05770	Human annexin V (ANX5) gene, exon 13.	annexin V

Fig 21

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1027	1027 41143_at	CALM1	U12022	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds.	calmodulin
1028	1028 239_at	CTSD	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	cathepsin D
3			704640	Human cellular oncogene c-fos (complete v-fos FBJ murine osteosarcoma viral	v-fos FBJ murine osteosarcoma viral
20 20 20 20 20 20 20 20 20 20 20 20 20 2	1029 1916_s_at	c-tos	212100	Sequence).	oncogene nomolog
1030	1030 1915_s_at	c-fos	V01512	bieid	v-tos FBJ mulling Ostgosarcuma viral oncogene homolog
1031	1031 32583_at	NOC	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1032	1032 1895_at	NON	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1033	1033 41604_at		U79297	Human clone 23589 mRNA sequence	
1034	1034 32185_at		U00946	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA	
1035	1035 33667_at	PPIA	X52851	Human cyclophilin gene for cyclophilin (EC 5.2.1.8).	рерtidylprolyl isomerase
1036	1036 38459_g_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1037	1037 38458_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	сутостоте Б5
1038	1038 36163_at	3; P	D; DUL13761	Human dihydrolipoamide dehydrogenase gene, exon 14.	dihydrolipoamide dehydrogenase
1039	1039 1424_s_at		/HA1{D78577	Human DNA for 14-3-3 protein eta chain, exon2 and complete cds.	14-3-3 protein eta chain
				Human DNA sequence from clone 73H22 on chromosome 6q23, complete	
1040	1040 31797_at	dJ73H22.1	AL035699	sequence.	dJ73H22.1 (TBP-like protein)
1041	1041 40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	human gamma enolase
1042	1042 38326_at	G0S2	M69199	Human G0S2 protein gene, complete cds. G0S2 protein	G0S2 protein
1043	1043 40567_at	TUBA3; FLJ25113X01703	X01703	Human gene for alpha-tubulin (b alpha 1). alpha-tubulin	alpha-tubulin

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4	8	ر		
1044 39775_at	SERPING1; C1IN;	1IN;X54486		C1 inhibitor
			gene for creatine kinase B (EC	
1045 40862_i_at	CKB; CKBB	X15334		creatine kinase B
			Human gene for hepatitis C-associated	reliation beginning of sisteman
		•	ate protein p44, exon	liepalilis C-associated Illiciotudulai
1046 37641_at	IF144; p44; MTAP4	AP4D28915	T	aggregate protein p44
			Human gene for heterogeneous nuclear	
			ribonucleoprotein (hnRNP) core protein	
1047 40211_at	HNRPA1; HNRNP	RNPX12671		hnrnp a1 protein
			Human gene for melanoma growth	melanoma growth stimulatory activity
1048 408 at	MGSA	X54489		preprotein
			Human gene for omithine decarboxylase	
1049 36203_at	opc1	X16277	ODC (EC 4.1.1.17).	ornithine decarboxylase (ODC)
			Human gene for very low density	
16873_at	VLDLR	D16532	lipoprotein receptor, exon 19.	very low density lipoprotein receptor
1051 34759_at		U68494	Human hbc647 mRNA sequence	
			Human hepatic dihydrodiol	
1052 32805_at	AKR1C1; DD1; DD	1; Dt U05861	dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
			Human HMG-17 gene for non-histone	
1053 41231_f_at	HMG17; MGC562	3562 X13546	chromosomal protein HMG-17.	put. HMG-17 protein
			Human HOX 5.1 gene for HOX 5.1	
1054 38294_at	HOXD4; HOX4; H	(4; HX17360	protein.	hox 5.1 protein
			Human hsc70 gene for 71 kd heat shock	
1055 40637_at	HSP73 HSC70 HS	0 HS Y00371	cognate protein.	71 Kd heat shock cognate protein
1056 232 at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
			Human lipoprotein-associated coagulation	٠
			inhibitor (LACI) gene, exon 9 and	
1057 40767_at	TFPI	M59499	complete cds.	lipoprotein-associated coagulation inhibitor
1058 38637 at	FOX	16895	Human lysyl oxidase (LOX) gene, exon 7. lysyl oxidase	lysyl oxidase
			Human medium-chain acyl-CoA	
1059 37532_at	MCAD	M91432	dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA dehydrogenase
			Human metallothionein-III gene, complete	
1060 870_f_at	MT3; GIF; GIFB	M93311	cds.	metallothlonein-III

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			>	Himen metayip (MTX) gene complete	
1061	1061 40890_at	MTX	U46920	cds.	metaxin
				Human mRNA for erythrocyte adducin	
1062	1062 32145_at	ADD1	X58141	alpha subunit.	erythrocyte alpha adducin
				Human mRNA for general transcription	
1063	1063 37381_g_at	TF2B	X59268	factor IIB.	IIB protein
<u>1</u>	1064 33683_at	TI-227H	D50525	Human mRNA for TI-227H.	
				Human myocyte-specific enhancer factor	myocyte-specific enhancer factor 2A, C9
				ene, last coding exon, and	form; myocyte-specific enhancer factor 2A,
1065	1065 41747_s_at	MEF2A	U49020	complete cds.	C4 form
				Human NAD(P)H:quinone oxireductase	
1066	1066 38066_at	NG01	M81600	gene, exon 6.	NAD(P)H:quinone oxireductase
				Human natural killer cell enhancing factor	
1067	1067 39729_at	NKEFB	L19185	(NKEFB) mRNA, complete cds.	enhancer protein
				= = = = = = = = = = = = = = = = = = = =	
				Human nonmuscle/smooth muscle alkali	non-muscie myosin light chain; smooth
1068	1068 33994_g_at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
				Human nucleic acid binding protein gene,	
1069	1069 32841_at	9; DM2;	CNB(U19765	complete cds.	nucleic acid binding protein
1070	1070 32590_at	NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1071 1782_s_at	Op18	M31303	complete cds.	oncoprotein 18
L				Human prostaglandin D2 synthase gene,	
1072	1072 216_at	PTGDS	M98539	өхоп 7.	prostaglandin D2 synthase (21kD, brain)
				Human protein phosphatase 2A catalytic	protein phosphatase-2A catalytic subunit-
1073	1073 237_s_at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
				Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1074	1074 812_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
				Human protein phosphatase inhibitor 2	-
				(PPP1R2) gene, exon 6 and complete	1 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
107.	1075 33180_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
,,	** 93030		W21684	Human putative ribosomal protein S1	
2	10/0 33350_8I		WZIOO	Signal Signal	

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				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1077	1077 491 at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1078	1078 492 g at	PTPRG	U46116		receptor tyrosine phosphatase gamma
	2			ill-type low molecular weight	
				acid phosphatase (ACP1) gene, exon 6	red cell-type low molecular weight acid
1079	1079 36611_at	ACP1	U25849		phosphatase
				Human SH3 domain-containing protein	
1080	1080 174 s. at	SH3P18	U61167	SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
				Human spermidine synthase gene,	
1081	1081 241 g at	SRM	M64231	complete cds.	spermidine synthase
				Human sterol carrier protein-X/sterol	
				carrier protein-2 (SCP-X/SCP-2) gene,	
1082	1082 36688_at	SCP-X/SCP-2	U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	1083 32587 at	ZFP36L2; BRF2; {U07802	U07802	Human Tis11d gene, complete cds.	Tis11d
1084	1084 31680 at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
				Human transformation-related protein	
1085	1085 36446_s_at	HMG1L2	124521	mRNA, 3' end	transformation-related protein
				Human transmembrane protein (CD59)	
1086	1086 39351_at	CD59	M84349	gene, exon 4.	CD59 protein
1087	1087 38727_at	THE	M23161	Human transposon-like element mRNA	
				Human vascular cell adhesion molecule-1	
1088	1088 41433_at	VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
<u>5</u>	40121 at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
<u> </u>	1090 35973 at	НУРН	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	1091 40196 at	HYA22	D88153 ·	HYA22 protein	HYA22
				hwdrowd-Congres	
				dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
	6	VIII VIII VIII VIII VIII VIII VIII VII	D16480	thiolase/enoyl-Coenzyme A hydratase	dehydrogenase alpha-subunit of trifunctional protein
200	1092 36952_at	ALIANI	Dioto	Children process, express care	

(Fig 2)

	A	8	ပ	Q	Ш
1093	1093 39741_at			hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
1094	1094 36626_at	HSD1784	X87176	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	17beta-hydroxysteroid dehydrogenase
				Hypothetical protein of unknown function, Hypothetical 52 kDa protein; Hypothetical	
				protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a	
				hypothetical cytochrome b5 containing	
				encoded by (Z81122) T13F2.1	
		,		[Caenorhabditis elegans] and (Z70271)	
				W08D2.4 [Caenorhabditis elegans]; DNA	
				structure-specials endonuclease FEN 1; FLAP ENDONUCLEASE-1;	
				MATURATION FACTOR 1 (MF1); DNase	
				IV; RAD2_HUMAN; Hypothetical human	
				Best's macular dystrophy relatedprotein;	
				Simulated translation extends ORF of	
				previously reported partial coding	
				sequence for Best's macular dystrophy	
				related protein (AF038536); Homo	
				sapiens chromosome 11, BAC CIT-HSP-	
				311e8 (BC269730) containing the hFEN1	BC269730_1; BC269730_2; FEN1_HUMAN;
109	1095 41583_at	FEN1	AC004770	gene, complete sequence.	BC269730_4

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		BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4 hypothetical protein CG018		hypothetical protein AF038182
<u> </u>		Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein (AF038536); Homo sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311-98 (BC269730) containing the hFEN1 gene, complete sequence.	himothetical dene supported by	AF038182; BC009203
C	\ \ \	AC004770	U50527	AF038182
	2	JEN 1	CG018	LOC90355
	V	096 34224_at	1097 1527_s_at	1098 33466_at
ŀ	-	1096	1097	1098

Fig 21

				_	-1	-	_
ш	H32184 1: R32184 3		hypothetical protein, similar to (AC007017) putative RNA helicase A (Arabidopsis	thaliana			
	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (AL021106) from Drosophila melanogaster; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRAIL predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor (Rattus norvegicus) and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) To1C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C- terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant hat-phase similarities whibits no significant hat-phase similarities whibits no significant	hypothetical protein			hypothetical protein	hypothetical protein 23851	nypotnetical protein 24050
Ğ		AA015605		AL079292	AF007130	AF035313	A1651368
	g	FL J20811		LOC54505	LOC54104	LOC56007	LOC55977
	A 90000	1100 38440 s at	41	1101 39140_at	1102 37819_at	a	1104 41561_s_at
				2	110	2	2



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1105 41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106 38972_at	LOC115207	AF052169	hypothetical protein BC013764	
1107 34864 at	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108 39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109 38837 at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110 35142_at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
1111 34830_at	==	822 W25986	hypothetical protein DKFZp564K0822	
1112 31852_at	DKFZP5640043	AL050390	hypothetical protein DKFZp5640043	
1113 33895_at	DKFZP586F1318 AL050373	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114 39692 at	DKFZP586F2423	423 AL080209	hypothetical protein DKFZp586F2423	
1115 35682_at	FLB6421	Al133727	hypothetical protein FLB6421	
1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118 36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
	at FLJ10849	T75292	hypothetical protein FLJ10849	
1122 39923_at	FLJ10971	Al935420	hypothetical protein FLJ10971	
			hypothetical protein FLJ11021 similar to	
1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	-
1124 33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125 35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126 38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127 40859_at	FLJ11806	AI561196	hypothetical protein FLJ11806	
1128 41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129 41434_at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130 36580_at		AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131 32222_at		AA152202	hypothetical protein FLJ14639	
1132 38710_at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133 38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134 40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135 34739_at		W26023	hypothetical protein FLJ20275	
1136 34857_at		Z24724	hypothetical protein FLJ20986	
1137 32251_at		AA149307	hypothetical protein FLJ21174	
1138 40615_at		AA780049	hypothetical protein FLJ21439	
113933915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

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11403	1140 35198 at		AF070596	hypothetical protein from clone 24796	hypothetical protein from clone 24796
11413	1141 38483 at	9		hypothetical protein HSA011916	hypothetical protein
11424	1142 41236 at	HSU79252		hypothetical protein HSU79252	hypothetical protein HSU79252
1143	1143 38443 at	MGC14433		hypothetical protein MGC14433	
144	1144 39811 at	MGC2749	AA402538	hypothetical protein MGC2749	
				hypothetical protein MGC2840 similar to a	
1145	1145 32051 at	MGC2840	AJ224875	putative glucosyltransferase	glucosyttransferase
1146	1146 35219 at	MGC3047	AL050202	hypothetical protein MGC3047	
1147	1147 41696 at	MGC3077	AI620381	hypothetical protein MGC3077	
				hypothetical protein MGC4276 similar to	hypothetical protein MGC4276 similar to
1148	1148 41147_at	MGC4276	AF038186	CG8198	CG8198
1149	1149 37242_at	MGC5149	U79260	hypothetical protein MGC5149	
1150	1150 36975_at	MGC8721	W26659	hypothetical protein MGC8721	
1151	1151 35677 at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	1152 32504 at	MY014	AW024812	hypothetical protein My014	
1153	1153 38106 at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
145	12 07640 of	T C C T	Matedo	hypoxanthine phosphoribosytransferase 1	hypoxanthine phosphoribosyttransferase 1
7	3/040_at		240 040		
1155	1155 1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
				IGF binding protein-4; Human insulin-like	,
1156	1156 30781 at	IGERPA	1120982	growth factor binding protein-4 (1975-4) leane, promoter and complete cds.	insulin-like growth factor binding protein-4
1157	1157 38046 at	三	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	1158 218_at	¥	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	1159 37690 at	ILVBL	U61263	ilvB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160	1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161	1161 1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	1162 34391 at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1 alpha 4 protein	1 alpha 4 protein

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Γ	A	В	ပ	Q	ı
			7 0 0 0 0 0	immunoglobulin superfamily containing	<u> </u>
1163	1163 38636_at	ISLR	AB003184	leucine-rich repeat	
				IMP (inosine monophosphate)	IMP (inosine monophosphate)
164	1164 40695 at	IMPDH1	J05272	dehydrogenase 1	dehydrogenase 1
1165			AL050018	inhibitor of Bruton's tyrsoine kinase	hypothetical protein
				inhibitor of DNA binding 1, dominant	inhibitor of DNA binding 1, dominant
1166	1166 36617_at	101	X77956	negative helix-loop-helix protein	negative helix-loop-helix protein
				inhibitor of DNA binding 2, dominant	,
1167	1167 41215_s_at	ID2	D13891	negative helix-loop-helix protein	Id-2H
				inhibitor of kappa light polypeptide gene	
				enhancer in B-cells, kinase complex-	
1168	1168 34344 at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169 37659 at	IMMI	L42572	(mitofilin)	transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
1170	1170 755 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
1171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
1172	1172 36154 at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
	I				lithium-sensitive myo-inositol
1173	1173 32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
			1		
1174	1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2	myo-mosnoi monopriospinatase z
1175	1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176	1176 41049_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
==	177 851_s_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
				insulin-like growth factor 1 (somatomedin	-
1178	1178 38737_at	IGF1	X57025	(၁)	insulin-like growth factor I
				insulin-like growth factor 1 (somatomedin	
1175	1179 1501_at	IGF1	X57025	(0)	insulin-like growth factor I
138	1180 160027 s at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
				insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2
2	1181 40422_at	IGFBF2	A16302	(SOND)	(cup)
118	1182 1737 s at	IGFBP4	M62403	insulin-like growth factor binding protein 4	insulin-like growth factor binding protein 4 insulin-like growth factor binding protein 4

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1183	1183 2062 at	IGEBP7	19182	insulin-like growth factor binding protein 7	
3					mtoan mombrono protein 1
1184	1184 37991_at	ITM1	L38961	integral membrane protein 1	integral memorane protein i
				integral membrane protein; swiss-prot	
1185	1185 37326 at	A4	U93305	differentiation in intestinal epithelium	LIM domain only 6
1186	1186 41163 at	P24B	AL 109672	integral type I protein	p24B protein
					integrin beta 1 isoform 1A precursor, integrin
					beta 1 isoform 1B precursor; integrin beta 1
					isoform 1C-1 precursor; integrin beta 1
				integrin beta 1 subunit precursor; Human	isoform 1D precursor; integrin beta 1 isoform
1187	1187 32808_at	ITGB1; CD29; FN	FN X07979	mRNA for integrin beta 1 subunit.	1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	1188 1195_s_at	ICAP-1A	AF012024	protein 1	protein
1189	1189 120 at	ITGA1	X68742	integrin, alpha 1	
1190	1190 37484 at	ITGA1	X68742	integrin, alpha 1	
1191	1191 36892 at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
	1			integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071 at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	39754 at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058 s at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
				integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681 at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	1196 35365 at	곳	U40282	integrin-linked kinase	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
			-	atternatively translated; short form; Homo	
119	1197 41743 i at	OPTN: NRP: FIP	FIP2AF061034	mRNA, complete cds.	FIP2
		. 1			

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				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
		*		zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				atternatively translated; short form; Homo	
1198	1198 41742_s_at	OPTN; NRP; FIP2	FIP2 AF061034	mRNA, complete cds.	FIP2
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1199	1199 676_g_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745_at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202	1202 1456_s_at	IFI16	M63838	interferon, gamma-inducible protein 16	interferon-gamma induced protein
1203	925_at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204	1204 39728 at	IF130	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
				interferon-induced protein with	interferon-induced protein with
1205	1205 32814_at	IEIT1	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679 at	IFRD1	Y10313	-	PC4 protein
1207	1207 1368 at	IL1R1	M27492	interleukin 1 receptor, type l	interleukin 1 receptor, type l
1208	1208 33228 g at	IL10RB	Al984234	interleukin 10 receptor, beta	
1209	1209 33227_at	IL 10RB	Al984234	interleukin 10 receptor, beta	
1210	1210 38969_at	11.27	AI828168	interleukin 27	
1211	1211 38299 at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r at	11.8	M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	1213 36189 at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030_at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776_at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431_at	S	AB023153	intestinal cell kinase	KIAA0936 protein
		000	1	IQ motif containing GTPase activating	TDoce-positional live material
121	1217 1825 at	IIGGAPT	L330/5	protein	ומא מיור מאס-מכוועמוווקיוועם טוטופווו

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r		C	ر		23
7	A	a		(NANA) 1 (NANA)	
- a c	1918 30093 at	DH1	AF020038		NADP-dependent isocitrate dehydrogenase
				eted (LONN) & concept Library	
219	1219 40112_at	ЮНЗВ	AA522698	Sociliate deliyatogenase s (1777) per	NAD+-specific isocitrate dehydrogenase
1000	1990 A0111 g at	DH3B	U49283	ata Ta	beta precursor
	1221 40478 at	KIAA1162	AL021396	T	hypothetical protein
222	32695 at	dJ196E23.1	297632	isoform 2 match: protein Q99991	bombesin-like receptor 3
223	1223 40827 at	IARS	U04953	isoleucine-tRNA synthetase	ISOIBUCYI-THINA SYIIIIBIASB
4001	1224 36985 at	IDI	X17025	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
1225	1225 41775 at	ICMT	AF064084	isoprenylcysteine carboxyl methyttransferase	prenylcysteine carboxyl methyltransferase
4004	1226 34877 at	.14K1	AL 039831	Janus kinase 1 (a protein tyrosine kinase)	
200	1007 24218 at	IMA	A.1005896	JM4 protein	JM4 protein
122	1227 34310_at	1.1471	D63881	joined to JAZF1	joined to JAZF1
1220	1220 41250 at	JTV1	U24169	JTV1 gene	JTV-1
1212	1230 41483 s at	ONDC	X56681	Jun D proto-oncogene	junD protein
123	1231 1612 s at	CNOC	X56681	jun D proto-oncogene	junD protein
	1232 40464 n at	KPNB2	U70322	karyopherin (importin) beta 2	transportin
123	1233 39028 at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_GTP binding protein 5
100	1234 35725 at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	karyopherin alnph 3
1235	1235 32487 s at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Cipi
				katanin p60 (ATPase-containing) subunit	
1236	1236 32708 g at	KATNA1	AI191768	A1	
				KDEL (Lys-Asp-Glu-Leu) endoplasmic	ZOE IZOS
1237	1237 37386_i_at	KDELR1	X55885	reticulum protein retention receptor 1	NDEL I REPUGI
١	** 00000	KDEI B2	M88458	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDEL receptor 2
<u> </u>	1238 39060_at	NUCLUS	200	KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1235	1239l33402 at	KDELR3	AL035081	reticulum protein retention receptor 3	hypothetical protein
124	1240 37150 at	AB026190	AB026190	Kelch motif containing protein	Keich motif containing protein
124	1241 32329 at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type il intermediate filament of nair keratili
				KH domain containing, RNA binding,	3
124	1242 39346_at	KHDRBS1	M88108	signal transduction associated i	pos

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1243 32679_at	KIAA0009	013634	KiAA0009 gene product	NIAAWW gene product
1244 34760_at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
1245 41129_at	KIAA0033	D26067	KIAA0033 protein	
1246 38797_at	KIAA0062	D31887	KIAA0062 protein	
1247 36978_at	KIAA0077	D38521	KIAA0077 protein	
1248 37718_at	KIAA0096	D43636	KIAA0096 protein	
1249 37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
			KIAA0098 is a human counterpart of	
	_		mouse changenin containing TCP-1	
			Thousa criaterories containing 1 of 1	
	_	-	gene, Start countries not identified.	
_			nau 1413 cultA civile for NAACOSO Has a	
			S-bb insertion between 735-737 of the	
			sequence of KIAA0098.; Homo sapiens	
1250 40417 at	KIAA0098	D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
1252 37359 at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
1253 38031 at	KIAA0111	D21853	KIAA0111 gene product	KIAA0111 gene product
1254 40279 at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
1255 36845 at	KIAA0136	D50926	KIAA0136 protein	
1256 32099 at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
1257 38472 at	KIAA0143	D63477	KIAA0143 protein	
1258 41728 at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
1259 37642 at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
1260 32661_s_at		D79992	KIAA0170 gene product	KIAA0170 gene product
1261 37225 at	KIAA0172	D79994	KIAA0172 protein	
1262 36942_at	KIAA0174	D79996	KiAA0174 gene product	KiAA0174 gene product
1263 31863_at	KIAA0179	D80001	KIAA0179 protein	
1264 37734_at	KIAA0184	D80006	KIAA0184 protein	
1265 41669 at	KIAA0191	D83776	KIAA0191 protein	
1266 36192 at	KIAA0193	083777	KIAA0193 gene product	KIAA0193 gene product
1267 38056_at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
1268 38419_at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
1269 38067_at	KIAA0202	D86957	KIAA0202 protein	
1270 32586_at	KIAA0217	D86971	KIAA0217 protein	
1271 38728 at	KIAA0225	D86978	KIAA0225 protein	

C D86982 H D86985 H D87077 H D87438 H D87446 H D87445 H D87445 H D87445 H D87446 H D87452 H D87452 H D87452 H D87452 H AB002319 H AB002319 H AB002319 H AB002319 H AB002347 H AB002348 AB002363 AB002363 AB002365 AB002365 AB002365 AB007900 AB007916 AB007916 AB007926 AB007926 AB007926 AB007926 AB007926 AB007926 AB007926 AB007926 AB007926 AB007938	C C C C C C C C C C C C C C C C C C C	KIAA0256 protein KIAA0256 gene product KIAA0350 protein KIAA0355 gene product
40971_at KIAA0229 D86982 H 37748_at KIAA0232 D86985 H 38892_at KIAA0240 D87077 H 40765_at KIAA0251 D87445 H 41634_at KIAA0255 D87446 H 41634_at KIAA0257 D87446 H 36971_at KIAA0265 D87446 H 32237_at KIAA0266 D87455 H 38592_at KIAA0284 AB02319 H 41381_at KIAA0284 AB002319 H 41381_at KIAA0329 AB002347 H 32592_at KIAA0349 AB002343 H 32592_at KIAA0355 AB002343 AB002348 32208_at KIAA0355 AB002348 AB002365 32208_at KIAA0355 AB002365 AB002363 3223_at KIAA0372 AB002363 AB02365 32583_at KIAA0438 AB007893 AB0516 32340_at KIAA0446 <th>10 10 10 10 119 119 119 119 119 119 119</th> <th>KIAA0256 protein KIAA0256 gene product KIAA0350 protein KIAA0355 gene product</th>	10 10 10 10 119 119 119 119 119 119 119	KIAA0256 protein KIAA0256 gene product KIAA0350 protein KIAA0355 gene product
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at KIAA0265 D87454 Italy I		KIAA0356 gene product KIAA0355 gene product KIAA0355 gene product
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KIAA0276		KIAA0350 protein KIAA0355 gene product
at KIAA0284 AI828210 I KIAA0308 AB002319 I KIAA0321 AB002321 I KIAA0320 AB002321 I KIAA0350 AB002347 I KIAA0355 AB002348 I KIAA0356 AB002348 I KIAA0357 AB002353 I KIAA0370 AB002368 I KIAA0370 AB002369 I KIAA0423 AB007369 AB007990 KIAA0446 AB007916 I KIAA0469 AB007926 I KIAA0469 AB007938 I KIAA0469 AB007938 I		KIAA0350 protein KIAA0355 gene product
KIAA0308 AB002306 I KIAA0321 AB002319 I KIAA0323 AB002321 I KIAA0350 AB002347 I KIAA0355 AB002348 I KIAA0355 AB002348 I KIAA0355 AB002348 I KIAA0367 AB002363 I KIAA0372 AB002374 I KIAA0376 AB002374 I KIAA0423 AB007883 I KIAA0440 AB007996 I KIAA0446 AB007916 I KIAA0447 AB007916 I KIAA0446 AB007916 I KIAA0446 AB007916 I KIAA0447 AB007920 I KIAA0469 AB007926 I KIAA0469 AB007928 I		KIAA0350 protein KIAA0355 gene product
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KIAA0367 AB002365 KIAA0370 AB002368 KIAA0372 AB002374 KIAA0423 AB007883 KIAA0438 AB007883 KIAA0438 AB007898 KIAA0440 AB007898 KIAA0446 AB007916 KIAA0447 AB007916 KIAA0451 AB007920 KIAA0469 AB007928 KIAA0469 AB007938 KIAA0469 AB007938		
KIAA0370 AB002368 KIAA0372 AB002370 KIAA0423 AB007893 KIAA0438 AB007898 KIAA0446 AB007990 KIAA0446 AB007916 KIAA0447 AB007916 KIAA0447 AB007920 KIAA0446 AB007938 KIAA0469 AB007938 KIAA0469 AB007938 AB007938 KIAA0469 AB007938 AB007938 AB007938 AB007938 AB007939 AB007938 AB007939 AB007938 AB007939		_
KIAA0372 AB002370 KIAA0376 AB002374 KIAA0423 AB007883 KIAA0438 AB007898 KIAA0440 AB007890 KIAA0446 AB007915 KIAA0447 AB007916 KIAA0451 AB007920 KIAA0469 AB007928 KIAA0469 AB007938 KIAA0469 AB007938		
KIAA0376 AB002374 KIAA0423 AB007883 KIAA0438 AB007898 KIAA0440 AB007990 KIAA0446 AB007915 KIAA0447 AB007916 KIAA0447 AB007920 KIAA0469 AB007928 KIAA0469 AB007938 KIAA0469 AB007938		KIAA0372 gene product
KIAA0423 AB007883 KIAA0433 AB007893 KIAA0438 AB007898 KIAA0440 AB007900 KIAA0446 AB007916 KIAA0451 AB007916 KIAA0451 AB007920 KIAA0469 AB007928 KIAA0469 AB007938 AKIAA0469 AB007938		
KIAA0433 AB007893 KIAA0438 AB007898 KIAA0440 AB007900 KIAA0446 AB007916 KIAA0447 AB007916 KIAA0451 AB007920 KIAA0469 AB007928 KIAA0469 AB007938 AKIAA0470 AB007939		
KIAA0438 AB007898 KIAA0440 AB007900 KIAA0446 AB007915 KIAA0447 AB007916 KIAA0451 AB007920 SRGAP2 AB007925 KIAA0469 AB007938 at KIAA0470		KIAA0433 protein
KIAA0440 AB007900 KIAA0446 AB007915 KIAA0447 AB007916 KIAA0451 AB007920 SRGAP2 AB007925 KIAA0469 AB007938 at KIAA0470		KIAA0438 gene product
KIAA0446 KIAA0447 KIAA0451 SRGAP2 KIAA0469 at KIAA0470		KIAA0440 protein
KIAA0447 KIAA0451 SRGAP2 KIAA0469 at KIAA0470		KIAA0446 protein
KIAA0451 SRGAP2 KIAA0469 at KIAA0470		KIAA0447 protein
SRGAP2 KIAA0469 at KIAA0470		KIAA0451 protein
KIAA0469 KIAA0470		KIAA0456 protein
KIAA0470	07938 KIAA0469 gene product	KIAA0469 protein
		KIAA0470 protein
1303 34445_at KIAA0471 AB007940		KIAA0471 protein
1304 35318_at KIAA0475 AB007944		KIAA0475 protein
		KIAA0476 protein
1306 35762_at KIAA0483 AB007952		KIAA0483 protein
1307 41830_at KIAA0494 AB007963	07963 KIAA0494 gene product	KIAA0494 protein

roduct	KIAA0532 protein KIAA0537 gene product KIAA0546 protein KIAA0564 protein
roduct	37 gene product 46 protein 54 protein
	46 protein 64 protein
	s4 protein
	KIAA0592 protein
	KIAA0594 protein
roduct	KIAA0605 gene product
	KIAA0610 protein
roduct	KIAA0618 gene product
	KIAA0625 protein
roduct	KIAA0626 gene product
	KIAA0630 protein
	KIAA0648 protein
_	KIAA0650 protein
roduc	KIAA0662 gene produc
roduc	KIAA0663 gene product
	KIAA0674 protein
_ ,	KIAA0678 protein
_	KIAA0692 protein
ا	KIAA0700 protein
produ	KIAA0716 gene product
è	KIAA0721 protein
ے	KIAA0725 protein
اے	KIAA0729 protein
Produ	KIAA0738 gene product
produ	KIAA0740 gene product
_	KIAA0746 protein
_	KIAA0747 protein
produ	KIAA0750 gene product
prod	KIAA0769 gene product
_	KIAA0776 protein
ء	KIAA0779 protein
<u>د</u>	KIAA0781 protein

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A	В	ပ	O	Ξ.
8	KIAA0788	AB018331	KIAA0788 protein	KIAA0788 protein
₹	KIAA0795	AB018338	KIAA0795 protein	KIAA0795 protein
X X	KIAA0802	AB018345	KIAA0802 protein	KIAA0802 protein
Σ¥	KIAA0810	AB018353	KIAA0810 protein	KIAA0810 protein
ΚIA	KIAA0826	AB020633	KIAA0826 protein	KIAA0826 protein
<u>X</u>	KIAA0830	AB020637	KIAA0830 protein	KIAA0830 protein
X A	KIAA0831	AB020638	KIAA0831 protein	KIAA0831 protein
KIA	KIAA0841	AB020648	KIAA0841 protein	KIAA0841 protein
¥₹	KIAA0843	AB020650	KIAA0843 protein	KIAA0843 protein
¥¥	KIAA0854	AB020661	KIAA0854 protein	KIAA0854 protein
XIX	KIAA0864	AB020671	KIAA0864 protein	KIAA0864 protein
¥¥	KIAA0877	AB020684	KIAA0877 protein	KIAA0877 protein
KIA	KIAA0878	AB020685	KIAA0878 protein	KIAA0878 protein
ΚIĀ	KIAA0882	AB020689	KIAA0882 protein	KIAA0882 protein
X	KIAA0893	AB020700	KIAA0893 protein	KIAA0893 protein
ΚI¥	KIAA0903	AB020710	KIAA0903 protein	KIAA0903 protein
¥¥	KIAA0909	AB020716	KIAA0909 protein	KIAA0909 protein
Σ¥	KIAA0911	AB020718	KIAA0911 protein	KlAA0911 protein
ΚĪĀ	KIAA0916	AF075587	KIAA0916 protein	protein associated with Myc
KI≹	KIAA0931	AB023148	KIAA0931 protein	KIAA0931 protein
Κ₩	KIAA0934	AB023151	KIAA0934 protein	KIAA0934 protein
ΧĀ	KIAA0937	AB023154	KIAA0937 protein	KIAA0937 protein
ΑŽ	KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
Rab	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
X §	KIAA0942	AB023159	KIAA0942 protein	KIAA0942 protein
X ₹	KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
ΚĮ	KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
ΚĮĄ	KIAA0978	AB023195	KIAA0978 protein	KIAA0978 protein
ΚĀ	KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
ΚĀ	KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
KIA	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
ΚĀ	KIAA0997	Al970189	KIAA0997 protein	-
KA A	KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
X X	KIAA1001	AW052084	KIAA1001 protein	
KIA	KIAA1012	AB023229	KIAA1012 protein	KIAA1012 protein
KIA	KIAA1014	AR023231	KIAA1014 protein	KIAA1014 protein

Fig 21

A 3,000	В	C PD038040	D VIAA1026 profein	KIAA1026 protein
了	KIAA1026	AB028949	KIAA 1026 protein	KIAA1030 protein
되	KIAA1030	AB028953	KIAA1030 protein	VIAA 1030 protein
로	KIAA1033	AB028956	KIAA1033 protein	NIAA 1035 protein
고	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
Y	KIAA1041	AB028964	KlAA1041 protein	KIAA1041 protein
Y	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
노	KIAA1049	AB028972	KIAA1049 protein	KIAA1U49 protein
Y	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
¥	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
X	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
ϫ	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
X	KIAA1091	AB029014	KiAA1091 protein	KIAA1091 protein
<u> -</u>	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
=	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
=	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
뜯	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
-	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
•	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
	KIAA1128	U90912	KIAA1128 protein	
_	KIAA1157	W29087	KiAA1157 protein	
	KIAA1240	A1830496	KIAA1240 protein	
-	KIAA1254	AI761567	KIAA1254 protein	
_	KIAA1354	AA115140	KIAA1354 protein	
-	KIAA1750	AL080059	KIAA1750 protein	
	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
	KIAA1966	N36997	KIAA1966 protein	
	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
	KIFC3	AL041493	kinesin family member C3	
	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
	KIFAP3	U59919	kinesin-associated protein 3	SMAP
	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
	Collage	VOGZEO	L-3-hydroxyacyl-Coenzyme A	3-hydroxyacyl-CoA dehydrogenase
_	HADHSC	76/064	deliyalogenase, short chair	

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1415	41485 at	DHA	X02152	lactate dehydrogenase A	actate dehydrogenase A
1416	288 s	LBR	125931		lamin B receptor
				laminin receptor 1 (67kD, ribosomal	
1417	1417 256 s at	LAMR1	M14199	protein SA)	laminin receptor 1
1418	1418 37671 at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419	1419 581 at	LAMB1	M61916		laminin B1
				LanC lantibiotic synthetase component C-	
1420	1420 39441 at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
				ing growth factor beta	latent transforming growth factor beta
1421	1421 1495 at	LTBP1	M34057		binding protein 1 precursor
				ing growth factor beta	
1422	1422 37906 at	LTBP2	237976		LTBP-2 precursor
				lectin, galactoside-binding, soluble, 1	
1423	1423 33412_at	LGALS1	AJ535946	(galectin 1)	
				lectin, galactoside-binding, soluble, 3	
1424	1424 35367 at	LGALS3	AB006780	(galectin 3)	galectin-3
				lectin, galactoside-binding, soluble, 3	
1425	1425 37754 at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
				lectin, galactoside-binding, soluble, 8	
1426	1426 1846 at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
1427	1427 34267 r at	LEPR	U50748	leptin receptor	leptin receptor
1428	1428 33830 at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	1429 33829 at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
7.30	20005 04	1 EPBOTI 1	AFORSAOS	lentin receptor overlapping transcript-like 1 brain my047 protein	brain my047 protein
	30000			leucine rich repeat (in FLII) interacting	
1431	1431 41320_s_at	LRRFIP1	609690	protein 1	transcription repressor
143	1432 30067 at	1 0001	AR019527	leucine zipper, down-regulated in cancer 1 LDOC1 protein	LDOC1 protein
	1433 41754 at	I RPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
	1434 37470 at	LAIR1	AF013249	leukocyte-associated lg-like receptor 1	leukocyte-associated Ig-like receptor-1
4	1435 38081 at	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	1436 36062 at	LPXN	AF062075	leupaxin	leupaxin
				libtest16.A02.r bynorm Homo sapiens	
143	1437 35278_at	RPS29	AI541542	CUNA 5, MRINA Sequence.	
1438	1438 39687_at	E46L	A1524873	like mouse brain protein E46	

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1439	1439 39686_g_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
84	1440 39685 at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
				likely homolog of rat kinase D-interacting	
1441	1441 39163_at	KIDINS220	W27233	substance of 220 kDa	
				likely ortholog of mouse suppressors of	
1442	1442 32669_at	SOCS5	AB014571		KIAA0671 protein
1443	1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
				likely ortholog of mouse TPR-containing,	
1444	1444 40844_at	TSBP	D63875		KIAA0155 gene product
				likely ortholog of mouse variant	
1445	1445 41248_at	CSTF2T	AB014589	polyadenylation protein CSTF-64	KIAA0689 protein
				likely ortholog of rat golgi stacking protein	
1446	1446 35805_at	GRASP55	AA447263	homolog GRASP55	
				LIM and senescent cell antigen-like	
1447	1447 39232_at	LIMS1	U09284	domains 1	PINCH protein
-448 8	1448 36181 at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
1449	1449 38617_at	LIMK2	D45906	LIM domain kinase 2	LIMK-2
1450	1450 1452 at	LMO4	U24576	LIM domain only 4	breast tumor autoantigen
1451	1451 31936 s. at	LKAP	AB007890		KIAA0430 protein
L				lipase A, lysosomal acid, cholesterol	
1452	1452 38745_at	LIPA	X76488		lysosomal acid lipase
1453	1453 38098 at	LPIN1	D80010	lipin 1	
1454	1454 37542 at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
1455	1455 41209 at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
1456	1456 1798 at	LIV-1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
				liver form; Homo sapiens glycogen phosphorylase (PYGL) gene exon 20 and	
1457	1457 37215 at	PYGL	AF046798		glycogen phosphorylase
	10 - 10				

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				long tailed isoform; individual exons 6-14	
				are atternative exons any of which can be	
				spliced out of the mRNA.; putative; long	
			•	tailed isoform; putative; long tailed	
			-	isoform; hemopoietic variant; putative;	
				long tailed isoform; epithelial form;	
				putative; Human cell surface glycoprotein	
1458	1458 40493 at	CD44	L05424		cell surface glycoprotein CD44
				low density lipoprotein-related protein-	
				associated protein 1 (alpha-2-	
				macroglobulin receptor-associated protein	macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated
1459	1459 36194_at	LRPAP1	M63959	1)	protein
				low molecular mass ubiquinone-binding	
1460	1460 34400_at	QP-C	AI540957	protein (9.5kD)	
1461	1461 37025_at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462	39017_at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463	38038_at	LUM	U21128	lumican	lumican
1464	38115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465	1465 39428_at	LNK	AF055581	lymphocyte adaptor protein	adaptor protein Lnk
1466	1466 39396_at	LYPLA1	AF081281	lysophospholipase I	lysophospholipase
1467	1467 33788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468	1468 39758 f at	I AMP1	.104182	Vsosomal-associated membrane protein 1 Nsosomal membrane glycoprotein-1	Nsosomal membrane glycoprotein-1
1460	1460 38403 et	I AMP?	X77196	Nsosomal-associated membrane protein 2	bsosomal-associated membrane protein 2 bsosome-associated membrane protein-2
1470	1470 38402 at	L AMP2	U36336	lysosomal-associated membrane protein 2	ysosomal-associated membrane protein 2 lysosome-associated membrane protein-2b
				lysosomal-associated protein	lysosomal-associated protein
1471	1471 39019_at	LAPTM4A	D14696	transmembrane 4 alpha	transmembrane 4 alpha
1472	33127_at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473	1473 34336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474	1474 32832_at	MAEA	AF084928	macrophage enythroblast attacher	erythroblast macrophage protein EMP
1475	147E 3E17A of	MACMABCKS	X70326	macrophage myristoylated alanine-rich C kinase substrate	macrophage mynstoylated alanıne-rich C. kinase substrate
	301/4-at	SUSUSUALISMA	V10050		

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Γ				MAD, mothers against decapentaplegic	
1476	1476 1453_at	MADH2	U68018	homolog 2 (Drosophila)	mad protein homolog
				decapentaplegic	
1477	1477 38944_at	MADH3	U68019		mad protein homolog
				MAD, mothers against decapentaplegic	
1478	1478 1433 g_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1479	1479 36953_at	MADH4	U44378	homolog 4 (Drosophila)	Dpc4
				MAD, mothers against decapentaplegic	
1480	1480 1013_at	MADHS	U59913	homolog 5 (Drosophila)	Smad5
				MAD, mothers against decapentaplegic	
1481	1481 1955_s_at	MADH6	AF035528	homolog 6 (Drosophila)	Smad6
				MAD, mothers against decapentaplegic	
1482	1482 1857_at	MADH7	AF010193	homolog 7 (Drosophila)	MAD-related gene SMAD7
				major histocompatibility complex, class I,	
1483	1483 41237_at	HLA-A	D32129	A	HLA-A26
				major histocompatibility complex, class II,	
1484	1484 41609_at	HLA-DMB	U15085	DM beta	HLA-DMB
				major histocompatibility complex, class II,	
1485	1485 38096 f_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	
1486	1486 38095 i at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	major histocompatibility complex, class II,
1487	1487 37039_at	HLA-DRA	J00194	DR alpha	DR alpha precursor
				major histocompatibility complex, class II,	
1488	1488 33261_at	HLA-DRB1	M16941	DR beta 1	
_				major histocompatibility complex, class I-	
1489	1489 34425_at	HLALS	AF031469	like sequence	MHC class I-related protein 1 isoform D
				major receptor for HIV-1; member of	
				immunoglobulin supergene family; T cell	
1490	1490 34003_at	CD4	U47924	surface glycoprotein T4	protein 'A', isoform 1
1401	1401 36608 at	MDH1	D55654	malate dehydrogenase 1. NAD (soluble)	cytosolic malate dehydrogenase
				malic enzyme 1, NADP(+)-dependent,	
1492	1492 837_s_at	ME1	U43944	cytosolic	cytosolic NADP(+)-dependent malic enzyme

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ME2 M55905 malic enzyme 2, NAD(+)-dependent, ninochondrial MPI X76057 minochondrial mainose phosphate isomerase P MKNK1 AB000409 MAP/misse-interacting serine/threonine Inamnose phosphate isomerase P MARK3 M80359 3 MAP/microtubule affinity-regulating kinase Inamnose phosphate isomerase In MAPK4 MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, in kinase kinase gene,		٨	8	ပ	O	u
ME2 M55905 mitochondrial MPI X76057 mannose phosphate isomerase MRNK1 AB000409 kinase interacting serine/threonine MAPI MAPImicrotubule affinity-regulating kinase MAPImicrotubule affinity-regulating kinase MAPI MAPIMICROTUBULE PRK; Homo sapiens mitogen activated protein Kinase activated protein kinase; PRK; Homo sapiens mitogen activated protein Kinase activated protein MAPICAPIK5; PRA AF032437 complete cds. Complete cds. complete cds. MAPICAPIK5; PRA AF032437 complete cds. Sw.P47337 Sw.P04040 Sw.P04762 Sw.P17338 Tr.O27487 Sw.P26531 Sw.P04830 Tr.C49133 Sw.P04040 Sw.P04390 Tr.C49133 Sw.P04040 Sw.P77872 Sw.P07820 Sw.P77872 Sw.P07820 Sw.P06831 Sw.P77872 Tr.C49133 Sw.P04040 Sw.P77872 Tr.C249133 Sw.P04040 Sw.P77872 Tr.C249133 Sw.P04040 Sw.P77872 Sw.P07820 Sw.P77872 Sw.P07820 Sw.P04309 Tr.C49133 Sw.P04040 Sw.P04389 Sw.P07820 Sw.P07820 Sw.P07820 Sw						nitochondrial NAD(P)+ -dependent malic
MPI X76057 mannose phosphate isomerase PR MKNK1 AB000409 kirase interacting serine/flhreonine APP/microtubule affinity-regulating kinase MAPK MAPK-activated protein kinase; PRK; PR MAPKAPK5; PRA AF032437 complete cds. PR-24270 Fr.062839 Sw.P0440 MAPKAPK5; PRA AF032437 complete cds. Fr.062839 Sw.P0440 MAPKAPK5; PRA AF032437 complete cds. Fr.062839 Sw.P0440 Sw.P17385 Tr.018193 Tr.077229 Tr.049133 Sw.P26901 Sw.P55306 Tr.049133 Sw.P26901 Sw.P55306 Sw.P07820 Sw.P77872 Tr.027710 Sw.D96528 Sw.O13289 Sw.P07820 Sw.P07820 Sw.P77872 Tr.059602 Tr.P77924 Sw.O35813 Sw.P07820 Sw.P15823 M.P153079 match ESTs W94164 N28621 match ESTs W94164 N28621 (NID:g1602189), and A167942 (NID:g3701112); H_RG041D11.1; Homo sapies Sequence. MUGSC:H_RG04AC005053 Tq21, complete sequence. Tq21, complete sequence. Tq21, complete sequence.	1493	36599 at		M55905		enzyme
MAP kinase-interacting serine/threonine MAP kinase-interacting serine/threonine MAP/MICTOTUBULE affinity-regulating kinase 3	1494	36673 at		X76057	sphate isomerase	shosphomannose isomerase
MKNK1 AB000409 kinase 1 MAP/microtubule affinity-regulating kinase 3 3 MAP/microtubule affinity-regulating kinase 3 MAP/microtubule affinity-regulating kinase 4 MAP/microtubule affinity-regulating kinase 5 MAP/microtubule affinity-regulating microtubule affinity-regulating microtubule affinity-regulating microtubule affinity-regulating microtubule affinity-regulating microtubule affinity-regulating microtubule affinity from 7q21, complete sequence.						
MAPKA MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, complete cds. MAPKAPKS; PRA AF032437 MAPK-activated protein kinase gene, complete cds. Figure activated protein kinase gene, complete sequence. Figure activated protein kinase gene, complete sequence. Figure activated protein kinase gene, complete sequence. Figure activated protein kinase protein. Figure activated protein kinase gene, complete sequence. Figure activated protein kinase protein. Figure activated protein. Fi	1495			AB000409		MNK1
MARK3 M80359 3 MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, homo sapiens mitogen activated protein kinase gene, complete cds. Homo sapiens witogen activated protein kinase gene, romplete cds. Complete com					_	
MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, rinase activated protein kinase gene, romplete cds. MAPKAPK5; PRA AF032437 complete cds. match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P04322 Sw:P04322 Sw:P17338 Tr:O18193 Tr:O177229 Tr:O27487 Sw:C61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O29133 Sw:P30263 Tr:P77924 Sw:C69170 Sw:P30263 Tr:O29602 Sw:P77924 Sw:C69170 Sw:P1389 Sw	1496	40826 at	MARK3	M80359		protein p78
Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, kinase activated protein kinase gene, complete cds. Complete co					MAPK-activated protein kinase; PRK;	
MAPKAPK5; PRA AF032437 Complete cds. Fig. 1978 Complete cds. Complete Sw:P04040 Sw:P04322 Sw:P04040 Sw:P04322 Complete Sw:P04330 Complete Sw:P0441011 Complete S		·				•
MAPKAPK5; PRA AF032437 complete cds. match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P0432 Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P5306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O49133 Sw:P30265 Sw:O13289 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O292405 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P7924 Sw:O59170 Sw:P15202 Tr:O59296 Tr:O33613 Sw:O92405 Sw:O59295 Sw:P81138 Tr:O59602 Tr:P7924 Sw:O59291 Sw:P15202 Tr:O59296 Tr:O33613 Sw:O92405 Sw:O59295 Sw:P81138 Match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from sapiens BAC clone STB-41D11 from ST						mitogen activated protein kinase activated
match proteins: Sw.P04040 Sw.P04762 Sw.P24270 Tr.O62839 Sw.P00432 Sw.P17336 Tr.P90682 Tr.O27487 Sw.O61235 Tr.O18193 Tr.O77229 Tr.Q49133 Sw.P26901 Sw.P55306 Sw.P30263 Tr.P95631 Sw.P44390 Tr.Q27710 Sw.G96528 Sw.O13289 Sw.P07820 Sw.P30265 Sw.P77872 Tr.Q59602 Tr.P77924 Sw.Q59170 Sw.P15202 Tr.C59296 Tr.O33613 Sw.G92405 Sw.G59635 Sw.P81138 match to ESTs A94164 N28621 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3165211), H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone GTB-41D11 from 7q21, complete sequence.	1497	/41506_at		AF032437		protein kinase
Sw.P24270 Tr.O62839 Sw.P00432 Sw.P17336 Tr.P90682 Tr.027487 Sw.O61235 Tr.O18193 Tr.O77229 Tr.O49133 Sw.P26901 Sw.P55306 Sw.P30263 Tr.P95631 Sw.P44390 Tr.O27710 Sw.O96528 Sw.O13289 Sw.P07820 Sw.P30265 Sw.P77872 Tr.O29602 Tr.P77924 Sw.O69170 Sw.P15202 Tr.O59602 Tr.O33613 Sw.O92405 Sw.O59635 Sw.P81138 CAT AL035079 match ESTs. W94164 N28621 match to ESTs AA316181 (NID:93165221), AA032221 (NID:93165221), AA032221 (NID:93165221), ABO41D111; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from					match proteins: SwrP04040 SwrP04762	
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Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P4330 Tr:O27710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P07820 Sw:P7872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C92291 (NID:93165221), AA032221 (NID:93165213), and Al167942 (NID:93165183), and Al167942 (NID:93701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone GTB-41D11 from 7021, complete sequence.					Sw:P17336 Tr:P90682 Tr:Q27487	
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Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:C96528 Sw:C013289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:C059170 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:C95296 Tr:O33613 Sw:C92405 Sw:P81138 match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3165213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Tr:Q49133 Sw:P26901 Sw:P55306	
Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q592405 Sw:Q59296 Tr:O33613 Sw:P0784051138 WUGSC:H_RG04 AC005053 7q21, complete sequence.					Sw:P30263 Tr:P95631 Sw:P44390	
Sw.P07820 Sw.P30265 Sw.P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw.P15202 Tr:Q59635 Sw.Q5913 Sw.Q92405 Sw:Q59635 Sw.P81138 CAT AL035079 match to ESTs: W94164 N28621 match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g31652218), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone GTB-41D11 from 7q21, complete sequence.					Tr:Q27710 Sw:Q96528 Sw:O13289	*
Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:G59296 Tr:C33613 Sw:Q92405 Sw:C59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g316521), HRG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P07820 Sw:P30265 Sw:P77872	
CAT AL035079 match ESTs: W94164 N28621 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g31652218), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Tr:Q59602 Tr:P77924 Sw:Q59170	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:93165221), AA032221 (NID:93165221), AA032221 (NID:93502112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from yq21, complete sequence.					Sw:P15202 Tr:Q59296 Tr:O33613	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:93165221), AA032221 (NID:91502183), and Al167942 (NID:93701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:Q92405 Sw:Q59635 Sw:P81138	
match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and A167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	149	3 37009 at	CAT	AL035079	match ESTs: W94164 N28621	රJ53C18.1 (Catalase)
(NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					match to ESTs AA316181	
(NID:g1502183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from WUGSC:H_RG04AC005053 7q21, complete sequence.					(NID:g3165221), AA032221	
(NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from WUGSC:H_RG04AC005053 7q21, complete sequence.	_				(NID:g1502183), and Al167942	
Sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					(NID:g3701112); H_RG041D11.1; Homo	•
WUGSC:H_RG04/AC005053 7q21, complete sequence.		_			sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
	149	9 40297 at		AC005053	7q21, complete sequence.	prostate

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	▼	8	O	Q	W
1500	1500 34860 g. at		Z98046	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 Q42141 P19823 Q02668 hepatocellular carcinoma associated protein: Dreast cancer associated gene 1
				match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039	·
1501	1501 35336_at	HS508115A	AL021707	Em:AA542125 Em:W41686 Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
1502	32658_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503	1503 31545_at	dJ1033B10.1	AL031228	match: protein O15214	BING4 UDP-galactose-4-epimerase
1504	36986_at	QJBB6KZ.1	ALU3 1295	match: proteins CE02000 059733	
1505	1505 38072_at	dJ465N24.1	AL031432	CE01999; supported by FGENES and GENSCAN	hypothetical protein dJ465N24.2.1
				match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of	dJ281H8.2 (PUTATIVE novel protein similar
1506	1506 32478_f_at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)

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: 1507	1507 39759_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 Cterminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3′ part of the atternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))
1508	508 39760_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein GKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein GKI-77 (isoform 3))
1509	1509 32573_at	COX6A	AL021546	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 cytochrome c oxidase subunit Vla P13182 O13085 O13082	cytochrome c oxidase subunit VIa polypeptide 1



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,			00,000	938533 Q03933 P38530 P38529 P38531 Q63717	Cachon footon
	1510 33443_at	HSF2	799129	P38532 Q99472	neat snock transcription factor &
				match: proteins Q14189 P15924 Q03001	
				P97395 P97396 P97394; Human DNA	
				sequence from clone 512811 on	
				chromosome 6p24-25. Contains the	
				Desmoplakin I (DPI) gene, ESTs, STSs	
1511	1511 36133_at	dJ512B11.1	AL031058	and GSSs, complete sequence.	dJ512B11.1 (Desmoplakin I (DPI))
				match: proteins Q14209 Q16254 O35261	
				O00716 Q61501 Q90977 Q01094	
1512	1512 37043_at	E2F-2	AL021154	Q27368	E2F transcription factor 2
				match: proteins Q15774; match: protein	
				Q01968 P32019; Homo sapiens DNA	
				sequence from PAC 454M7 on	
				chromosome Xq25-26.3. Contains the	
				OCRL1 gene for Lowe Oculocerebrorenal dJ454M7.1.2 (Lowe Oculocerebrorenal	dJ454M7.1.2 (Lowe Oculocerebrorenal
				Syndrome protein OCRL-1. Contains	Syndrome protein OCRL-1) (isoform 2);
				ESTs, STSs and GSSs, complete	dJ454M7.1.1 (Lowe Oculocerebrorenal
1518	1513 41227_at	OCRL1	AL022162	sequence.	Syndrome protein OCRL-1) (isoform 1)
					dJ341E18.1 (Serine/Threonine Protein
				match: proteins Q62726 P20793 Q04859 Kinase (presumptive isolog of Rat protein	Kinase (presumptive isolog of Rat protein
1514	1514 38990_at	dJ341E18.1	AL031178	Q39423 P43294 O49669	Q62726))

(7,57)

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m	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))	non-histone chromosome protein 2 (S. cerevisiae)-like 1		((TREB5))
D	match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 as further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	match: proteins Q99795 Q91665 Q91664 C09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence 180040 dJ889N15.1 (novel protein similar to X. supported by GENSCAN and FGENES laevis Cortical Thymocyte Marker CTX) annimonatein in the control of	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	match: proteins: Sw:P12956	match: proteins: Sw.P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete	sequence.
၁	AL021938	77	AL049699			Z93930
В	ICNOMUL	15.1	ME1	OTK27 SSFA1		XBP1
٧	1515 34782_at	1516 37350_at	1517 39738_81 1518[31824_at	1519 32766 at		1520 39756_g_at
	1515	1516	151	151		152

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1521	1521 39755_at	·	293930	Bu	bK292E10.1 (X-box binding protein 1 (TREB5))
t Con	77771 of	Z	708046	match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26043 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane- organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island,	dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein))
1523	''	RPL3	AL022326	match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598	ribosomal protein L3
1524	1524 33136 at	UBE21	AL031714	match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867	C358B7.1 (ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9))
1525	1525 36607_at	bK250D10.3	Z99716	match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352 match: proteins: Sw:Q28038 Sw:Q16674 Tr-P97591 Sw:O61865	septin 3 small nuclear ribonucleoprotein polypeptide B"
1524	1526 38399_at	SNHPBZ	ALU34428	11.P9/391 3W.do1003	a

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-	A	88	3	Q	U
\dagger				match: proteins: Tr:054791 Sw:Q90595	
				Sw:Q61827 Sw:Q90596 Tr:O54790	
				15.05.05.10 See Card	
_					A demonstrate the second secon
1527 36711	26711 at	HSSOGA DKFZPS AL021977	AL021977	Ī	chromosome 22 open readility liaille 3
250	i to	DIAM 4	AI 008583	29	chromobox homolog 6
350					
					dJ738P15.2 (CD39-like 2 (a nucleoside
	10 070 OF	4 1738D15 1	AI 035252		phosphatase))
12C1	1529 39670 81	100 100		sins: Tr:O94136 Sw:Q99798	
					dJ347H13.1 (aconitase 2, mitochondrial
					(Aconitate Hydratase, EC 4.2.1.3, Citrate
1001	4E90/37480 at	AC.02	AL 023553		Hydrolyase))
3	07 103_at	7005		527	
7	4504 44005 04	TAYBERGY TYRE	YEE A1 022312		activating transcription factor 4
	41235 at	- 1			dJ117516.1 (Ras inhibitor JC265 (Has
				match: proteins: Tr:Q00425 Sw:Q13671	association (RaIGDS/AF-6) domain
	400	A 14 47516 4	AI OAGE38		containing protein))
1532	1532 36550 at	20071	2000	4621 Tr:Q64012	
				Sw.P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
4500	te 0200000	D5.42	AI 031668	Sw:Q14011 Sw:P26686	isoform
3	33300 at	1 342		match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
7627	2000	A MASKIE 1	AI 034374	Sw.P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
7	1334 3302 1 - at	210	1111861	maternal G10 transcript	maternal G10 transcript
1000	1333 39029 at	MANT	X96401	MAX binding protein	ROX protein
	33143_at	I NII NI			MAX interacting protein 1, isoform a; MAX
1	20070	NAVI4	107648	MAX interacting protein 1	interacting protein 1, isoform b
20	1537 39072 at	INVIN			MAX interacting protein 1, isoform a; MAX
4520	4E20 CEA 24	MXII	107648	MAX interacting protein 1	interacting protein 1, isoform b
3	5			MCM2 minichromosome maintenance	
1530	1530 35312 at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
				MCM3 minichromosome maintenance	
				deficient 3 (S. cerevisiae) associated	
1540	1540 40469 at	MCM3AP	AB011144	protein	KiAA0572 protein
3					

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Τ				MCM6 minichromosome maintenance	
				deficient 6 (MIS5 homolog, S. pombe) (S.	
341	1541 40117_at	MCM6	D84557	cerevisiae)	HsMcm6
				Meis1, myeloid ecotropic viral integration	
342	1542 41388_at	MEIS2	AF017418	site 1 homolog 2 (mouse)	homeobox protein MEIS2
Γ				Meis1, myeloid ecotropic viral integration	
543	1543 37486_f_at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
Γ				mel transforming oncogene (derived from	
44	1544 35340_at	MEL	AI819948	cell line NK14)- RAB8 homolog	
Γ				melanoma antigen, family A, 2, copy a;	
				similar to GenBank Accession Number	
545	1545 36500_at	MAGEA2A	AF027974	L18920	melanoma antigen family A2a
546	1546 41139_at	MAGED1	W26633	melanoma antigen, family D, 1	
547	1547 39327 at	D2S448	D86983	Melanoma associated gene	
				membrane cofactor protein (CD46,	membrane cofactor protein (CD46,
				trophoblast-lymphocyte cross-reactive	trophoblast-lymphocyte cross-reactive
548	1548 38441_s_at	MCP	X59408	antigen)	antigen)
				membrane component, chromosome 11,	
549	1549 39471 at	M11S1	Z48042	surface marker 1	GPI-anchored protein p137
				membrane component, chromosome 17,	
				surface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
550	1550 33444 at	M17S2	D30756	antigen CA125)	surface marker 2
				membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	
551	1551 1389_at	MME	J03779	CALLA, CD10)	membrane metallo-endopeptidase
				mesenchyme homeo box 2 (growth arrest-	
552	1552 40399 r at	MEOX2	AI743406	specific homeo box)	
				Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
				initiation codon in vitro; Homo sapiens	
				porin (por) mRNA, complete cds and	,
1553	1553 37697_s_at	por	T08666	truncated cds.	porin
1554	1554 40244 s at	MPPE1	AI743654	metallo phosphoesterase	

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metallothionein (MT)-like gene; H.sepiens pseudogene for metallothionein and research MTZA AI547258 metallothionein 2A methodogene for methodogene for methodogene for methodogene for methodogene methodogene methodogene for methodogene for methodogene for methodogene for methodogene for methodogenes (NAD+ dependent). MMDZ X16396 methodogenes (NAD+ dependent), me	r			(w
MT2A AI547258 metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and MT2A AI547258 metallothionein 2A metallothionein 2A MT7A AF053551 metallothionein 2A metal-regulatory transcription factor 1 metal-regulatory transcription factor 1 metasitasis associated 1 metasin 2 AF053551 metasis associated 1 metasin 2 AF053551 metasis associated 1 metasin 2 AF072242 methionine-tRNA synthetase 1 methiony aminopeptidase 1 methiony aminopeptidase 1 methyl-CpG binding domain protein 1 MBD1 AF072242 methyl-CpG binding domain protein 2 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 2 methylene tetrahydrofolate cyclohydrolase 1 methylene tetrahydrofolate cyclohydrolase 1 methylene tetrahydrofolate cyclohydrolase 1 methylmaloryl Coenzyme A methodomain protein 1 methylmaloryl Coenzyme A mutasa 1 methylmaloryl Coenzyme A mutasa 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A mutasa 2 molecule (MICB) gene, complete 1 methylmaloryl Coenzyme A microsimking factor 1 microthylle-associated protein 1 micro	┪	4	20	,		
MT2A X55503 AG/CT repetitive element. Interpretation MT2A AIS47258 metallothionein 2A MTA1 U35113 metallothionein 2A MTX2 AF053551 metalothionein 2A MMT2 AF053551 metalothionein 2A MBD1 V10746 methionine-tRNA synthetase MBD2 AF072250 methiol-CpG binding domain protein 1 MBD3 AF072250 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 1 MBD4 AF072250 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 1 MTHFD1 AF072250 methyl-CpG binding domain protein 4 MTHFD2 X16396 methyl-CpG binding domain protein 4 MMTHFD1 J04031 (NADP+ dependent), methylitetrahydrofolate cyclohydrolase, with the acceptance for the accepta					metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and	
MT2A AIS47256 metallothionein 2A MT71 X78710 metalregulatory transcription factor 1 in metaxin 2 MTA1 U35113 metaxin 2 MARS X94754 methionine-tRNA synthetase 1 MBD1 X10746 methionine-tRNA synthetase 1 MBD2 AF072242 methionine-tRNA synthetase 1 MBD4 AF072240 methyl-CpG binding domain protein 1 1 MBD4 AF072250 methyl-CpG binding domain protein 4 4 MBD4 AF072250 methyl-CpG binding domain protein 4 4 MBD4 AF072250 methyl-CpG binding domain protein 4 4 MMB04 AF072250 methyl-CpG binding domain protein 4 4 MMTH-D2 X16396 methyl-dependent), methyl-dependent), methylitetrahydrofolate cyclohydrolase, (NAD+ dependent), methylmianetetrahydrofolate cyclohydrolase, (NAD+ dependent), methylmianetetrahydrofolate synthetase MMC5131 Methylmianetetrahydrofolate cyclohydrolase, (NAD+ dependent), methylmianetet	55					metallothionein
MTF1 X78710 metal-regulatory transcription factor 1 Information MTA1 U35113 metasitasis associated 1 Information MARS X94754 methionine-tRNA synthetase Information MBD1 Y10746 methionine-tRNA synthetase Information MBD2 AF072242 methyl-CpG binding domain protein 1 MBD4 AF072250 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 MBD4 AF072250 methyl-CpG binding domain protein 4 MMD4 AF072250 methyl-CpG binding domain protein 4 MMD4 AF072250 methylenglese 1 MMD4 AF072250 methylenglese 2 MMTHD1 J04031 formyletrahydrofolate cyclohydrolase MUT M65131 methylmalonyl Coenzyme A mutase MMC class I chain-related gene B; CDNA sequence deposited under GenBank Accession Number X91625; Human MHC Lat MFAP1 U04209 microfibrillar-associated protein 1 MGS12 U074209 microfibrillar-associated	18	39081 at	MT2A			
MTA1 U3513 metastasis associated 1 metastasis associated 1 metasta metasin 2 metasin 2 metasin 2 metasin 2 methologe	57	38945 at	MTF1		-	metal-regulatory transcription factor
MTX2 AF053551 metaxin 2 MARS X94754 methionine-tRNA synthetase 1 MEDA MEDA methyl-CpG binding domain protein 1 MBD1 Y10746 methyl-CpG binding domain protein 2 MBD2 AF072242 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 methyl-CpG binding domain protein 4 methyl-cpG binding domain protein 4 methyl-CpG binding domain protein 4 methyl-cpG binding domain protein 4 MTH-Cp1 J04031 methyl-cpG binding domain protein 4 MTH-Dp1 J04031 methylenetathydrofolate cyclohydrolase MUT MES131 methylinalonyl Coenzyme A mutase MICB U04203 methylinalonyl Coenzyme A mutase MFAP1 U04209 microfibrillar-associated protein 1 MACF1 MACF1 MES00599 microfibrillar-associated protein 1 <	58	1643 q at	MTA1			metastasis associated protein
MARS X94754 methionine-tRNA synthetase MBD1 D42084 methionyl aminopeptidase 1 MBD1 Y10746 methyl-CpG binding domain protein 1 MBD2 AF072250 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 methylene tetrahydrofolate dependent), methylene tetrahydrofolate eyclohydrolase (NAD+ dependent), methylenetarahydrofolate cyclohydrolase, (NADP+ dependent), methylenetarahydrofolate cyclohydrolase, comylete case, iormyltetrahydrofolate cyclohydrolase, comylete case, iormyltetrahydrofolate cyclohydrolase, complete case, indicated protein 1 microfubule-associated protein 1 mic	59	35642_at	MTX2	AF053551		metaxin 2
METAP1 DA2084 methionyl aminopeptidase 1 MBD1 Y10746 methyl-CpG binding domain protein 1 MBD2 AF072242 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 MBD4 AF072250 methyl-CpG binding domain protein 4 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 4 methyl-CpG binding domain protein 2 methyl-CpG binding domain protein 4 methyl-CpG binding domain protein 2 methyl-CpG binding domain protein 4 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 methyl-CpG binding domain protein 1 microtubule-associated protein 1 methyl-CpG binding domain protein 1 microtubule-associated protein 1	99	39342 at	MABS	X94754		yeast methionyl-tRNA synthetase homolog
MBD1 Y10746 methyl-CpG binding domain protein 1 MBD2 AF072242 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 MBD4 MAD4 MAD4 MBD4 AF072250 methylenghydrofolate synthetaenge (NAD4 dependent), methylenghydrofolate cyclohydrolase, methylenghydrofolate cyclohydrolase, methylenghydrofolate synthetaenge (NAD4 methylenghydrofolate cyclohydrolase, synthetaenghydrofolate synthetaenghydrofolatenghydrof	<u>Ş</u>	37619 at	METAP1	D42084		
MBD2 AF072242 methyl-CpG binding domain protein 2 MBD4 AF072250 methyl-CpG binding domain protein 4 MBD4 AF072250 methyl-CpG binding domain protein 4 MTHFD1 X16396 methylene tetrahydrofolate cyclohydrolase (NAD+ dependent), methylenetarahydrofolate cyclohydrolase (NAD+ dependent), methylenetarahydrofolate cyclohydrolase, methonyletrahydrofolate cyclohydrolase, methonyletrahydrofolate synthetase t MUT M65131 methylenetarahydrofolate cyclohydrolase, methonyletrahydrofolate synthetase t MUT M65131 methylmalonyl Coenzyme A mutase t MICB Sequence deposited under GenBank Accession Number X91625, Human MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625, Human MHC class I molecule (MICB) gene, complete cds. tt MGS12 U04209 microfibrillar-associated protein 1 microphthalmia-associated protein 1 microphthalmia-associated protein 1 microphyllamia-associated protein 1 microtubule-associated protein 1 microt	18	41828 at	MBD1	Y10746	protein 1	methyl-CpG binding protein
MBD4 AF072250 methyl-CpG binding domain protein 4 methylene tetrahydrofolate dehydrolase dehydrogenase (NAD+ dependent). MTHFD2 X16396 methylenetetrahydrofolate cyclohydrolase (NAD+ dependent). methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase formyltetrahydrofolate formyltetrahydrofolate formyltetrahydrofolate formyltetrahydrofolate formyltetrahydrofolate formyltetrahydrofolate formyltetrahydrofolate synthetase formyltetrahydrofolate formylthalminetrahydrofolate formylthalminetrahydrofolate formylthalmin	8	33905_at	MBD2	AF072242		methyl-CpG binding protein MBU2
MTHFD2 X16396 methylene tetrahydrofolate dehydrolase methylenetrahydrofolate cyclohydrolase methylenetrahydrofolate cyclohydrolase (NAD+ dependent), methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase methylmalonyl Coenzyme A mutase MUT M65131 methylmalonyl Coenzyme A mutase MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds. MICB U65416 cds. MICB U65416 cds. MITF AB006909 factor microphthalmia-associated transcription factor MACF1 AB007934 microtubule-actin crosslinking factor 1 microtubule-associated protein 1A microtubule-associated protein 1A microtubule-associated protein 1A microtubule-associated protein 4	8	34386_at	MBD4	AF072250		methyt-CpG binding protein MBU4
tt MUT MG5131 It MUT M65131 It MICB U65416 It MFAP1 U04209 It MFAP1 U04209 It MAST2 U77604 It MACF1 AB007934 It MAP1A W26631 It MAP1A W26631	565	40074_at	MTHFD2	X16396	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyitetrahydrofolate cyclohydrolase, precursor
MUT MEST31 methylmatonyl Coenzyme A mutase MUT MEST31 methylmatonyl Coenzyme A mutase MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds. MICB U65416 cds. MICB U65416 cds. MITF AB006909 microphthalmia-associated protein 1 microphthalmia-associated transcription factor MGST2 U77604 microtubule-actin crosslinking factor 1 at MACF1 AB007934 microtubule-actin crosslinking factor 1 at MAP1A W26831 microtubule-associated protein 1A microtubule-associated protein 1A microtubule-associated protein 1A microtubule-associated protein 1A					methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase,	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
MUT MOT MEST 31 mennyimalonyi Coencyme A mutase MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds. MICB U65416 cds. MEAP1 U04209 microphthalmia-associated protein 1 microphthalmia-associated transcription factor microphthalmia-associated transcription microtubule-actin crosslinking factor 1 microtubule-actin crosslinking factor 1 microtubule-associated protein 14	8	674 g at	MIHFD1	J04031	Tormyletranydrologae synnierase	mothylmologid CoA mittee
sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete at MFAP1 U04209 microfibrillar-associated protein 1 microphthalmia-associated transcription microphthalmia-associated transcription factor at MACF1 AB006909 factor at MAP14 W26631 microtubule-associated protein 1A	267	40105_at	MOT	M65131	MHC class I chain related gene B; cDNA	
MICB U65416 Cds. Implement As 1023, Further Mic Leas I molecule (MICB) gene, complete					sequence deposited under GenBank	
at MICB U65416 cds. at MFAP1 U04209 microfibrillar-associated protein 1 g MITF AB006909 factor MGST2 U77604 microsomal glutathione S-transferase 2 at MACF1 AB007934 microtubule-associated protein 1A at MAP1A W26631 microtubule-associated protein 1A at MAP4 W28892 microtubule-associated protein 4					Accession number As Iozo, numer mino class I molecule (MICB) gene, complete	
MFAP1 U04209 microfibrillar-associated protein 1 microphthalmia-associated transcription microphthalmia-associated transcription factor MGST2 U77604 microsomal glutathione S-transferase 2 microtubule-actin crosslinking factor 1 at MAP1A W26631 microtubule-associated protein 1A microtubule-associated protein 1A microtubule-associated protein 4	565	35937 at	MICB	U65416	cds.	MHC class I molecule
microphthalmia-associated transcription MITF AB006909 factor		36535 at	MEAP	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
1_at MITF AB006909 factor MGST2 U77604 microsomal glutathione S-transferase 2 at MACF1 AB007934 microtubule-actin crosslinking factor 1 at MAP1A W26631 microtubule-associated protein 1A at MAP4 W28892 microtubule-associated protein 4	3				microphthalmia-associated transcription	A-type microphthalmia associated
MGST2 U77604 microsomal glutathione S-transferase 2 AB007934 microtubule-actin crosslinking factor 1 MAP1A W26631 microtubule-associated protein 1A at MAP4 W28892 microtubule-associated protein 4	57) 38228 g_at	MITE	AB006909	factor	transcription factor
at MACF1 AB007934 microtubule-actin crosslinking factor 1 at MAP1A W26631 microtubule-associated protein 1A at MAP4 W28892 microtubule-associated protein 4	57	1 820 at	MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
at MAP1A W26631 at MAP4 W28892	57,	2 38704_at	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
MAP4 W28892	57,	3 35917_at	MAP1A	W26631	microtubule-associated protein 1A	
	57	4 33850_at	MAP4	W28892	microtubule-associated protein 4	

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Γ				ciated protein, RP/EB	
1575	1575 33456_at	MAPREI	U24166		EB1
Γ				microtubule-associated proteins 1A/1B	
1576	1576 39370_at	MAP1A/1BLC3	W28807		
1577	1577 34296 at	MID1	AF041210		midline 1 fetal kidney isoform 3
1578	1578 34403 at	MFGE8	U58516		BA46
Γ				mitochondrial ATP synthase regulatory	
1579	1579 40027_at	ATPW	W52999		
1580	37174_at	MRPL19	D14660	6	mitochondrial ribosomal protein L19
1581	37726 at	MRPL3	X06323		mitochondrial ribosomal protein L3
1582	1582 39717 g at	MRPL33	AI597616		
1583	1583 32221_at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	1584 38899 s at	MFN1	U95822	mitofusin 1	putative transmembrane GTPase
1585	1585 34369_at	MFN2	D86987		KIAA0214 protein
1586	1586 36577 at	MIG2	Z24725	lucible 2	mitogen inducible gene mig-2
1587	1587 37733 at	MAPK14	L35263	rotein kinase 14	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692		p97mapk
1589	1589 38431 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1590 1238 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1591 1130_at	MAP2K1	L11284	-	mitogen-activated protein kinase kinase 1
				mitogen-activated protein kinase kinase	
1592	1592 1327_s_at	MAP3K5	U67156	kinase 5	mitogen-activated kinase kinase kinase 5
				mitogen-activated protein kinase kinase	
1593	1593 36905_at	MAP3K7	AB009356	kinase 7	I GF-Deta activated Kinase 1a
				mitogen-activated protein kinase kinase	
1594	1594 38980_at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	
1595	1595 35694_at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179_at	MAPKAPK2	U12779	protein kinase 2	MAP Kinase activated protein Kinase 2
				mitogen-activated protein kinase-activated	
1597	1597 1637_at	MAPKAPK3	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1599	1599 38437 at	MLN51	X80199	MLN51 protein	MLN51 protein

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1		٥		MMS19-like (MET18 homolog, S.	
909	1600 35273_at	MMS19L	AF007151		MMS19 (MET18 S. cerevisiae)-like
<u>8</u>	1601 34767_at	MAP-1	Al670788	modulator of apoptosis 1	
1602	1602 41771 g_at	MAOA	AA420624		
1603	1603 41772_at	MAOA	M68840	monoamine oxidase A	monoamine oxidase A
1604	1604 41770 at	MAOA	AA420624		
188	1605 37628 at	MAOB	M69177		monoamine oxidase B
				ge differentiation-	monocyte to macrophage differentiation-
1606	1606 37565 at	MMD	X85750	associated	associated, precursor
1607	1607 40861 at	MRGX	D14812	MORF-related gene X	MORF-related gene X
				M-phase phosphoprotein 10 (U3 small	
1608	1608 33797_at	MPHOSPH10	X98494	nucleolar ribonucleoprotein)	M phase phosphoprotein 10
1609	1609 34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
1610	1610 35992 at	MSC	AF087036	musculin (activated B-cell factor-1)	musculin
1611	1611 31884 at	MLH3	L40399	mutt homolog 3 (E. coli)	mutL homolog 3
				mutS homolog 2, colon cancer,	
1612	1612 860 at	MSH2	U03911	nonpolyposis type 1 (E. coli)	mutS homolog 2
1613	1613 2003 s at	MSH6	U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
1614	1614 33769 at	MPZL1	AF087020	myelin protein zero-like 1	protein zero related protein
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1615	1615 33146 at	MCL1	L08246	related)	related)
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1616	1616 277 at	MCL1	L08246	related)	related)
				myeloid/lymphoid or mixed-lineage	myeloid/lymphoid or mixed-lineage leukemia
				leukemia (trithorax homolog, Drosophila);	(trithorax homolog, Drosophila); translocated
1617	1617 39037_at	MLLT2	L13773	translocated to, 2	to, 2
1618	1618 41637 at	MYLE	AF108145	MYLE protein	DEXI
1619	1619 41439 at	MYO1B	AJ001381	myosin IB	myh-1c
1620	1620 35729_at	MYO1D	AB018270	myosin ID	KiAA0727 protein
1621	1621 37631_at	MYO1E	U14391	myosin IE	myosin-IC
1622	2 38251 at	MLC1SA	Al127424	myosin light chain 1 slow a	
1623	1623 41187_at	MLC-B	U26162	myosin regulatory light chain	myosin regulatory light chain
1624	1624 35362_at	MYO10	AB018342	myosin X	KIAA0799 protein
100	1000 00447 04	80	XE4304	myosin, light polypeptide, regulatory, non- serromeric (20kD)	myosin, light polypeptide, regulatory, non- Imyosin, light polypeptide, regulatory, non- serromenic (20kD)
162	1626 35739 at	MTMR3	AB002369	myotubularin related protein 3	myotubularin related protein 3
		211111111			

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	A	В	2		
1627	39707_at	MTMR4	AB014547		KIAA0647 protein
1628	1628 38035 at	MTMR6	AF072928		myotubularin related protein 6
1629	1629 39607 at	MTMR8	AL080178		hypothetical protein
88	1630 36692 at	MTMR8	AF052099	myotubularin related protein 8	
				mynistoylated alanine-rich protein kinase C	
1831	1631 32434_at	MARCKS	D10522	substrate	80K-L protein
1632	1632 39267 at	AGM1	AF102265	N-acety/glucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
				N-acylsphingosine amidohydrolase (acid	
1633	1633 36938_at	ASAH	U70063	ceramidase)	acid ceramidase
				N-acylsphingosine amidohydrolase (acid	de di marco
<u>4</u>	1634 461_at	ASAH	0/0003	ceraminase)	מטומ לסומווותמסס
1635	36169_at	NDUFA1	N47307	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	
				NADH dehydrogenase (ubiquinone) 1	NADH-ubiquinone oxidoreductase subunit Cl
1636	1636 40546_s_at	NDUFA2	AF047185	alpha subcomplex, 2 (8kD, B8)	88
				NADH dehydrogenase (ubiquinone) 1	NADPH:ubiquinone oxidoreductase subunit
1637	1637 38462_at	NDUFAS	U64028	aípha subcomplex, 5 (13kD, B13)	B13
				NADH dehydrogenase (ubiquinone) 1	
1638	1638 32752_at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	1639 38605_at	NDUFB1	AI345944	subcomplex, 1 (7kD, MNLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981_at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 beta NADH-ubiquinone oxidoreductase subunit Ci
1641	1641 32232_at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGUH
				NADH dehydrogenase (ubiquinone) 1 beta	
1642	1642 32774_at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
1643	1643 38485_at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NAUH denydrogenase
<u>\$</u>	1644 38395_at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
1645	1645 38695 at	NDUFS4	AA203303	reductase)	
	m=-				

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				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 5 (15kD) (NADH-coenzyme Q	
1646	1646 38060_at	NDUFS5	AI541336	reductase)	
				NADH dehydrogenase (ubiquinone)	
1647	1647 34893_at	NDUFV2	AI557064	flavoprotein 2 (24kD)	
				natriuretic peptide receptor C/guanylate	
				cyclase C (atrionatriuretic peptide receptor	
1648	1648 34519_at	NPR3	M59305	_	atrial natriuretic peptide clearance receptor
1649	1649 34234 1 at	NKIH	Al688640	common sedneme	
1650	1650 41795_at	NCK1	X17576		NCK adaptor protein 1
1651	1651 33357_at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652	1652 36073_at	NDN	U35139	necdin homolog (mouse)	NECDIN related protein
1653	1653 34202 at	DKFZP566B0846	846 AL050071	nectin 3	hypothetical protein
1654	1654 34264 at	NESCA	AB026894	nesca protein	NESCA
1655	1655 38719 at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
				neural precursor cell expressed,	
1656	1656 39356 at	NEDD4L	AB007899	developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
					neural precursor cell expressed,
1657	1657 40281 at	NEDDS	D63878	developmentally down-regulated 5	developmentally down-regulated 5
L				neural precursor cell expressed,	
1658	1658 1695 at	NEDD8	D23662	18	ubiquitin-like protein
					neuroblastoma, suppression of
1659	1659 37005 at	NBL1	D28124		tumorigenicity 1
1660	1660 31896 at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
99	1661 37286 at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
166	1662 37673_at	NSMAF	X96586	activation associated factor	FAN protein
				NGFI-A binding protein 1 (EGR1 binding	
<u> </u>	1663 38692_at	NAB1	AF045451	\neg	transcriptional regulatory protein p54
1664	4 34835 at	NCSTN	D87442	nicastrin	
166	1665 37032_at	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyttransferase
			00707		asenanoshudanast abitoaloma pinamitosin acononoshudanast abitaalama elimenista
8	1666 41722_at	I N	040490	nicolinamide nucieoude (Ialistiyatogeliase	miconialina maranta maranyarasa
166	1667 35366_at	QIN	M30269	inidogen (enactin)	magonii
166	8 753_at	NID2	D86425	nidogen 2	osteonidogen

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1669	37047_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670	1670 980_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671	39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
	35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673 36047	36047_at	NEK1	AL050385	kinase 1	
1674	1674 35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675	1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677	39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
1678	1678 36472_at	IMN	U32849	N-myc (and STAT) interactor	Nai
1679	1679 36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680	1680 41656_at	NMT2	AF043325	N-myristoyftransferase 2	N-myristoyltransferase 2
				non-canonical ubquitin conjugating	
1681	1681 39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
1682	1682 39039_s_at	NCUBE1	AI557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683 1521	1521_at	NME1	X17620	expressed in	Nm23 protein
				non-metastatic cells 2, protein (NM23B)	
1684	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685	1685 1980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
1686	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687	1687 38750_at	NOTCH3	N97669	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	1689 40122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	1690 33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
				N-sulfoglucosamine sulfohydrolase	
1691	35626_at	SGSH	U30894	(sulfamidase)	N-sulphoglucosamine sulphohydrolase
1692	1692 37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	1694 40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1605	1605 30780 of	NCBB3	A A 1 4 G A 2 B	nuclear cap binding protein subunit 2,	
2	32/09_all	INCOFE	143450	·	

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\sqcap		homolog	C1D protein	NDP52	_				int 3 cytoplasmic, calcineurin-dependent 3	eb	nuclear factor kappa-B DNA binding subunit		nuclear factor Kappa-B DIVA binding Subunin				r 4 CAGH1 alternate open reading frame	_	IEF SSP 9502		Amplified in Breast Cancer	Ret fused gene	ein 1 nuclear factor RIP140					nuclear RNA export factor 1	ıta	binding	ox binding NFX1	binding
Q	nuclear distribution gene C homolog (A.	nidulans)	nuclear DNA-binding protein	nuclear domain 10 protein	nuclear factor (erythroid-derived 2)-IIKe 2	nuclear factor NF-IL6 (AA 1-345); Human	gene for nuclear factor NF-IL6.	nuclear factor of activated T-cells,	cytoplasmic, calcineurin-dependent 3	nuclear factor of kappa light polypeptide	gene enhancer in B-cells 1 (p105)	nuclear factor of kappa light polypeptide	gene enhancer in B-cells 1 (p105)	nuclear factor of kappa light polypeptide	gene enhancer in B-cells inhibitor, alpha	nuclear factor, interleukin 3 regulated	nuclear matrix transcription factor 4	nuclear phosphoprotein similar to S.	cerevisiae PWP1	nuclear receptor coactivator 2	nuclear receptor coactivator 3	nuclear receptor coactivator 4	nuclear receptor interacting protein 1	nuclear receptor subfamily 2, group F,	member 2	nuclear receptor subfamily 3, group C,	member 1	nuclear RNA export factor 1	nuclear transcription factor Y, beta	nuclear transcription factor, X-box binding	nuclear transcription factor, X-box	nuclear transcription factor, X-box 1 nuclear. Homo saniens tyrosine
0		AB019408	X95592		S74017		CRIX52560		L41067		M58603		M58603		M69043	X64318	U80760		L07758	A1040324	AF012108	X77548	X84373		M64497		M10901	AJ132712	AA621555		U15306	U15306
В		NUDC		52	NFE2L2		CEBPB: LAP: CRI	-I	NFATC3		NFKB1		NFKB1		NFKBIA				PWP1	NCOA2	NCOA3	NCOA4	NRIP1		NR2F2		NR3C1	NXF1	NFYB		NFX1	NFX1
A		1696 35836 at			1699 853_at		1700 38354 at		1701 40822 at		1702 38438 at		1703 1377_at		1704 1461 at	1705 37544 at	1706 38648 at		1707 40816 at	708 34312 at	1709 33381 at	1710 39174 at	1711 40088 at		1712 39397 at		1713 36690 at	1714 35302 at	1715 37928 at		1716 34667_at	34667_at
r	\vdash	16963	16973	16984	1699		1700 :		1701		1702		1703		1704	1705	1706		1707	1708	1709	1710	?		1712		1713	1714	1715		1716	1716

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_				nuclease sensitive element binding protein	
<u>।718िड</u>	1718 32340_s_at	NSEP1			nuclease sensitive element binding protein-i
1719	1719 35643_at			nucleobindin 2	NEFA protein
-	10101	0	031262	OBE	
Ş	1/20 3639/_at	NOLO!		Hadiodai antoino ich protoin	Avetaina-rich profein
1721	1721 37520_at		AJUUGSSI	ווכון אוסיפוויו	Cystolic TPace
1722	36930_at	INTIG	L05425		illucional del aso
1723	1723 39390_at	NUP133	AF052123		
1724	1724 32850_at	NUP153	Z25535	0	nuclear pore complex protein nnup 153
1725	39024 at	NUP98	AF042357	nucleoporin 98kD	
1726	1726 571 at	NAP1L1	M86667	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1727	1727 743 at	NAP1L3	D50370	nucleosome assembly protein 1-like 3	nucleosome assembly protein
1728	1728 32575 at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	1729 36127 g at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
	ľ			nudix (nucleoside diphosphate linked	diphosphoinositol polyphosphate
1730	1730 41584 at	NUDT3	AF062529	moiety X)-type motif 3	phosphohydrolase
1731	1731 37693 at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
				ob15e02.s1 NCI_CGAP_Kid3 Homo	
				sapiens cDNA clone IMAGE:1323770 3'	
				similar to SW:ROA3_HUMAN P51991	
				HETEROGENEOUS NUCLEAR	
				RIBONUCLEOPROTEIN A3;, mRNA	
1732	35916 s at	INHBC	AA877215	sequence.	
1733	1733 34169 s at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocr11
				offactory receptor; Human offactory	Ç.
1734	1734 31921_at	OLF3	U56421	receptor (OLF3) gene, complete cds.	TSOLTS
				O-linked N-acetylglucosamine (GlcNAc)	
				transferase (UDP-N-	
				acetylglucosamine:polypeptide-N-	
1735	1735 39507_at	OGT	AL050366	acetyiglucosaminyi transferase)	hypothetical protein
1736	40332 at	OGFR	AF109134	opioid growth factor receptor	
1737	1737 39745 at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
1738	1738 41744 at	OPTN	AF070533	optineurin	optineurin
				OR11-3; offactory receptor; Homo sapiens	
				OR7E12P pseudogene, complete	
1739	1739 34539 at	OR7E12P	AF065854	sequence.	

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	V	B	د		Figo cinconolos ceimais o t
\$	1740 AFFX-BioC-3_at bioA		J04423	- THO	7 o dismino polorgonic acid
					, o diaminio por a gone dois
1741	1741 AFFX-BIOB-M_atbloA		104423		7 8-diamino-nelardonic acid
1742	1740 AEEX. Bio Dn. 5 abio 4		.104423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFFX-BioDn-3 abioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5 at bioA	bioA	J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	
1745	1745 32412 at	RPS14	M13934 °		unknown protein; ribosomal protein 514
				ORF1; ORF 2; no start codon; Human	
				ylase	
1746	1746 1315 at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
				> Time to be a control of the contro	
				2	edulo reference > bionitar
1747	1747 32800_at	RXRA; NR2B1	U66306	╗	retirioid A receptor, aipiria
				ecognition complex, subunit 5-like	ongin recognition complex subunit 3
1748	1748 38155_at	ORCSL	U92538	(yeast)	Bolomon
				ornithine aminotransferase (gyrate	
1749	1749 36636_at	OAT	M12267	atrophy)	omithine aminotransferase
					وماناتان وسيدناس
1750	1750 1959_at	OAZIN	D88674	ornithine decarboxylase antizyme initionor	anazyma mmonol
1751	33367 s at	OAZIN	D88674	omithine decarboxylase antizyme inhibitor antizyme inhibitor	antizyme inhibitor
				ornithine decarboxylase; Human ornithine	omithine decemboxylase 1
1752	1752 1081_at	00001	M33/64	decarboxykase gene, complete cus.	
				orphan G protein-coupled receptor; normo	
1759	1753 31700 at	GPB35	AF027957	(GPR35) gene, complete cds.	G protein-coupled receptor
	m=00110	201			
1754	1754 1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciciin I-like) osteoblast specific factor 2	osteoblast specific factor 2
476	: 307774 ot	OXA1	X80695	oxidase (cytochrome c) assembly 1-like	oxidase (суtосhrome с) assembly 1-like
ř	1/32/33/14_a	COMILE	NOOON .	(C)	

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T	V	a		<u> </u>	п
1756	1756 39136 at			nsive 1	oxidative-stress responsive 1
1757	1757 41438 at	18			oxysterol-binding protein-like protein 8
1758	1758 34329_at			9.2	
1759	1759 39710_at		U30521		P311 HUM
1760	36136_at		AF010315	p53-induced protein	Pig11
1761	1761 40441 g at	8P1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1762	1762 40440_at	1	AL080119		hypothetical protein
1763	1763 32001 s at	PACE4	M80482	paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
					paired box gene 8, isoform PAX8A; paired
					box gene 8, isoform PAX8B; paired box
					gene 8, isoform PAX8C; paired box gene 8,
					isoform PAX8D; paired box gene 8, isoform
1764 121	121_at	PAX8	66969X	paired box gene 8	PAX8E
1765	1765 40127_at		M95929	paired mesoderm homeo box 1	homeobox protein
1766	1766 41191_at	1992	AB023209	palladin	KIAA0992 protein
1767	1767 40504_at	PON2	AF001601	paraoxonase 2	paraoxonase
				ted by FGENES and	
1768	1768 36032_at	dJ167A19.1	AL031427		hypothetical protein
1769	39243_s_at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	1770 41665_at	PCF11	AB020631	PCF11p homolog	KIAA0824 protein
1771	1771 38758_at	PDAP1	R98910	PDGFA associated protein 1	
1772	1772 36937_s_at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	1773 32026_s_at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745_at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF; Human pigment epithelium-derived	
1775	1775 40856_at	SERPINF1; PEDF	EDF U29953	factor gene, complete cds.	pigment epithelium-derived factor
4776	776 1401 21	DTV3	Marree	pentaxin-related gene, rapidly induced by	tumor necrosis factor
?	1431_01	SVI	31.0%	1-1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	mondish dah sing alah samidating
				peptidylgiycine alpna-amidaung	peptidyigiycine alpha-amidating
	1/// 38465_at	PAM	M3//21	monooxygenase	IIIOIIOOXYgeriase
1778	1778 35823 at	PPIB	Me3573	peptidyfprofyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein

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	A	В	O	Q	ш
1	37499 at	Cidd	S71018	pentid/brolyl isomerase C (cyclophilin C)	cyclophilin C
	0) 76.E. CI	2		1	
1780	1780 37385 at	PPIG	U40763	(clophilin G	CARS-Cyp
1781	1781 36829 at	PER1	AF022991	period homolog 1 (Drosophila)	Rigui
1782	1782 35835 at	PDL-108	AB019409	protein	
					peripheral benzodiazapine receptor;
					peripheral benzodiazapine receptor short
1783	1783 32806_at	BZRP; MBR; PBR	PBR M36035	receptor (hpbs) mRNA, complete cds.	form
1784	38653_at		D11428	in protein 22	PMP-22(PAS-II/SR13/Gas-3)
1785	1785 41213 at	PRDX1	X67951		peroxiredoxin 1
					Aop1_Human, MER5(Aop1_Mouse)-like
1786	1786 36631_at	PRDX3	D49396	peroxiredoxin 3	protein
1787	1787 38435 at	PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788	1788 37900 at	PEX118	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789	1789 36864 at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
				peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790	1790 36625 at	ZAP128	L40401	thioesterase	thioesterase
				peroxisomal membrane protein 3 (35kD,	
1791	1791 33265_at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792	1792 36502_at	PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793	1793 37694_at	PHF3	D87685	PHD finger protein 3	PHD finger protein 3
					PHD zinc finger protein XAP135, isoform a;
1794	1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	PHD zinc finger protein XAP135, isoform b
,	1	ŭ L	1100436	phosphatase and tensin homolog	WWAC1
4706	1735 1454_at	PPAPOA	AF014402	phosphatidic acid phosphatase type 2A	type-2 phosphatidic acid phosphatase alpha-
2 2	1707 23862 at	DDADOR	AE017786	phosphatidic acid phosphatase type 2B	phosphatidic acid phosphohydrolase homolog
				phosphatidylinositol 4-kinase, catalytic,	
1798	1798 40783_s_at	PIK4CA	L36151	alpha polypeptide	phosphatidylinositol 4-kinase
1799	1799 37685 at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	CALM

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PIGA D11466		V	ď	O	Q	n
PIGA D11466 (paroxysmal noctumal hemoglobinuma)	T					
PIGB D42138 phosphatidylinositol glycan, class B PIGC D85418 phosphatidylinositol glycan, class F at PIGH L19783 phosphatidylinositol glycan, class F PIGH L19783 phosphatidylinositol glycan, class F phosphatidylinositol glycan, class F phosphatidylinositol glycan, class F phosphatidylinositol glycan, class F phosphatidylinositol transfer protein, phosphatidyliserine synthase 1 phosphatidylinositol transfer protein, phosphatidylinositide carboxykinase 2 phosphatidylinositide carboxykinase 1 at PGM1 V00572 phosphatide stransfer protein, at PGAM1 J04173 phosphatidylicente kinase 1 (brain) phosphatidylicentein entriched in astrocytes 15 phosphatidylicentein entriches 1 phosphatidyl	800	19993 at	PIGA			PIG-A protein
PIGC D85418 phosphatidylinositol glycan, class C PIGF D13435 phosphatidylinositol glycan, class F PIGH L19783 phosphatidylinositol glycan, class H phosphatidylinositol glycan, class H phosphatidylinositol transfer protein, membrane-associated phosphatidylinositol transfer protein, membrane-associated phosphatidylinositol transfer protein, membrane-associated phosphatidylinositol-thosphate 5- phosphatidylinositol-thosphate 5- phosphatidylinositol-thosphate 5- phosphatidyliserine synthase 1 phosphatidyliserine synthase 2 phosphatidio-syntae carboxykinase 2 phosphatidio-syntae 2 phosphatidio-syntae 2 phosphatidio-syntae 2 phosphatidio-syntae 2 phosphate 3 phosphatidio-syntae 2 phosphate 3 phosphatidio-syntae 3 phosphate 3 phosph	8013	114 at	PIGB			PIG-B
19 PIGE D13435 phosphatidylinositol glycan, class F phosphatidylinositol glycan, class H pige L19783 phosphatidylinositol glycan, class H phosphatidylinositol transfer protein, phosphatidylinositol transfer protein, phosphatidylinositol transfer protein, phosphatidylinositol d-phosphate 5- phosphatidylinositol-4-phosphate 5- phosphatidylinositol-4-phosphate 5- phosphatidylisenine synthase 1 phosphatidylisenine synthase 1 (phosphatidylisenine synthase 1 phosphatidylisenine synthase 1 (phosphatidylisenine synthase 1 phosphatidylisenine synthase 2 phosphatidylisenine synthase 2 phosphatidylisenine synthase 2 phosphatidylisenine synthase 2 phosphatidylisenine synthase 3 phosphatidylisenine synthase 1 phosphatidylisenine synthase 3 phosphatidid scramblase 1 (prain) subunit, polypeptide 3 (p55, gamma) phosphatidid scramblase 1 (past alphate synthase phosphatidsyl pyrophosphate synthase phosphatidsyl pyrophosphate synthase phosphatidsyl phosphatesyl pyrophosphate synthase phosphatidsyl phosphatesyl pyrophosphate synthase phosphatidsyl phosphatesyl pyrophosphate synthase phosphatidsyl phosphatesyl pyrophosphate synthase phosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesyl pyrophosphatesy	2	, T	Ceja			phosphatidylinositol-glycan-class C (PIG-C)
PIGH L19783 phosphatidylinositol glycan, class H	700	10.1	200			PIG-F
PITPNM X98654 membrane-associated phosphatidylinositol transfer protein, membrane-associated phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphatidyliserine synthase 1 phosphodiesterase 48, cAMP-specific (phosphodiesterase 48, cAMP-specific (phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, phosphodiestera		//b_ar	FIGE			phosphatidylinositol glycan, class H
PITPNIM X98654 membrane-associated phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphatidylinositol-4-phosphate 5-phosphodiesterase 4B, cAMP-specific (phosphodiesterase 4B, carboxykinase 2 (phosphodiesterase 4B, carboxykinase 2 (phosphodiesterase 4B, carboxykinase 3 (phosphodiesterase 4B, carboxykinase 3 (phosphodiesterase 4B, carboxykinase 4 (ph	2	40029 at	בפונ	3612		homologue of Drosphila retinal degeneration
PIPSK2B U85245 kinase, type II, beta hrosphate 5- to hosphatidylinositol-4-phosphate 5- to hosphatidyliserine synthase 1 to hosphatidyliseriase E4 dunce homolog, hosphatidyliseriase E4 dunce homolog, hosphatidiseriase E4 dunce homolog, hosphate synthetase phosphatidiseriase E4 dunce homolog, hosphatidiseriase E4 dunce homolog, hosphatidiseriase E4 dunce homolog, hosphatese E4 dunce homolog, hosphateseriase	1805	38297 at	MNdTid	X98654		B gene
PIPSK2B U85245 kinase, type II, beta PTDSS1 D14694 phosphatidylserine synthase 1 phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, 120971 Drosophila) PDE4BB L20971 Drosophila) PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphodiesterase		- Caro			phosphate 5-	phosphatidylinositol-4-phosphate 5-kinase
PTDSS1 D14694 phosphatidylserine synthase 1 PDE4B L20971 phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, phosphodiesterase BA PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A POKZ X92720 (mitochondrial) PGK1 V25328 phosphodiucornutase 1 PGM1 M83088 phosphoglucornutase 1 PGM1 V00572 phosphoglucornutase 1 PGAM1 J04173 phosphoglucornutase 1 PIK3R1 M61906 phosphoglycerate finase 1 (brain) PIK3R3 Z46973 phosphoglycerate finase 1 (brain) PIK3R1 M61906 subunit, polypeptide 1 (p85 alpha) PIK3R3 U90907 subunit, polypeptide 3 (p55, gamma) PEA15 X86809 phosphoprotein enriched in astrocytes 15 PRPR51 D00860 1	1806	35741 at	PIP5K2B	U85245		type II beta
PDE4B L20971 Drosophia) PDE4B L20971 Drosophia) PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphodiesterase 9A phosphodiesterase 9A phosphodiesterase 1 phosphodiesterate 6A phosphodiesterase 1 phosphodiesterate 6A phosphodiesterate 7A ph	1807	37320 at	PTDSS1	D14694		phosphatidylserine synthase 1
PDE4B L20971 Drosophila) PDE4B PDE4B L20971 Drosophila) PDE4DIP AB007923 (myomegalin) PDE8A AF056490 Phosphodiesterase 4D interacting protein PDE8A AF056490 Phosphodiesterase 8A PGK2 X92720 Posphoenolpyruvate carboxykinase 2 PGM1 M83088 Phosphofructokinase 1 PGM1 M83088 Phosphofructokinase 1 PGM1 J04173 Phosphoglucomate dehydrogenase PGK1 V00572 Phosphoglucomate dehydrogenase PGK1 V00572 Phosphoglycerate kinase 1 PK3C3 Z46973 Phosphoinositide-3-kinase , regulatory PIK3C3 Z46973 Phosphoinositide-3-kinase , regulatory PIK3R1 M61906 Subunit, polypeptide 1 (p85 alpha) PEA15 X86809 Phosphoprotein enriched in astrocytes 15 PRPS1 D00860 1					phosphodiesterase 4B, cAMP-specific	
PDE4B 120971 Drosophila) PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphodiesterase 1025328 phosphodiesterate 8A phosphodiesterase 1025328 phosphodiesterate 8A phosphodiesterase 10253 phosphodiesterate 8A phosphodiesterase 10253 phosphomiostitide-3-4Grase, class 3 phosphomiostitide-3-4Grase, class 3 phosphomiostitide-3-4Grase, class 3 phosphomiostitide-3-4Grase, regulatory 8 phosphomiostitide-3-4Grase, regul					(phosphodiesterase E4 dunce homolog,	
PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphoriosterase 8A phosphoriosterase 8A phosphoriosterase 8A phosphoriosterase 8A phosphoriosterase 8A phosphoriocondial) PCK2 X92720 (mitochondrial) PGM1 M83088 phosphorioconate dehydrogenase 1 phosphoglucomate dehydrogenase 1 phosphoglucomate dehydrogenase 1 phosphoglucomate dehydrogenase 1 phosphoglucomate dehydrogenase 1 phosphoglycerate kinase 1 (brain) phosphorioconate dehydrogenase 1 phosphoglycerate mutase 1 (brain) phosphoriositide-3-kinase, class 3 phosphoriositide-3-kinase, regulatory phosphoriositide-3-kinase, regulatory phosphoriositide-3-kinase, regulatory phosphoriositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) phosphoriositide-3-kinase, regulatory phosphoriositide-3-kinase, regulatory phosphoriositide-3-kinase, regulatory phosphoriosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase	1808	33705 at	PDE4B	120971	Drosophila)	phosphodiesterase
PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A PCK2 X92720 (mitochondrial) PCK2 X92720 (mitochondrial) PGM1 M83088 phosphoglucomutase 1 PGM2 U30255 phosphoglucomutase 1 PGM1 V00572 phosphoglycerate kinase 1 PGM1 J04173 phosphoglycerate kinase 1 PGM1 J04173 phosphoglycerate kinase 1 PGAM1 J04173 phosphoinositide-3-kinase, regulatory PIK3R1 M61906 subunit, polypeptide 1 (p85 alpha) phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulat					phosphodiesterase 4D interacting protein	
PDE8A AF056490 phosphodiesterase 8A phosphoenolpyruvate carboxykinase 2 phosphoenolpyruvate carboxykinase 2 (mitochondrial) PCK2 X92720 (mitochondrial) PGM1 M83088 phosphofructokinase, platelet PGM1 U30255 phosphoglucomutase 1 PGM1 V00572 phosphoglycerate kinase 1 PGM1 J04173 phosphoglycerate kinase 1 PGAM1 J04173 phosphoinositide-3-kinase, regulatory phk3R1 M61906 subunit, polypeptide 1 (p85 alpha) phosphoinositide-3-kinase, regulatory phosphoin	1809	39422 at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
PCK2 X92720 (mitochondrial) PCK2 X92720 (mitochondrial) PGM1 M83088 phosphofructokinase, platelet PGM1 M83088 phosphoglucomutase 1 PGM1 V00572 phosphoglucomutase 1 PGM1 V00572 phosphoglucomate dehydrogenase PGM1 J04173 phosphoglycerate kinase 1 PGAM1 J04173 phosphoglycerate intase 1 (brain) PGAM1 J04173 phosphoinositide-3-kinase, regulatory PIK3R1 M61906 subunit, polypeptide 1 (p85 alpha) phosphoinositide-3-kinase, regulatory	E	37676 at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
PCK2 X92720 (mitochondrial) PFKP D25328 phosphofructokinase, platelet PGM1 M83088 phosphoglucomutase 1 PGD U30255 phosphoglucomutase 1 PGM1 V00572 phosphoglucomutase 1 PGM1 V00572 phosphoglucomate dehydrogenase PGM1 V00572 phosphoglycerate kinase 1 (brain) PGAM1 J04173 phosphoinositide-3-kinase, regulatory PIK3R1 M61906 subunit, polypeptide 1 (p85 alpha) phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, re					phosphoenolpyruvate carboxykinase 2	
PFKP D25328 PGM1 M83088 PGD U30255 PGAM1 V00572 PIK3A3 Z46973 PIK3R1 M61906 PIK3R3 U90907 PEA15 X86809 PRPS1 D00860	1811	37188 at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
PGM1 M83088 PGD U30255 PGAM1 V00572 PIK3C3 Z46973 PIK3R1 M61906 PIK3R3 U90907 AT PEA15 X86809 PRPS1 PRPS1 D00860	1812	39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
PGD U30255 PGAM1 V00572 PGAM1 J04173 PIK3C3 Z46973 PIK3R1 M61906 PIK3R3 U90907 AR V86809 PRPS1 D00860	1813	32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
PGK1 V00572 PGAM1 J04173 PIK3C3 Z46973 PIK3R1 M61906 PIK3R3 U90907 AT PEA15 X86809 X86809 PRPS1 D00860	1814	36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
PGAM1 J04173 PIK3C3 Z46973 PIK3R1 M61906 PIK3R3 U90907 ABO06746 ABO06746 PEA15 X86809 PRPS1 D00860	1815	37677 at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
at PIK3R1 M61906 at PIK3R1 M61906 r at PLSCR1 AB006746 at PEA15 X86809 at PRPS1 D00860	1816	41221 at	PGAM1	J04173	phosphoglycerate/mutase 1 (brain)	phosphoglycerate mutase 2
PIK3R1 M61906 PIK3R3 U90907 at PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860	1817		PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
PIK3R1 M61906 PIK3R3 U90907 at PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860					phosphoinositide-3-kinase, regulatory	
at PLSCR1 U90907 AB006746 PEA15 X86809 PRPS1 D00860	1818	1269_at	PIK3R1	M61906	Subunit, polypeptide 1 (pos dipila)	
PIK3R3 U90907 at PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860					phosphoinositide-3-kinase, regulatory	
at PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860	1819	37961_at	PIK3R3	U90907	subunit, polypeptide 3 (p55, gamma)	
PEA15 X86809 PRPS1 D00860	1820	32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramplase 1
PRPS1 D00860	182	32260 at	PFA15	86809	phosphoprotein enriched in astrocytes 15	
PRPS1 D00860					phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase
	1822	36489_at	PRPS1	D00860		subunit I

Fig. 2

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Γ				phosphate synthetase-	phosphoribosypyrophosphate synthetase-
1823	1823 37338_at	PRPSAP1	D61391		associated protein 39
				phosphoribosylaminoimidazole	
				carboxylase,	phosphoribosylaminoimidazole carboxylase,
				phosphoribosylaminoimidazole	phosphoribosylaminoribosylaminoimidazole
1824	1824 39056 at	PAICS	X53793	•	succinocarboxamide synthetase
1825	1825/37392 at	PHKB	X84908		phosphorylase kinase
1826	1826 36667 at	PYGB	U47025	rain	glycogen phosphorylase B
				phytanoyl-CoA hydroxylase (Refsum	peroxisomal phytanoyl-CoA alpha-
1827	1827 32724 at	РНУН	AF023462	disease)	hydroxylase
1828	1828 33543 s at	PNN	U777718	pinin, desmosome associated protein	pinin
				pituitary tumor-transforming 1 interacting	
1829	1829 39003_at	PTTG11P	Z50022	protein	putative surface glycoprotein
1830	1830 34793_s_at	PLS3	M22299	plastin 3 (T isoform)	T-plastin polypeptide
				platelet-activating factor acetylhydrolase,	
1831	1831 32569_at	PAFAH1B1	L13385	isoform lb, alpha subunit (45kD)	Miller-Dieker lissencephaly protein
				platelet-derived growth factor receptor,	platelet-derived growth factor receptor A
1832	1832 1731 at	PDGFRA	M21574	alpha polypeptide	chain
				pleckstrin homology, Sec7 and coiled/coil	cytohesin 1, isoform 1; cytohesin 1, isoform
1833	1833 38666 at	PSCD1	M85169	domains 1(cytohesin 1)	2
				pleckstrin homology, Sec7 and coiled/coil	
<u>18</u>	1834 38741 at	PSCD2	U70728	domains 2 (cytohesin-2)	cytohesin-2
1835	1835 36943 r at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	C2H2 zinc finger protein PLAGL1
1836	1836 34780_at	PLXNB2	AB002313	plexin B2 '	plexin B2
183	1837 32193 at	PLXNC1	AF030339	plexin C1	VESPR
183	1838 38270 at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	poly(ADP-ribose) glycohydrolase
183	1839 31951 s at	PABPC1	Z48501	poly(A) binding protein, cytoplasmic 1	polyadenylate binding protein II
<u>\$</u>	ă	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytoplasmic 1
				poly(A)-specific ribonuclease	
18	1841 36003 at	PARN	AJ005698	(deadenylation nuclease)	poly(A)-specific ribonuclease
1842	1842 34305 at	PCBP1	229505	poly(rC) binding protein 1	sub2.3
\$	1843 35746_r_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
\$	1844 35745_f_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
<u>18</u>	1845 39868 at	PCBP3	AL046394	poly(rC) binding protein 3	

1.5.2

	V	В	ပ	Q	3
		1		polycystic kidney disease 2 (autosomal	
1846	1846 38120_at	PKD2	U50928	dominant)	polycystin 2
1847	1847 33380_at	POLS	AB005754	polymerase (DNA directed) sigma	LAK-1
				DNA directed), epsilon 3	polymerase (DNA directed), epsilon 3 (p17
1848	1848 38702_at	POLE3	AF070640	(p17 subunit)	(junans
				polymerase (RNA) II (DNA directed)	
1849	1849 40791_at	POLH2A	X63564	polypeptide A (220kD)	KNA polymerase II largest subunit
0	2000			polymerase (RNA) II (DNA directed)	DNA notworses II 140 kDs enting
200	1850 39740 at	rochze	Accobs	Canata a control of the control of t	winder box of it of the control with
				polymerase (HNA) II (UNA directed)	
1851	1851 36027_at	POLR2F	AA418779	polypeptide F	
				polymerase (RNA) II (DNA directed)	,
1852	1852 35631_at	POLRZH	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1853	1853 1248_at	POLR2H	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1854	1854 503_at	POLR2L	U37690	polypeptide L (7.6kD)	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1855	1855 35841_at	POLR2L	N24355	polypeptide L (7.6kD)	
1856	1856 34320_at	PTRF	AL050224	polymerase I and transcript release factor	
1857	1857 34005_at	PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
70.7	000	7 007 0	1000	Coli C become a cite and cite	
ဂို ဗ	1839 31600_s_at	LIMSTL I	U38433	אייים שלים שלים שלים שלים שלים שלים שלים	
				pot. ORF1 (as 1-73); ORF2, put. cre	
1860	18EN AEEX-Crox.s of		XO3453	process (ag 1-3-2), paccentingers of contractions	
	1 - COLO X - COLO		2000	pot. ORF1 (aa 1-73); ORF2, put. cre	
			_	protein (aa 1-343); Bacteriophage P1 cre	
1861	1861 AFFX-CreX-3_at		X03453	gene for recombinase protein.	
4 96.0	1000001		D46132	De domain containing 2 with ZNE domain zinc-finger DNA-binding protein	 zinc-finger DNA-binding protein
200	313 at	r noivie	20105		
1863	1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3 homeobox protein	homeobox protein

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T				precursor, Human prolyl 4-hydroxylase	
				beta-subunit and disulfide isomerase	
				(P4HB) gene, exon 11, clones 6B-	,
864	1864 36666 at		M22806		prolyl 4-hydroxylase beta-subunit
1885	at at	GS3786	D87120	predicted osteoblast protein	GS3786
7998	at a	PFDN4	U41816	prefoldin 4	C-1
128		PREI3	AL080070	ation protein 3	hypothetical protein
898		PRP18		ctor 18	hPrp18
				ephalin	
1869	1869 38291 at	PENK	J00123		proenkephalin
1870		PSEN1	L76517	sease 3)	presenilin 1
1871	at	PAWR	0889A		prostate apoptosis response protein par-4
1872		PCOLN3	U58048		PRSM1
1873	at	PCOLCE	L33799	_	procollagen C-proteinase enhancer protein
1874	1874 34795 at	PLOD2	U84573		hsyl hydroxylase isoform 2
				procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
1875	1875 36184 at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876 37037 at	P4HA1	M24486	alpha polypeptide I	polypeptide l
				procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390_at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
		-		procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxogiutarate 4-
				dioxygenase (proline 4-hydroxylase), beta	dioxygenase (proline 4-hydroxylase), beta
				polypeptide (protein disuffide isomerase;	polypeptide (protein disulfide isomerase;
1878	1878 691 g at	P4HB	J02783	thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1879	1879 38840 s at	PFN2	L10678	profilin 2	profilin II
1880	1880 38839 at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	
1881	1881 38802_at	PGRMC1	Y12711	component 1	putative progesterone binding protein
				progesterone receptor membrane	
1882	1882 38821_at	PGRMC2	AJ002030	component 2	progresterone pinding protein

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1883	30035	חחי		progrestin induced protein	progestin induced protein
3 2	39036 a at	DDS		progestin induced protein	progestin induced protein
1885	1885 35218 at	PDCD10		programmed cell death 10	TFAR15
1886	1886 37569 at	PDCD6		programmed cell death 6	calcium binding protein
				(apoptosis-	
1887	32212_at	PDCD8	AL049703		hypothetical protein
1888	1888 36592_at	器	S85655	prohibitin	prohibitin
1889	1884_s_at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890	4160	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
				proline-rich Gla (G-carboxyglutamic acid)	
1891	1891 35978_at	PRRG1	AF009242	polypeptide 1	proline-rich Gla protein 1
1892	1892 36023_at	PRH1	A1864120	proline-rich protein Haelll subfamily 1	
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing membrane
1893	1893 40803_at	PORIMIN	AL050161	injury gene	injury gene
				propionyl Coenzyme A carboxylase, alpha	Propionyl-Coenzyme A carboxylase, alpha
1894	1894 1348_s_at	PCCA	S79219	polypeptide	polypeptide precursor
				propionyl Coenzyme A carboxylase, beta	
1895	1895 36561_at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
	11000	DOCKE	1156307	proprotein convertase subtilisin/kexin type	projesse PC6 isoform A
ŝ	41035 at	222	100000		
				prosaposin (variant Gaucher disease and	prosaposin (variant Gaucher disease and
1897	1897 36795_at	PSAP	J03077	variant metachromatic leukodystrophy)	variant metachromatic leukodystrophy)
1898	1898 38406 f at	PTGDS	AI207842	prostaglandin D2 synthase (21kD, brain)	
				prostaglandin E receptor 2 (subtype EP2),	
1895	1899 828_at	PTGER2	U19487	SakD	prostaglandin E2 receptor
1900	1900 1890_at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
<u>6</u>	1901 32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
190	1902 719 g at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
199	1903 718_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
190	1904 33368_at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
190	1905 40078_at	SPUVE	AF015287	protease, serine, 23	serine protease
190	1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
1907	1907 688 at	PSMC1	L02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit



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				proteasome (prosome, macropain) 26S	. Cook
1908	1908 35353_at	PSMC2	D11094	T	MOST Protein
				ne, macropain) 26S	proteasome (prosome, macropain) zoo
1909	1909 592_at	PSMC3	M34079	٦	subunit, A I Pase, 3
				proteasome (prosome, macropain) 26S	
1910	1910 37766_s_at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	
1911	1911 949 s at	PSMCe	D78275		proteasome subunit p42
	1			ne, macropain) 26S	
1912	1912 1314 at	PSMD1	D44466		proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192 at	PSMD12	AB003103	subunit, non-ATPase, 12	26S proteasome subunit p55
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 26S
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
			·	390 (1)	
1045	1015 045 04	DCM07	ווייייייייייייייייייייייייייייייייייייי	proteasome (prosome, macropain) 263 subjinit non-ATPase, 7 (Mov34 homolod) (proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
	343_al	OMO L	20000		
				proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
L				proteasome (prosome, macropain) 26S	
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	AI347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	1919 41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
L				proteasome (prosome, macropain)	
192(1920 1184_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
L				proteasome (prosome, macropain)	
192	1921 36974 at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
192	1922 38371 at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
192	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
192	1924 1448_at	PSMA3	D00762	subunit, alpha type, 3	laipna type, 3



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				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1925	1925 1450_g_at	PSMA4	D00763	subunit, alpha type, 4	alpha type, 4
				e, macropain)	proteasome (prosome, macropain) subunit,
1926	1926 1449_at	PSMA4	D00763	subunit, alpha type, 4	alpha type, 4
				proteasome (prosome, macropain)	
1927	1927 37046_at	PSMA5	AI246726	subunit, alpha type, 5	
				e, macropain)	
1928	1928 36122_at	PSMA6	X59417		prosomal P27K protein
				, macropain)	proteasome (prosome, macropain) subunit,
1929	1929 1447_at	PSMB1	D00761	subunit, beta type, 1	beta type, 1
				me, macropain)	
1930	1930 1310_at	PSMB2	D26599	subunit, beta type, 2	proteasome subunit HsC7-I
				ю, macropain)	
1931	1931 33154_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
				ne, macropain)	
1932	1932 1311_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
L				proteasome (prosome, macropain)	
1933	37666_at	PSMB5	D29011	subunit, beta type, 5	proteasome subunit X
L				proteasome (prosome, macropain)	
1934	1934 941_at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
				proteasome (prosome, macropain)	
1935	1935 39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
1936	936 1313_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
				subunit, beta type, 9 (large multifunctional	
1937	1937 38287_at	PSMB9	AA808961	protease 2)	
1938	1938 41750 at	Ps	D49489	protein disultide isomerase-related protein human P5	human P5
1936	1939 32558 at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
				protein kinase (cAMP-dependent,	
1940	1940 34376_at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
194	1941 36957_at	PRKC8P1	W22296	protein kinase C binding protein 1	
194	1942 1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
194	3 1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
194	1944 36835_at	PRKCL2	U33052	protein kinase C-like 2	PRK2

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1945	1945 41768 at	PRKAR1A	M33336	ecific	cAMP-dependent protein kinase type I-alpha subunit
				cAMP-dependent, e I. alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1946	1946 227 g at	PRKAR1A	M33336		subunit
				Decific	cAMP-dependent protein kinase type I-alpha
1947	1947 226_at	PRKAR1A	M33336		subunit
				protein kinase, interferon-inducible double protein activator of the interferon-induced	protein activator of the interferon-induced
1948	1948 32205_at	PRKRA	AF072860	stranded RNA dependent activator	protein kinase
				bunit,	serine /threonine specific protein
1949	1949 37725_at	PPP1CC	X74008	\neg	phosphatase
				itase 1, regulatory	
1950	1950 40438_at	PPP1R12A	D87930	(inhibitor) subunit 12A	myosin phosphatase target subunit 1
				protein phosphatase 1, regulatory	
1951	1951 39366_at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540_at	PPP1R7	Z50749		yeast sds22 homolog
1953	1953 857_at	PPM1A	S87759		protein phosphatase 2C alpha
1954	1954 36501_at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305		Wip1
				protein phosphatase 2 (formerly 2A),	
1956	1956 924_s_at	PPP2CB	J03805	catalytic subunit, beta isoform	
				protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PR 52), alpha	
1957	1957 41167_at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
				protein phosphatase 2 (formerly 2A),	•
4 0 10	1000	Acadaa	MEADOO	regulatory subulin D (r n 32), alpina	protein phosphatase-2A subunit-alpha
	1302 at	ורובחבא	141043C3	Solominia thousand of roundations subjustit	
1959	1959 32734 at	PPP2R5E	L76703	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon



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				egulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1960	960 40786_at	PPP2R5C	U37352		subunit
				egulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1961	1961 176_at	PPP2R5C	U37352	B (B56), gamma isoform	subunit
				protein phosphatase 2A, regulatory	
1962	1962 39127 f. at	PPP2R4	X73478	subunit B' (PR 53)	phosphotyrosyl phosphatase activator
				se 3 (formerly 2B),	protein phosphatase 3 (formerly 2B),
				neurin	catalytic subunit, beta isoform (calcineurin A
1963	1963 38277_at	PPP3CB	M29550	A beta)	beta)
				protein phosphatase 3 (formerly 2B),	
				catalytic subunit, gamma isoform	
1964	964 32541 at	PPP3CC	S46622	(calcineurin A gamma)	calcineurin A catalytic subunit
				protein phosphatase 4, regulatory subunit	
1965	34371_at	PPP4R1	U79267		
1966	37581_at	PPP6C	X92972	protein phosphatase 6, catalytic subunit	protein phosphatase 6
1967	1967 35752_s_at	PROS1	M15036	protein S (alpha)	protein S (alpha)
1968	1968 32564_at	SEC61B	AA083129	protein translocation complex beta	
1969	1969 1064 at	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
				protein tyrosine phosphatase type IVA,	
1970	1970 843 at	PTP4A1	U48296	member 1	protein tyrosine phosphatase PTPCAAX1
				protein tyrosine phosphatase type IVA,	
1971	1971 38415 at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase type IVA,	
1972	1972 1241_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
1973	1973 40137_at	PTPN1	M31724	receptor type 1	type 1
				protein tyrosine phosphatase, non-	
1974	1974 1463_at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
				protein tyrosine phosphatase, non-	
1075	1075 34198 at	PTPN13	1112128	receptor type 13 (AFC-1) CC33 (Fas)- lassociated phosphatase)	protein tyrosine phosphatase 1E
			23.2.0		protein tyrosine phosphatase, receptor type.
				-	A, isoform 1 precursor; protein tyrosine
		1		protein tyrosine phosphatase, receptor	phosphatase, receptor type, A, isoform 2
1976	1976 1496_at	PTPRA	M34668	lype, A	precursor

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T				protein tyrosine phosphatase, receptor	
1977	1977 36204_at	PTPRF	Y00815		put. LAR preprotein (AA -16 to 1881)
T				protein tyrosine phosphatase, receptor	
				PRF), interacting	
1978	1978 41780_at	PPFIA1	U22816		LAK-interacting protein 10
T				protein tyrosine phosphatase, receptor	
1979	1979 1488 at	PTPRK	L77886	type, K	protein tyrosine phosphatase
				tyrosine phosphatase, receptor	
1980	1980 995_q_at	PTPRM	X58288		protein-tyrosine phosphatase
				protein tyrosine phosphatase, receptor	-
1981	1981 31892 at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
				protein-kinase, interferon-inducible double	
				stranded RNA dependent inhibitor,	
1982	1982 41141 at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
				protein-L-isoaspartate (D-aspartate) O-	
1983	1983 37737 at	PCMT1	D25547	methyttransferase	PIMT isozyme I
				protein-L-isoaspartate (D-aspartate) O-	
1984	1984 37736 at	PCMT1	D13892	methyttransferase	carboxy/ methyttransferase
1985	1985 32227 at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
198	1986 38590 r at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1087	1087 38580 i at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
	1000 27036 24	DPDDAD	A1184802	IPRP4/STK/WD splicing factor	
1969	3/330_al		711010		
				pseudoferritin H protein; Human ferritin H	
1989	1989 31697 s at	FTHP1	J04755	processed pseudogene, complete cds.	
1990	1990 36117 at	PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
1991	1991 40048 at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992	1992 35359 at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993	1993 35221 at	PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-	
				340); Human liver mRNA for beta-subunit	
			_	signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
1994	33341 at	GNB1	X04526	G).	subunit
1995	1995 33720 at	LOC56902	L48692	putatative 28 kDa protein	
				putative breast adenocarcinoma marker	C-2 protein
1996	1996 39363_at	BC-2	AF042384	((32KD)	bos place

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1997	39884_g_at	HSA9761	AF091078	П	putative dimethyladenosine transferase
		-		<u>.</u>	putative glialblastoma cell differentiation-
1998	1998 38841_at	GDBR1	AF068195		related protein
1999	1999 41188_at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984_at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
2002	2002 35286 r at	RY1	X76302	putative nucleic acid binding protein RY-1	nucleic acid binding protein
				Putative prostate cancer tumor	
2003	2003 36852_at	N33	U42349	suppressor	
				ein similar to nessy	
2004	2004 33710_at	C3F	U72515		C3f
2005	2005 40203_at	SUI1	AJ012375	putative translation initiation factor	putative translation initiation factor
2006	2006 37678_at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
				putative transmembrane protein; homolog	
_				of yeast Golgi membrane protein Yif1p	
2007	2007 35326_at	54TM	AF004876		54TMp
L				putative; Homo sapiens PTS gene,	
2008	2008 35697_at	PTS	L76259	complete cds.	6-pyruvoyttetrahydropterin synthase
				putative; originaly identified as an	
				oncogene, product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2009	2009 40887_g_at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				'oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2010	2010 40886_at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
201	2011 33219_at	VDU1	AB029020		KIAA1097 protein
				Pyruvate dehydrogenase complex, lipoyl-	
				containing component X; E3-binding	pyruvate dehydrogenase complex protein X
201,	2012 36164_at	PDX1	U82328	protein	subunit precursor
201;	2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate kinase, muscle
2014	2014 260_at	QDPR	M16447	quinoid dihydropteridine reductase	quinoid dihydropteridine reductase

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1			>	RaH domain (hinds single-stranded	
2015	2015 36610 at	R3HDM	D21852		KIAA0029 protein
2016;	2016 39030 at	RABAC1	AJ133534	(þe	prenylated Rab acceptor 1 (PRA1)
				ase, beta	
2017	2017 37703_at	RABGGTB	Y08201	subunit	rab geranyigeranyi transferase
2018	2018 38264_at	RABIF	U74324	RAB interacting factor	guanine nucleotide exchange factor mss4
	100000	4,50	A 1000004	May a concord of the	that 1 a
200	2019 30000 at	HABIIA	AFOODESI	J	51.75
2020	2020 35325_at	RAB14	AF052113		
2021	2021 34393_r_at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2022	2022 34392_s_at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2023	2023 33326_at	RAB21	D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
2024	2024 809 at	BAB27A	U57094	BAB27A. member RAS oncogene family	Rab27a
2025	2025 33371 s at	RAB31	U59877	RAB31, member RAS oncogene family	low-Mr GTP-binding protein Rab31
2026	2026 36110 at	RABSA	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
				rabe GTPase activating protein (GAP and	
2027	2027 35289_at	GAPCENA	AJ011679	centrosome-associated)	Rabe GTPase activating protein, GAPCenA
2028	2028 35304_at	RABGA	AF052130	RAB6A, member RAS oncogene family	
2029	2029 39628 at	RAB9A	AI671547	RAB9A, member RAS oncogene family	
2030	2030 41716_at	RC3	AB020663	rabconnectin-3	KIAA0856 protein
	1 07 150	01.04	100	Rac/Cdc42 guanine nucleotide exchange	
2031	2031 37543 at	AHHGEF6	025304	DADA homolog (S. nombo)	DNA repair exemple lease
2032	2032 36857_at	KAUI	AFU84513	HAD I nomong (3. pompa)	DADOT L
2033	2033 38114_at	RAD21	D38551	RAD21 homolog (S. pombe)	HAUZ1 nomolog
2034	2034 1874_at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
2035	2035 32757 at	RAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
	1			RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible	
				coding regions; Human renal cell	
				carcinoma antigen RAGE-4 mRNA,	
2036	2036 1524_at		U46194	complete putative cds.	
2037	2037 36628_at	RALBP1	L42542	ralA binding protein 1	RLIP76 protein
2038	2038 37539_at	RGL	AB023176	RalGDS-like gene	KIAA0959 protein

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2030	2030 41342 at	RANRP1	D38076		Ran-BP1(Ran-binding protein 1)
2000		RANBP16	AB018288	9	KIAA0745 protein
i k	2041 41174 at	RANBP21 1	AF012086	ke 1	Ran binding protein 2
Š	2042 35255 at	RANBP7	AF098799		RanBP7/importin 7
200	2043 32602 at	RAPIGNS1	XE3465	BAP1 GTP-GDP dissociation stimulator 1 smg GDS	smq GDS
	4040	4,040	Monope	DAD4A member of DAS oncorene family ras-related profein	ras-related profein
3	2044 040 at	¥1.150	CECTAIN		
2045	2045 40146_at	RAP1B	AL080212	RAP1B, member of RAS oncogene family hypothetical protein	hypothetical protein
2046	2046 39601 at	RASSF1	AF061836	Ras association (RaIGDS/AF-6) domain family 1	putative tumor suppressor protein
				Ras association (RaIGDS/AF-6) domain	Ras association (RaIGDS/AF-6) domain
2047	2047 37598_at	RASSF2	D79990	family 2	family 2
2048	2048 1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049	2049 37309_at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	2050 1394_at	ARHA	L25080	ras homolog gene family, member A	GTP-binding protein
2051	2051 35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
				RAS p21 protein activator (GTPase	
2052	2052 36935_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675_at	RASA1	M23379	activating protein) 1	GT Pase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793_at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 botulinum toxin substrate 1	
1	200E 40864 at	200	N25274	(rho family, small GTP binding protein Bact)	
	- TOOOT	2	17070	ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	isoform Rac1; ras-related C3 botulinum toxin
2056	2056 2050 s at	RAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316 at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	2058 33234_at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	2060 34684 at	RECOL	L36140	RecQ protein-like (DNA helicase Q1-like) DNA helicase	DNA helicase
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†	A	B)		
2061	2061 34685_at	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
				regulated at the translational level; contains I-mfa domain; untilizes unique	
				GTG start codon; Homo sapiens HIC protein isoform n40 and HIC protein	HIC protein isoform p40: HIC protein isoform
2062	2062 37842_at	呈	AF054589		p32
				in signalling 19	
88	2063 35756_at	RGS19IP1	AF089816	T	RGS-GAIP meracting protein GIPO
2064	2064 37701_at	RGS2	L13463	24KD	heix-loop-heilx phosphoprotein
2065	2065 35722_at	RENT2	AL080198		hypothetical protein
	-			related RAS viral (r-ras) oncogene	
2066	2066 32827_at	RRAS2	Al365215	homolog 2	
				remainder of gene in clone 549K18	
2067	2067 34845_at	dJ796117.4	AL035398	(AL023654)	CGI-51 protein
2068	2068 1055 g at	RFC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2069	2069 38481 at	RPA1	M63488		replication protein A, 70-kDa subunit
2070	652_g_at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071	2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
		e e			٠
2072	2072 34350_at	RSN	X64838	ent-associated protein)	restin
2073	2073 31851_at	RFP2	AJ224819	ret finger protein 2	tumor suppressor
				reticulocalbin 1, EF-hand calcium binding	
2074	2074 40556_at	RCN1	D42073	domain	reticulocalbin
				reticulocalbin 2, EF-hand calcium binding	
2075	2075 37727_i_at	RCN2	X78669	domain	EF-hand protein
				reticulocalbin 2, EF-hand calcium binding	
2076	37728_r_at	RCN2	X78669	domain	EF-hand protein
2077	2077 31536_at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078	2078 39964 at	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive) XRP2 protein	XRP2 protein
2079	2079 38164_at	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
6	2080	180	M15400	retinoblastoma 1 (including	retinoblastoma 1 (including osteosarcoma)
	ZO44 S BI	ופע	00+C1W	Categorial)	

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2081	35227 at	RBBP8	U72066		CtBP interacting protein CtIP
2082	2082 33860 at	RBAF600	AB007931	. 600	KIAA0462 protein
ğ	32597 at		X76061		130K protein
8	2084 35848 at		AL049432	retinoic acid induced 17	
	•			retropseudogene; Human	
				DNA, complete	
2085	2085 31672 g at	RBMS1P; MSSP1	P1 D82351	$\overline{}$	MSSP-1
				REV3-like, catalytic subunit of DNA	
2086	2086 38908 s at	REV3L	AL096744		hypothetical protein
				reversion-inducing-cysteine-rich protein	
2087	2087 35236 g at	RECK	AA099265	with kazal motifs	
Γ				reversion-inducing-cysteine-rich protein	
2088	2088 35235_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2089	2089 35234_at	RECK	D50406	with kazal motifs	RECK protein precursor
2090	2090 553_g_at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	2091 39700 at	ARHGAP1	Al961929	Rho GTPase activating protein 1	
				Rho guanine nucleotide exchange factor	Of refresh engaged on the section of
2092	2092 34180_at	ARHGEF10	AB002292	(GEF) 10	Hno guanine nucleotide excriatige factor to
				Rho guanine nucleotide exchange factor	
2093	2093 40828_at	ARHGEF7	D63476	(GEF) 7	PAK-interacting exchange factor beta
				rho/rac guanine nucleotide exchange	
2094	2094 40100_at	ARHGEF2	U72206	factor (GEF) 2	guanine nucleotide regulatory tactor
				Rho-specific guanine nucleotide exchange	
2095	2095 36537_at	P114-RHO-GEF	AB011093	factor p114	KIAA0521 protein
2096	2096 41040 at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	2097 32664 at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
2098	2098 36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
3000	2000 34314 at	BBM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
200	2100 2016 s at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	2101 41178 at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	2102 33668 at	RPL12	AF037643	ribosomal protein L12	
2103	2103 31509 at	RPL13	X64707	ribosomal protein L13	ribosomal protein L13
219	2104 35119_at	RPL13A	X56932	ribosomal protein L13a	23 kD highly basic protein
2106	2105 31907_at	RPL14	D87735	ribosomal protein L14	Iribosomal protein L14

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2106	32432_f_at	RPL15	L25899	ribosomal protein L15	ribosomal protein L10
2107	32440_at	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108	31546_at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109	33614_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110	2110 32435_at	RPL 19	X63527	ribosomal protein L19	ribosomal protein L19
2111	2111 32337_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
2112	33451_s_at	RPL22	AI526079	ribosomal protein L22	
2113	32395	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2114	2114 32394_s_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2115	2115 32341_f_at	RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
2116	2116 33677_at	RPL24	M94314	ribosomal protein L24	ribosomal protein L30
2117	2117 32444_at	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118	2118 39830_at	RPL27	AA044823	ribosomal protein L27	
2119	2119 32436_at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120	2120 31708_at	RPL30	L05095	ribosomal protein L30	ribosomal protein L30
2121	2121 33676_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122	32276_at	RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123	2123 33657_at	RPL34	L38941	ribosomal protein L34	ribosomal protein L34
2124	2124 41765_at	RPL35	AI541285	ribosomal protein L35	
2125	2125 41152_f_at	RPL36A	T89651	ribosomal protein L36a	
2126	2126 33656_at	RPL37	D23661	ribosomal protein L37	ribosomal protein L37
2127	31962_at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128	34085_at	RPL38	Z 26876	ribosomal protein L38	ribosomal protein
2129	2129 33485 at	RPL4	D23660	ribosomal protein L4	ribosomal protein
				_	human homologue to yeast ribosomal
2130	2130 32466_at	RPL41	Z12962	ribosomal protein L41	protein YL41
2131	33660_at	RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132	31952_at	RPL6	X69391	ribosomal protein L6	ribosomal protein L6
2133	2133 36333_at	RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134	31505_at	RPL8	Z28407	ribosomal protein L8	ribosomal protein L8
2135	2135 31568_at	RPS10	U14972	ribosomal protein S10	ribosomal protein S10
2136	32330_at	RPS11	X06617	ribosomal protein S11	ribosomal protein S11
2137	33116_f_at	RPS12	AA977163	ribosomal protein S12	
2138	33619_at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
2139	34317_g_at	RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
2140	2140 38061_at	RPS16	Al541256	ribosomal protein S16	

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2141	34593_g_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2142	2142 34592_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2143	2143 31330_at	RPS19	M81757		S19 ribosomal protein
2144			X17206		ribosomal protein S2
2145	32438_at	RPS20	L06498	0	ribosomal protein S20
2146		RPS23	D14530		ribosomal protein
2147	32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	31573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
				ribosomal protein S27 (metallopanstimulin	
2149	32748_at	RPS27	2	1)	
2150	2150 34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
2151	2151 39798_at	RPS28	R87876	ribosomal protein S28	
2152	2152 34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153	2153 1653_at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
2154	34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155	32437_at	RPSS	U14970	ribosornal protein S5	ribosomal protein S5
2156	2156 31511_at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	31538	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158	31956_f_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
				ribosome binding protein 1 homolog	
2160	2160 33213_g_at	RRBP1	AF006751	180kD (dog)	ES/130
				Ric-like, expressed in many tissues	
2161	2161 38331_at	RIT	Y07566	(Drosophila)	Ric-like, expressed in many tissues
2162	2162 35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163	2163 39150_at	RNF11	U69559	ring finger protein 11	
2164	2164 35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165	2165 33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein 14
2166	2166 33484_at	RNF2	Y10671	ring finger protein 2	ring finger protein 2
2167	2167 37964_at	RNF3	W25793	ring finger protein 3	
2168	2168 35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X	
				chromosome inactivation; Human ring zinc	
				finger protein (ZNF127-Xp) gene and 5'	
2169	2169 37650_at	ZNF127-Xp	U41315	flanking sequence.	ZNF127-Xp
2170	2170 37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

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11/2	38073 at		AB007858	RNA (guanine-7-) methyttransferase	RNA (guanine-7-) methyltransferas
2172	172 41460 at	4	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
2173					RNPL
2174		RBM4	U89505		Hlark
2175			AF091263		RNA binding motif protein 5
2176	at		AF069517	RNA binding motif protein 6	RNA binding protein DEF-3
2177		RBM9		RNA binding motif protein 9	hypothetical protein
2178	2178 39731 at	RBMX	723064	RNA binding motif protein, X chromosome hnRNP G protein	hnRNP G protein
				RNA binding motif, single stranded	RNA binding motif, single stranded
2179	2179 33867_s_at	HBMS1	X//494	meracing protein i	melaculig protein 1, 150 cm
2180	2180/36186 at	BNPS1 ~	1.37368	RNA binding protein S1, serine-rich domain	RNA-binding protein
				RNA guanylytransferase and 5'-	
2181	2181 35202 at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
2182	2182 33237 at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	2183 36045 at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	2184 38762 at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
				RNA-binding protein gene with multiple	
2185	38049 g at	RBPMS	D84110	splicing	RBP-MS/type 4
	<u> </u>			RNA-binding protein gene with multiple	
2186	2186 38047_at	RBPMS	D84109	splicing	RBP-MS/type 3
2187	2187 38974 at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
	,			RNA-binding region (RNP1, RRM)	
2188	2188 39725_at	RNPC2	L10910	containing 2	splicing factor
2189	2189 38011_at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
2190	2190 35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
				runt-related transcription factor 1 (acute	
2191	943_at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML 1b protein
2192	2192 40124 at	BUVBL 1	Y18418	RuvB-like 1 (E. coli)	erythrocyte cytosolic protein of 54 kDa, ECF- 54
2193	2193 35758 at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
	!			S100 calcium binding protein A10 (annexin II ligand, calpactin I, light	
2194	2194 39338_at	S100A10	A(201310	polypeptide (p11))	

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				ntaining inositol	::0000 A N J
2195 3	36089_at	SAC2	AB023183		NAKOSOO DIOCEILI
				ntaining inositol	
2196 41101	11101_at	SAC3	D87464	_	KIAA0274 gene product
				SAC1 suppressor of actin mutations 1-like	
2197 36511	36511_at	SACM1L	AB020658	(yeast)	KIAA0851 protein
2198	2198 34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1 hypothetical protein	hypothetical protein
3.00	2199 41302 at	AHCYL1	R59606	S-adenosylhomocysteine hydrolase-like 1	
Š	2200 36685 at	AMD1	W63793		
					S-adenosylmethionine decarboxylase 1
2201	2201 263_g_at	AMD1	M21154	ıе decarboxylase 1	precursor
2202	2202 41449_at	SGCE	AJ000534		epsilon-sarcogiycan
2203	2203 36083_at	SAS	U01160		SAS
2204	2204 36536 at	SCHIP1	AF070614	schwannomin interacting protein 1	schwannomin interacting protein 1
2205	2205 33423 g at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	2206 33422 at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	2207 36207 at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	2208 39099 at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
				SEC24 related gene family, member A (S.	
2209	2209 34199 at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
				SEC24 related gene family, member B (S.	
2210	2210 35845 at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
				SEC24 related gene family, member D (S.	
2211	2211 32770 at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
2212	2212 34349 at	SEC63L	AJ011779	SEC63 protein	SEC63 protein
2213	2213 32521 at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
				secreted phosphoprotein 1 (osteopontin,	
				bone statoprotein 1, early 1-tymphocyte	- citaconocio
2214	2214 34342_s_at	SPP1	AF052124	activation 1)	Osteopolitiii
1	0015 671 04	CDABC	IN3040	secreted protein, acidic, cysteine-rich (cysteine-rich)	(osteonectin)
	10/ 1_at	2	2	secretory granule, neuroendocrine protein	secretory granule, neuroendocrine protein secretory granule, neuroendocrine protein 1
2216	2216 34265 at	SGNE1	Y00757	1 (7B2 protein)	(7B2 protein)
22.7	2217 37405 at	SELENBP1	U29091	selenium binding protein 1	selenium-binding protein



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2218	2218 39078 at	SPS2	U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
2219			211793		selenoprotein P
				obulin domain	
				(lg), short basic domain, secreted,	
2220	2220 377_g_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	
2221	2221 376 at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2222	2222 35666_at	SEMA3F	U38276	(semaphorin) 3F	semaphorin III family homolog
2223	2223 38826 at	2-Sep	Sep D50918	septin 6	septin 2
					phosphotyrosine independent ligand for the
2224	2224 40898_at	SQSTM1	U46751	sequestosome 1	Lck SH2 domain p62
				serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
				clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125_at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor,	
				clade H (heat shock protein 47), member	
2227	2227 39167_r_at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyftransferase, long chain	
2228	2228 38818_at	SPTLC1	Y08685	base subunit 1	serine palmitoyttransferase, subunit l
				serine threonine kinase 39 (STE20/SPS1	
2229	40966_at		AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737 at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	36019 at		126260	serine/threonine kinase 19	RP protein
				serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424	homolog, yeast)	MST2
				serine/threonine-protein kinase PRP4	
2234	2234 32784_at	PRP4	AB011108	homolog	KIAA0536 protein

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SRF J03161 factor) SRR AF059617 serum-inducible kinase SARS X91257 serum-inducible kinase SET M93651 serum in absentia homolog 1 (Drosophila) SIAH1 U76247 seven in absentia homolog 2 (Drosophila) SIAH2 U76248 seven in absentia homolog 2 (Drosophila) SCML2 V18004 seven transmembrane domain protein seventh subunit (rpb-7) pb-7 U52427 seven transmembrane domain protein seventh subunit (rpb-7) SCML2 SH3BGR AI337192 seven transmembrane domain protein seventh subunit (rpb-7) SH3BGR AI337192 seven binding glutamic acid-rich sh3BGR AB005047 seven fanding glutamic acid-rich sh3BGR AB005047 sexombo on midleg-like 2 (Drosophila) SHC1 AF042081 protein SH3G domain binding glutamic acid-rich sh3GR AB005047 sexombo on midleg-like 2 (Drosophila) SHC1 AF042081 protein sexocitated) SHC1 AF042081 protein sexocitated) SHC1 AB007380 SHC (Src homology 2 domain containing) SHC1 AB07385 signal recognition particle 14kD signal recognition particle 14kD signal recognition particle 54kD signal recognition particle 54kD signal recognition particle 54kD signal recognition particle 54kD						
SRF J03161 factor response element-binding transcription response element-binding transcription factor		¥	മ	ပ	O	u
SRF J03161 Factor) SRF J03161 Factor					serum response factor (c-fos serum	serum response factor (c-tos serum
SRF J03161 factor) SRF J03161 factor) SRF J03161 factor) SRF J03161 factor) SARS X91257 serum-inducible kinase SARS X91257 serum-inducible kinase SARS X91257 serum-inducible kinase SET M93651 serum-inducible kinase RET M93651 serum-inducible kinase RET M93651 serum-inducible kinase RET M93651 serum-inducible kinate RESCARL2 Y18007 serven in absentia homolog 1 (Drosophila) RESCARL2 Y18004 serven kinate RH337192 SH3 domain binding glutamic culdrich <t< td=""><td></td><td></td><td></td><td></td><td>response element-binding transcription</td><td>response element-binding transcription</td></t<>					response element-binding transcription	response element-binding transcription
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SRF J03161 factor) factor fac					serum response factor (c-fos serum	serum response factor (c-fos serum
at SRF J03161 factor) at SARS X91257 serum-inducible kinase factor) at SARS X91257 serum-inducible kinase factor) at SET M93651 serum-inducible kinase factor at SET M93651 serum-inducible kinase factor at SET M93651 serum-inducible kinase factor at SET M93651 serventive factor at SIAH2 U76247 seven in absentia homolog 1 (Drosophila) factor at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) factor at SCML2 Y18007 seven in absentia homolog 2 (Drosophila) factor at SCML2 Y18004 seven in absentia homolog 2 (Drosophila) factor at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) factor at SH3BGR Al337192 SH3 domain binding gutamic acid-rich factor at SH3GLB AF042081 SH3 domain binding gutamic acid-rich factor at SH3GLB AB005047 associated) SH3 domain binding			-			response element-binding transcription
at SNK AF059617 serum-inducible kinase s at SARS X91257 senyi-RNA synthetase s at SET M93651 associated) seven in absentia homolog 1 (Drosophila) at SIAH1 U76247 seven in absentia homolog 2 (Drosophila) seven in absentia homolog 2 (Drosophila) at SIAH2 U76247 seven in absentia homolog 2 (Drosophila) seven in absentia homolog 2 (Drosophila) at SIAH2 U76247 seven in absentia homolog 2 (Drosophila) seven in absentia homolog 2 (Drosophila) at SIAH2 U76247 seven in absentia homolog 2 (Drosophila) at SIAH2 U76247 seventh in absentia brotein (Tp-7) at SCML2 Y18004 seventh subunit (Tp-7) at SCML2 Y18004 sex comb on midleg-like action of the construction glutamic acid-rich at SH3BGR AF042081 SH3 domain binding glutamic acid-rich at SH3BGR AF042081 sassociated) sassociated) at SHC1 AB007960 SH3-domain bindin	2236	1409 at	SRF	J03161		factor)
at SARS X91257 seryl-tRNA synthetase at SET M93651 associated) at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76247 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seven transmembrane domain protein at NIFIE14 Y18007 seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) at DU52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SH3BGR AF042081 protein sex comb on midleg-like 2 (Drosophila) at SH3BGR AF042081 protein SH3 domain binding glutamic acid-rich protein like at SH3BGR AF042081 protein SH3 domain binding glutamic acid-rich protein like at SH3GLB1 AB005047 associated) sex comb at SHGLB1 AB005047 associated) at SHGLB1 AB007360 SH3-domain binding protein 5 (BTP-rich language) <t< td=""><td>2237</td><td></td><td>SNK</td><td>AF059617</td><td>serum-inducible kinase</td><td>serum-inducible kinase</td></t<>	2237		SNK	AF059617	serum-inducible kinase	serum-inducible kinase
SET M93651 seven in absentia homolog 1 (Drosophila) is seven in absentia homolog 2 (Drosophila) in properties in absentia homolog 2 (Drosophila) in seven in absentia in absentia acid-rich in shall in shall in seven in absentia in a signal in a sign	2238		SARS	X91257	servi-tRNA synthetase	seryl-tRNA synthetase
at SET M93651 seven in absentia homolog 1 (Drosophila) at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seventh tansmembrane domain protein at NIFIE14 Y18004 seventh tansmembrane domain protein at PD-7 U52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) Al337192 SH3 domain binding glutamic acid-rich SH3 domain binding glutamic acid-rich at SH3BP5 AB005047 sasociated 0 at SH3GLB1 AB007960 SH3-domain binding glutamic acid-rich at SHC1 U73377 transforming protein 1 at SHC1 AB018356 siahyltra		i-20			SET translocation (myeloid leukemia-	SET translocation (myeloid leukemia-
at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seven transmembrane domain protein seventh largest subunit, Human RNA polymerase II seventh subunit (rpb-7) gene, complete cds. at SCML2 Y18004 sex complete cds. at SCML2 Y18004 sex complete cds. SH3 domain binding glutamic acid-rich protein at SH3BGR AI337192 SH3 domain binding glutamic acid-rich at SH3BGR AB005047 associated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK- at SH3CLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 slay/transferase 9 (CMP- NeuAc:lactosylceramide alpha-2,3- signal peptidase complex (18kD) at SRP14 AI525652 signal recognition particle 19kD stans SRP14 SI279 signal recognition particle 19kD stans SRP14 SI279 signal recognition particle 54kD	2239	40189 at	SET	M93651	associated)	associated)
at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFE14 Y18007 seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) at rpb-7 U52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) sex comb on midleg-like 2 (Drosophila) SH3 domain binding glutamic acid-rich at SH3BGR AI337192 SH3 domain binding glutamic acid-rich at SH3BGR AB005047 sex comb on midleg-like acid-rich at SH3BFS AB005047 sex comb on midleg-like endophilin B1 at SH3BFS AB005047 sex-ciated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK- at SH3BFS AB007960 SH3-domain grotein 1 sianyltransferase 9 (CMP- NeuAc:lactosyfceramide alpha-2,3- signal recognition particle 14kD at SRP14 AI357653 signal recognition particle 14kD at SRP14 AI357650 signal recognition particle 15kW signal recognition particle 15kW	2240		SIAH1	U76247	seven in absentia homolog 1 (Drosophila)	hSIAH1
at higher a higher seven transmembrane domain protein seventh largest subunit, Human RNA polymerase II seventh subunit (rpb-7) at rpb-7 U52427 gene, complete cds. SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SH3 domain binding glutamic acid-rich protein SH3BGR A1337192 protein SH3 domain binding glutamic acid-rich protein like sH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-associated) at SHC1 U73377 transforming protein 1 siayltransferase 9 (CMP-neut SPC18 AB018356 signal recognition particle 14kD signal recognition particle 14kD signal recognition particle 19kD signal recognition particle 54kD	2241	33799 at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila)	hSIAH2
at pb-7 U52427 gene, complete cds. at pb-7 U52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SH3BGR Al337192 protein SH3BGRL AF042081 protein Bixen SH3BGRL AF042081 protein like SH3BGRL AB005047 associated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-associated) at SH3GLB AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 sialyltransferase 9 (CMP-Neudolays 2 domain containing) at SPC18 AB01836 signal peptidase complex (18kD) at SRP14 Al357653 signal recognition particle 14kD at SRP19 X12791 signal recognition particle 19kD signal recognition particle 54kD	2242	39088_at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
rpb-7 U52427 gene, complete cds. SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SH3BGR AI337192 SH3 domain binding glutamic acid-rich protein SH3BGRL AF042081 Protein SH3 domain binding glutamic acid-rich protein like SH3BP5 AB005047 SSH3-domain binding protein 5 (BTK-SH3GLB1 SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 N73377 transforming protein 1 NeuAc:lactosylceramide alpha-2.3-siayltransferase; GM3 synthase) siayltransferase; GM3 synthase) RSPC18 AB357653 signal peptidase complex (18kD) SRP14 AI357653 signal recognition particle 19kD SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 19kD Signal recognition particle 19kD signal recognition particle 19kD					seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7)	
SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SH3BGR Al337192 SH3 domain binding glutamic acid-rich SH3BGRL AF042081 Protein SH3BGRL AF042081 Protein like SH3BP5 AB005047 SSOciated) SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-ssociated) SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 NeuAc:lactosylceramide alpha-2.3-sialyltransferase 9 (CMP-sialyltransferase) NeuAc:lactosylceramide alpha-2.3-sialyltransferase: GM3 synthase) SPC18 AB357653 signal peptidase complex (18kD) SRP14 AI355652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	2243		rpb-7	U52427	gene, complete cds.	RNA polymerase II seventh subunit
SH3BGR Al337192 protein SH3BGRL AF042081 protein SH3BGRL AF042081 protein like SH3BBB SH3-domain binding glutamic acid-rich SH3BBB AB005047 SSH3-domain binding protein 5 (BTK-SH3GLB1 SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-SH3GLB1 SH3GLB1 AB007960 SH3-domain card-rich SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-SH2GS) SH3GLB1 AB007960 SH3-domain card-rich SH3GLB1 AB007960 SH3-domain card-rich SHAC1 U73377 transforming protein 1 NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) SPC18 AB018356 sightransferase; GM3 synthase) SRP14 AI357653 signal recognition particle 14kD SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	224	38518 at	SCML2	Y18004	sex comb on midleg-like 2 (Drosophila)	SCML2 protein
SH3BGR AI337192 protein SH3BGRL AF042081 protein like SH3BGRL AF042081 protein like SH3BBGRL AB005047 associated) SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-associated) SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 SHC (Src homology 2 domain containing) TAB018377 Stansforming protein 1 SIAT9 AB018356 siah/Itransferase 9 (CMP-asia) NeuAc:lactosylceramide alpha-2.3-asignal peptidase complex (18kD) signal recognition particle 14kD SRP14 AI357653 signal recognition particle 14kD SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					SH3 domain binding glutamic acid-rich	
SH3BGRL AF042081 protein like SH3BGRL AF042081 protein like SH3BP5 AB005047 associated) SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-associated) SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 SH3-domain GRB2-like endophilin B1 SHC1 U73377 Ivansforming protein 1 RSHC1 AB018356 siayltransferase 9 (CMP-asiayltransferase) NeuAc:lactosylceramide alpha-2,3-asignal peptidase complex (18kD) signal peptidase complex (18kD) RSPC18 AI357653 signal recognition particle 14kD RSRP19 X12791 signal recognition particle 19kD RSRP19 SRP19 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	2248	36040_at	SH3BGR	Al337192	protein	
SH3BGRL AF042081 protein like SH3BF5 AB005047 associated) SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 sialytransferase 9 (CMP-new or sialytransferase) NeuAc:lactosylceramide alpha-2,3-new or sialytransferase; GM3 synthase) t SPC18 AB018356 sialytransferase; GM3 synthase) t SPC18 AB357653 signal peptidase complex (18kD) t SRP14 AI525652 (homologous Alu RNA binding protein) t SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					SH3 domain binding glutamic acid-rich	SH3 domain binding glutamic acid-rich-like
SH3BP5 AB005047 associated) SH3BP5 AB007960 SH3-domain GRB2-like endophilin B1 SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 sialyttransforming protein 1 sialyttransforming alpha-2,3- NeuAc:lactosylceramide alpha-2,3- sialyttransforase (GMP- NeuAc:lactosylceramide alpha-2,3- signal peptidase complex (18kD) signal recognition particle 14kD signal recognition particle 14kD transform SRP14 AI525652 transform signal recognition particle 19kD signal recognition particle 19kD signal recognition particle 54kD	224	39714_at	SH3BGRL	AF042081	protein like	protein
SH3BP5 AB005047 associated) SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 SHC1 U73377 transforming protein 1 SIAT9 AB018356 sialyftransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-signal peptidase complex (18kD) SPC18 AB018356 siahyftransferase; GM3 synthase) SPC18 AB357653 signal peptidase complex (18kD) SRP14 AB525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					SH3-domain binding protein 5 (BTK-	
SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 SHC1 U73377 transforming protein 1 SHC1 U73377 transforming protein 1 SIAT9 AB018356 sialyttransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-signal peptidase complex (18kD) SPC18 AB357653 signal peptidase complex (18kD) SRP14 AI525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	224	7 38968_at	SH3BP5	AB005047	associated)	SH3 binding protein
at SHC1 U73377 transforming protein 1 at SHC1 U73377 transforming protein 1 sialyltransferase 9 (CMP- NeuAc:lactosylceramide alpha-2,3- NeuAc:lactosylceramide alpha-2,3- sialyltransferase; GM3 synthase) at SPC18 Al357653 signal peptidase complex (18kD) at SRP14 Al525652 (homologous Alu RNA binding protein) at SRP19 X12791 signal recognition particle 19kD	224	3 39691_at	SH3GLB1	AB007960	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLB1
SHC1 U73377 transforming protein 1	L				SHC (Src homology 2 domain containing)	
SIAT9	224	9 38118_at	SHC1	U73377	transforming protein 1	p66shc
NeuAc:lactosylceramide alpha-2,3- SIAT9					sialyttransferase 9 (CMP-	
SIAT9 AB018356 sightransferase; GM3 synthase) SPC18 Al357653 signal peptidase complex (18kD) signal recognition particle 14kD SRP14 Al525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD					NeuAc:lactosylceramide alpha-2,3-	
SPC18 Al357653 signal peptidase complex (18kD) signal recognition particle 14kD SRP14 Al525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 (151920 signal recognition particle 54kD	225	0 34256_at	SIAT9	AB018356	sialyttransferase; GM3 synthase)	GM3 synthase
SRP14 AI525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD	225	1 39139_at	SPC18	Al357653	signal peptidase complex (18kD)	
SRP14 Al525652 (homologous Alu HNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					signal recognition particle 14kD	
SRP19 X12791 signal recognition particle 19kU SRP54 U51920 signal recognition particle 54kD	225	2 41194_at	SRP14	AI525652	(nomologous Alu RINA binding protein)	3
SBP54 IU51920 Isignal recognition particle 54KD	225	335231_at	SRP19	X12791	signal recognition particle 19kU	signal recognition particle 19KD
	225	2254 36060_at	SRP54	U51920	signal recognition particle 54kD	signal recognition particle

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2555		SRP72	AF069765	0	signal recognition particle 72
256	2256 36981 at	SRP9	AF070649		
				aptor	signal recognition particle receptor (docking
2257	2257 36679_at	SRPR	X06272		protein')
				signal transducer and activator of	
2258	2258 AFFX-HUMISGF STAT1	STAT1	M97935		transcription factor ISGF-3
T				d activator of	
2259	2259 32860 q at	STAT1	M97935		transcription factor ISGF-3
				d activator of	
2260	2260 32859 at	STAT1	M97935		transcription factor ISGF-3
				signal transducer and activator of	
2261	2261 33338_at	STAT1	M97936	transcription 1, 91kD	
				signal transducer and activator of	
				transcription 3 (acute-phase response	
2262	2262 39708_at	STAT3	129277	factor)	DNA-binding protein
				signal transducing adaptor molecule (SH3	
2263	2263 160 at	STAM	U43899	domain and ITAM motif) 1	STAM
				similar to Drosophila ash2 gene; Homo	
				sapiens ASH2L gene, complete cds,	
2264	2264 35804 at	ASH2L	AB022785	similar to Drosophila ash2 gene.	
2265	2265 41552 q at	RER1	AW044624	similar to S. cerevisiae RER1	
2266	2266 41551 at	RER1	AW044624	similar to S. cerevisiae RER1	
2267	2267 33632 g at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
				similar to SW:GOLI_DROME Q06003	
2268	2268 35083 at	G1L	AL031670	GOLIATH PROTEIN	ring finger protein 24
2269	2269 37178 at	na	M74089	similar to TB1	
				similar to Wiskott-Aldrich syndrome	
2270	2270 40787 at	WIRE	U90911	protein interacting protein	
2271	2271 34705 at	BET3	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	2272 39131 at	UPF3A	N36842	similar to yeast Upf3, variant A	
2273	2273 41277 at	SAP18	AW021542	sin3-associated polypeptide, 18kD	
2274	33859 at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2275	2275 40992 s at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
				sine oculis homeobox homolog 1	sine oculis homeobox (Drosophila) homotog
2276	2276 40004_at	SIX1	X91868	(Drosophila)	

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				singed-like (fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057	(Drosophila)	actin bundling protein
2278	2278 39086_g_at	SSBP1	AA768912	single-stranded DNA binding protein	
2279		SSBP2	AL080076	2	hypothetical protein
2280	2280 35294_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
				Sjogren syndrome antigen A2 (60kD,	
2281	2281 35295_g_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
				Sjogren syndrome antigen B (autoantigen	Sjogren syndrome antigen B (autoantigen
2282	38450_at	SSB	X69804	(La)	La)
2283	2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389_at	IMAGE145052	A1346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	
2287	2287 37337_at	SNRPG	AI803447	potypeptide G	
				small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
				small nuclear RNA activating complex,	
2289	2289 35247_at	SNAPCS	AI557062	polypeptide 5, 19kD	
				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	-
2291	2291 32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	
				SMT3 suppressor of mif two 3 homolog 1	
2292	2292 38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185_f_at	SMT3H2	Al971724	(yeast)	
2294	2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2206	2296 A0928 at	WSB1	WORAGE	SOCS box-containing WD protein SWiP-1	
25.75	10350 at	10011	1120430		

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	A	В	O	Q	E C
2297	2297 36609_at		D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298	2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 NRAMP2	NRAMP2
2299	2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	monocarboxylate transporter
2300	2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301	2301 36979_at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302	2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303	2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
				solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),
2304	2304 32822_at	SLC25A4	J02966	member 4	member 4
				solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator),
S	2305 37 /40_r_at	SLC25A5	202083	solute carrier family 25 (mitochondrial	
2306	2306 40436_g_at	SLC25A6	J03592	member 6	
2307	2307 40435 at	SLC25A6	103592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308	2308 37675 at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	phosphate carrier protein
2305	2309 33901 at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310	2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein



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†	5			(copper	
표	2311 34749_at	SLC31A2	U83461		putative copper uptake protein
				solute carrier family 35 (CMP-stalic acid	
312	2312 37895_at	SLC35A1	D87969		CMP-sialic acid transporter
				solute carrier family 35 (UDP-N-	
				acetylglucosamine (UDP-GlcNAc)	
313	2313 38208 at	SLC35A3	AB021981		UDP-N-acety/glucosamine transporter
T				odium bicarbonate	
314	2314 34936_at	SLC4A7	AB012130		sodium bicarbonate cotransporter2
				solute carrier family 6 (neurotransmitter	
315	2315 34166_at	SLC6A7	S80071		brain-specific L-proline transporter
					bigo onime dincitor) Tylimol seimes shills
				no acid	Solute carrier lainily / (carloine aniii)
316	2316 32186_at	SLC7A5	M80244	transporter, y+ system), member 5	transporter, y+ system), member 5
				DO acid	Solute carrier tarminy / (cationic animio acid
317	2317 39533_at	SLC7A6	D87432	transporter, y+ system), member 6	transporter, y+ system), member o
				appropriate (continuo o continuo	
				Solute carrier falling 9 (sociality in yellogen	*
				exchanger), isotorm 1 (antiponer, Na+/n+,	
318	2318 32681_at	SLC9A1	S68616	amiloride sensitive)	Na+/H+ exchanger INTE-1 isoloffit
				colute corrier femily 9 (seedium/hydroden	
			207.0001	Solute called failing 5 (southerny disease)	sodium-hydronen exchanger 6
319	2319 36542_at	SLC9A6	AF030409	exchanger), Isolorin o	Sociality angles of the second
2320	2320 39097_at	SON	X63753	SON DNA binding protein	SON UNA-binging protein
Š	11	8000	10000	son of seventees homolog 2 (Diosophila)	guanina nucleotide exchange factor
	2321 32037 at	2005	AFACEAGO	1	sorting nexin 2
3	41405 81	SIVAC	Aroo-102	2 invalidation	S divor prince
2323	2323 39360_at	SNX3	Ar034546	Sorting nextit 3	O HINDE DE LIBOR
2324	2324 40605_at	SNX4	AA524345	sorting nexin 4	
2325	37808 at	SNX7	AL049989	sorting nexin 7	hypothetical protein
				Source: H.sapiens genes for histones	
2326	2326 33352_at	HZA	X57985	H2B.1 and H2A.	histone H2A
2327	2327 36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	2328 36111 s at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2



一	V	8	S	D	Ш
329	2329 1173 g at		HG172-HT3924	Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces.	·
				Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete	hynothetical protein FL120274
088	2330 4061 / _at	44MZ.1	AC004381	sequence.	inpolitional places in the second sec
				Source: Homo sapiens clk2 kinase (CLK2), propin1, cote1,	
				glucocerebrosidase (GBA), and metaxin	
_				genes, complete cds; metaxin	
				pseudogene and glucocerebrosidase	
				pseudogene; and thrombospondin3	Company and the contract of th
<u>88</u>	2331 33740_at	COTEI	AF023268	(THBS3) gene, partial cds.	CITOTIOSOTTIO I OPET TOWNING TIGHTO Z
		_		Source: Homo sapiens hJ l B gene,	
2332	2332 41834_g_at	HJTB PAR	AB016492	complete cds.	jumping translocation preakpoint
				Source: Homo sapiens hJTB gene,	
2333	2333 41833_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
				Source: Homo sapiens mRNA for	
2334	2334 32335_r_at	Ubc2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Homo sapiens mRNA for	
2335	2335 32334_f_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Human CCAAT-box-binding	
2336	2336 32194_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human CCAAT-box-binding	
2337	2337 229_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-101F10, complete	•
2338	2338 41791_at	101F10.3	AC002550	sequence.	hypothetical protein
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-211C6, complete	
2339	2339 41488_at	A-211C6.1	AC002394	sequence.	hypothetical protein A-211C6.1
<u> </u>				Source: Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete	
2340	2340 35742 at	A-362G6.1	U95740	sednence.	hypothetical protein A-362G6.1

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I			,	Source: Himen Chamasome 16 BAC	
				clone CIT987SK-A-61E3, complete	
2341	2341 41733_at	61E3.1	AC003007	sequence.	Unknown gene product (partial)
				Source: Human DNA sequence from	
2242	2242 26904 24		A1 034046	clone RP4-742C19 on chromosome 22,	
7	20024_all		ALUS 1040	complete sequence.	
0,00		•		Source: Human mRNA for HLA class I	
3	2343 37383_1_at	HLA class I - locus	ocus X58536	locus C neavy chain.	HLA class I neavy chain
		-		Source: Human N-	
				acetylglucosaminyltransferase I (GlcNAc-	acetylglucosaminytransferase I (GlcNAc- mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
2344	2344 39778_at	T1 GLCN	AC-1M55621	TI) mRNA, complete cds.	N-acetylglucosaminyltransferase
2345	2345 41573_at	SP3	X68560	Sp3 transcription factor	
				spastic ataxia of Charlevoix-Saguenay	
2346	2346 32102_at	SACS	AB018273	(sacsin)	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
2347	2347 35171_at	SPG4	AB029006	spastin)	KIAA1083 protein
2348	39423_f_at	SPOP	AJ000644	speckle-type POZ protein	SPOP
2349	2349 38924_s_at	SSH3BP1	AF001628	spectrin SH3 domain binding protein 1	interactor protein AbIBP4
2350	33886_at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351	2351 39556_at	SPTBN1	M96803	spectrin, beta, non-enythrocytic 1	beta-spectrin
2352	2352 34304 s at	SAT	AL050290	spermidine/spermine N1-acetytransferase	
				sphingomyelin phosphodiesterase 1, acid	
2353	2353 32574_at	SMPD1	X59960	lysosomal (acid sphingomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
				(olivopontocerebellar ataxia 1, autosomal	
2354	2354 36142_at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
				spinocerebellar ataxia 2	
				(olivopontocerebellar ataxia 2, autosomal	
2355	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
				splicing factor 30, survival of motor neuron	
2356	2356 38040 at	SPF30	AF107463	related	splicing factor
2357	2357 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein



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35.8	2358 36224 A at		A1827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
	2000 October 19-01		X70944	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	PTB-associated splicing factor
380	2360 36098 at		M72709	lor, arginine/serine-rich 1 tor 2, atternate splicing factor)	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361	2361 140_s_at	0	U68063	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362	2362 32183_at	SFRS11	M74002	splicing factor, arginina/serine-rich 11	argillite-tich nacreal process
2363	2363 35258_f_at	۵	AF030234		splicing factor Sip1
2364	40457_at	SFRS3	AF038250		
2365	2365 36991_at	SFRS4	L14076	splicing factor, arginine/serine-nch 4	pre-mina splicing factor SRp40-1
7366	40453_s_at	STROD	020020	1	
2367	2367 40262_at	SRP46	AF031166	Splicing factor, arginine/senne-nch, 40kD	sanalana anoxidasa
2368	2368 35839_at	SOLE	0,813/0	squaiene epoxidase	squares openings
2369	2369 39047 at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370	2370 41784 at	DKFZp564B0769	AL080186	SR rich protein	hypothetical protein
2371	2371 36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	2372 41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	2373 32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	2376 41823 at	STAU	AJ132258	staufen, RNA binding protein (Drosophila)	
2377	2377 38669 at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378	2378 37147 at	SCGF	AF020044	stem cell growth factor, tymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379	2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380	2380 38034 at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid sultatase (microsomai), aryisultatase C, isozyme S
	10000 I				

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SRD5A1 M32313 A-dehydrogenase alpha SRD5A1 M32313 A-dehydrogenase alpha SCAMOL AI53563 stencid-5-alpha-reductase, alpha SCAMOL AI53563 stenci-C4-methy oxidase-life stenci-C4-methy oxidase-lif			c	ļ		L
SRD5A1 M32313 Adehydrogenase alpha SRD5A1 AI535653 stenot-C4-methyl oxidase-like SC4MOL AI535653 stenot-C4-methyl oxidase-like SC4MOL AI535653 stenot-C4-methyl oxidase-like SC4MOL AB016247 desaturase homolog, tungal)-like stenot-C5-desaturase (ERG3 delta-5-sacociated endoplesmic reticulum stress-associated endoplesmic reticulum		¥	B	כ		
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SRD5A1 M32313 4-dehydrogenase alpha 1) of case alpha 1 strip SCAMOL Al535653 sterol-C3-desaturase (ERG3 defra-5-3 sterol-C3-desaturase (ERG3 defra-5-3 sterol-C5-desaturase (ERG4 description (ER) subcritate defravorprotein (ER) subcritate subcritate defravorprotein (ER) subcritate subcritate defravorprotein subcritate defravorprotein subcritate defravorprotein subcritate subcritate defravorprotein subcritate defravorprotein subcritate defravorprotein subcritate defravorprotein subcritate defravorprotein subcrit						1 (3-oxo-5 alpha-steroid detta 4-
SC4MOL Al535653 sterol-C4-methyl oxidase-like	2381	589 at	SRD5A1	M32313		dehydrogenase alpha 1)
at SC5DL AB016247 desaturase (ERG3 delta-5-rike) at EPB72 X85116 stomatin; H.sapiens epb72 gene exon 1. Item at SFN X57348 stratflin at SFN X57348 stratflin at SFN X57348 stratflin protein 1; ribosome associated membrane protein 1; ribosome associated membrane protein 4. at SDF1 AF035272 protein 1; ribosome associated membrane protein 4. at SDF1 AF035287 stromal cell-derived factor 1 at SDF1 L36033 stromal cell-derived factor 1 at SDF2 D50845 stromal cell-derived factor 1 at SDF3 subunit A flavoprotein (Fp) subunit A flavoprotein (Fp) succinate dehydrogenase complex, subunit A flavoprotein (Fp) at SDHD AB006202 subunit A flavoprotein (Fp) at SULA2 AF058953 subunit A membrane protein succinate Gelydrogenase complex, subunit A flavorating enzyme subunit B subunit A flavorating enzyme subunit B subunit A flavorating enzyme subunit B suberxilian at SKIVZL U09877 <td>2382</td> <td>33369 at</td> <td>SC4MOL</td> <td>AI535653</td> <td>sterol-C4-methyl oxidase-like</td> <td></td>	2382	33369 at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
s. at SC5DL AB016247 desaturase homolog, fungal)-like at EPB72 X85116 stomatin; H.sapiens epb72 gene exon 1. Lat SFN X57348 stratifin at SERP1 AF035272 protein 1; ribosome associated membrane protein 1; ribosome associated membrane protein 4 at SDFR1 AF035287 stromal cell derived factor 1 at SDF1 L36033 stromal cell-derived factor 1 at SDF1 at SDF2 D50845 stromal cell-derived factor 1 at SDF2 stromal cell-derived factor 1 at SDF2 succinate cell-derived factor 1 at SDF2 at SDHA L21936 subunit A, flavoprotein (Fp) succinate dehydrogenase complex, subunit A, flavoprotein (Fp) at SDHC U57877 15kD succinate dehydrogenase complex, subunit C, integral membrane protein at SUHD AB006202 subunit D, integral membrane protein at SULTAt AB029000 sulfatase FP at SULTAt AB039000 sulfatase FP at SKIVZL AL041443 SUMO-1 activating enzyme subunit 2 sulfatase PP at SC						
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SFN X57348 stratifin	2384	40419 at	EPB72	X85116		band 7 integral membrane protein
at SERP1 AI557272 protein 1; ribosome associated membrane protein 1; ribosome associated membrane protein 4 at SDFR1 AF035287 stromal cell derived factor 1 at SDF1 L19495 stromal cell-derived factor 1 at SDF2 L21936 stromal cell-derived factor 1 at SDF2 D50645 stromal cell-derived factor 1 at SDF2 D50645 stromal cell-derived factor 1 at SDF2 D50645 stromal cell-derived factor 1 at SDF2 stromal cell-derived factor 1 at CAPA	2385	l.—	SFN	X57348		stratifin
SERP1 AI557272 protein 4 SDFR1 AF035287 stromal cell derived factor 1 SDF1 U19495 stromal cell-derived factor 1 SDF1 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 1 SDF2 Subunit A, flavoprotein (Fp) SUDHA L21936 subunit C, integral membrane protein, subunit C, integral membrane protein, subunit D, integral membrane protein, subunit D, integral membrane protein, subunit D, integral membrane protein, subunit A, member 1 SULT4A1 AB029000 sulfotransferase family 4A, member 1 SKIV2L AL04443 SUMO-1 activating enzyme subunit 2 SKIV2L U09877 cerevisiae) SVIIL AR051850 superviller viralicidic activity 2-like (S. cerevisiae) SVIIL AR051850 supervi		11			stress-associated endoplasmic reticulum protein 1; ribosome associated membrane	
SDFR1 AF035287 stromal cell derived factor 1 SDF1 U19495 stromal cell-derived factor 1 SDF1 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 2 SDF2 D50645 stromal cell-derived factor 2 SDF2 D50645 stromal cell-derived factor 2 SUF2 Succinate dehydrogenase complex, submit A, flavoprotein (Fp) SDHA L21936 submit A, flavoprotein (Fp) SDHC U57877 15kD SUCLA2 AB006202 submit C, integral membrane protein submit C, integral membrane protein submit D, integral membrane protein succinate -CoA ligase, ADP-forming, beta submit D, submit D, integral membrane protein submit C, submit D, integral membrane protein submit D, sulfatase FP SULT4A1 N63574 sulfatase FP SKIV2L U09877 superkiller viralicidic activity 2-like (S. cerevisiae) SOD1 X02317 supervillin SVIL AF051850 supervillin SUMO-1 activating enzyme submit 2 superviller selerosis 1 (adult)) SVIL AF051850 superviller selerosis 1 (adult))	2386	37035 at	SERP1	AI557272	protein 4	
SDFR1 AF035287 stromal cell derived factor 1 SDF1 U19495 stromal cell-derived factor 1 SDF1 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 2 SDF2 succinate dehydrogenase complex, subunit A, flavoprotein (Fp) SDHA L21936 subunit A, flavoprotein (Fp) SDHC U57877 subunit C, integral membrane protein, subunit C, integral membrane protein SDHC AB006202 subunit D, integral membrane protein SULTAA1 AB029000 sulfatase FP SULTAA1 AB029000 sulfatase FP SULTAA1 AL041443 sulfotransferase family 4A, member 1 SWIV2L AL041443 SUMO-1 activating enzyme subunit 2 SCD1 superoxide dismutase 1, soluble SOD1 X02317 cerevisiae) SVIL AF051850 supervillin GHRF GRF AL031659 supported by FGENESH						stromal cell derived factor receptor 1 isoform
SDFR1 AF035287 stromal cell derived factor 1 SDF1 U19495 stromal cell-derived factor 1 SDF1 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 2 SDF2 D50645 stromal cell-derived factor 2 SDF2 D50645 stromal cell-derived factor 2 SDF2 succinate dehydrogenase complex, subunit A, flavoprotein (Fp) SDHA L21936 subunit A, flavoprotein (Fp) SDHC U57877 15kD SUCIA2 AB006202 subunit C, integral membrane protein, succinate dehydrogenase complex, subunit D, integral membrane protein SUCIA2 AF058953 subunit Membrane Protein SULT4A1 AB029000 sulfotransferase family 4A, member 1 SULT4A1 NG3574 sulfotransferase family 4A, member 1 SKIV2L U09877 cerevisiae) SCD1 X02317 cerevisiae) SVIL AF051850 suppervillin GHRF GRF AL031659 supported by FGENESH			-			b; stromal cell derived factor receptor 1
SDF1 U19495 stromal cell-derived factor 1 SDF2 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 2 SDF2 D50645 succinate dehydrogenase complex, subunit A, flavoprotein (Fp) SDHA L21936 subunit A, flavoprotein (Fp) SDHC U57877 15kD SDHC U57877 subunit C, integral membrane protein, subunit C, integral membrane protein, subunit D, integral membrane protein, subunit D, integral membrane protein SDHD AR006202 subunit D, integral membrane protein, subunit D, integral membrane protein, subunit D, integral membrane protein, subunit D, integral membrane protein SUCLA2 AR029000 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 SURIO2 SUMO-1 activating enzyme subunit 2 supervisie) SCD1 X02317 cerevisie) SVIL AR051850 supervillin GHRF GRF AL031659 suppervillen	2387	35747_at	SDFR1	AF035287	stromal cell derived factor receptor 1	isoform a
SDF1 L36033 stromal cell-derived factor 1 SDF2 D50645 stromal cell-derived factor 2 SDHA L21936 subunit A, flavoprotein (Fp) SDHA L21936 subunit A, flavoprotein (Fp) SDHC U57877 t5kD SDHC U57877 succinate dehydrogenase complex, subunit C, integral membrane protein SDHC AB006202 subunit D, integral membrane protein SUCLA2 AF058953 subunit D, integral membrane protein SULT441 N63574 sulflotransferase FP SULT443 SUMO-1 activating enzyme subunit 2 SWIV2L superkiller viralicidic activity 2-like (S. SCD1 X02317 cerevisiae) SVIL AF051850 supervillin GHRF GRF AL031659 supported by FGENESH	2388	32666_at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
SDF2 D50645 stromal cell-derived factor 2 succinate dehydrogenase complex, SDHA L21936 subunit A, flavoprotein (FP) SUCINATOR SUCINATE dehydrogenase complex, SUCLA2 AB006202 sucinate dehydrogenase complex, SUCLA2 AF058953 subunit D, integral membrane protein SUCLA2 AF058953 subunit D, integral membrane protein SUCLA2 AF058953 subunit D, integral membrane protein SULT4A1 AB029000 sulfatase FP SULT4A1 AB029000 sulfatase FP SUMO-1 activating enzyme subunit 2 SUMO-1 activating enzyme 2 SUMO-1 activating enzyme 3 SUMO-1 activati	2389	33834 at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
SDHA (L21936 subunit A, flavoprotein (FP) SUCCINATO (L21936 subunit A, flavoprotein (FP) SUCCINATO (L27877 SUCCINATE dehydrogenase complex, subunit C, integral membrane protein, 15kD SUCLA2 ABO06202 subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit D (L4A1 AB029000 sulfatase FP) SULTAA1 AB029000 sulfatase FP subunit D (L4A1 AB029000 sulfatase FP) SULTAA1 AB029000 sulfatase FP subunit 2 subunit 2 superkiller viralicidic activity 2-like (S. SCNV2L U09877 cerevisiae) SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH	2390	41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
SDHA L21936 subunit A, flavoprotein (FP) SUCCINATOR Succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD succinate dehydrogenase complex, subunit D, integral membrane protein succinate dehydrogenase complex, subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit D sulfatase FP KIAA1077 AB029000 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 superviller suralicidic activity 2-like (S. Supervillin SVIL SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) supervillin supervillin supervillin GHRF GRF AL031659 supported by FGENESH					succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
SDHC U57877 15kD succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD succinate dehydrogenase complex, subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit AB029000 sulfatase FP sulfotransferase family 4A, member 1 SULT4A1 N63574 sulfotransferase family 4A, member 1 SULT4A1 AL041443 SUMO-1 activating enzyme subunit 2 superkiller viralicidic activity 2-like (S. SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH	2391	34826_at	SDHA	121936	subunit A, flavoprotein (Fp)	subunit
SDHC U57877 15kD SDHC 15kD succinate dehydrogenase complex, subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit AIA1077 AB006202 subunit D, integral membrane protein succinate-CoA ligase, ADP-forming, beta subunit AIA1077 AF058953 subunit AIA2 Subunit AIA3 sulfatase FP sulfatase family 4A, member 1 sulfatase FP superviller activity 2-like (S. superviller viralicidic activity 2-like (S. superviller (amyotrophic lateral sclerosis 1 (adult)) supervillin SVIL AF051850 supported by FGENESH supported by FGENESH					succinate dehydrogenase complex,	
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SDHD AB006202 subunit D, integral membrane protein SUCLA2 AF058953 subunit KIAA1077 AB029000 sulfatase FP SULT4A1 N63574 sulfatase FP SULT4A1 N63574 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SKIV2L U09877 cerevisiae) SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH GHRF GRF AL031659 supported by FGENESH	2392	34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
SDHD AB006202 subunit D, integral membrane protein SUCLA2 AF058953 subunit KIAA1077 AB029000 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SKIV2L SUPRO-1 activating enzyme subunit 2 SKIV2L superkiller viralicidic activity 2-like (S. cerevisiae) SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH					succinate dehydrogenase complex,	
SUCLA2 AF058953 subunit KIAA1077 AB029000 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SKIV2L superkiller viralicidic activity 2-like (S. cerevisiae) SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH	2393	40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
SUCLA2 AF058953 subunit KIAA1077 AB029000 sulfatase FP SULT4A1 N63574 sulfotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SKIV2L U09877 cerevisiae) SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH					succinate-CoA ligase, ADP-forming, beta	ATP-specific succinyl-CoA synthetase beta
KIAA1077 AB029000 sulflatase FP SULT4A1 N63574 sulflotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SKIV2L L09877 cerevisiae) SCD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH	2394	40893_at	SUCLA2	AF058953	subunit	subunit
SULT4A1 N63574 sulfotransferase family 4A, member 1 UBA2 AL041443 SUMO-1 activating enzyme subunit 2 SUMO-1 activating enzyme subunit 2 superkiller viralicidic activity 2-like (S. SKIV2L U09877 cerevisiae) SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supported by FGENESH GHRF GRF AL031659 supported by FGENESH	2395	35832_at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
UBA2 AL041443 SUMO-1 activating enzyme subunit 2 superkiller viralicidic activity 2-like (S. SKIV2L U09877 cerevisiae) superoxide dismutase 1, soluble superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supervillin supervi	2396	33712 at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
SKIV2L U09877 cerevisiae) SKIV2L U09877 cerevisiae) SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supervillin SVIL AF031659 supported by FGENESH	2397	34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
SKIV2L U09877 cerevisiae) SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supervillin GHRF GRF AL031659 supported by FGENESH		1			superkiller viralicidic activity 2-like (S.	
SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supervillin GHRF GRF AL 031659 supported by FGENESH	2398	37998_at	SKIV2L	U09877	cerevisiae)	helicase-like protein
SOD1 X02317 (amyotrophic lateral sclerosis 1 (adult)) SVIL AF051850 supervillin GHRF GRF AL 031659 supported by FGENESH					superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
SVIL AF051850 supervillin SUPPRINT SUPP	2399	36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
GHRF GRF AL031659 Supported by FGENESH	2400	40069 at	SVIL	AF051850	supervillin	supervillin
	2401	36676 at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

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2402	2402 33297 at	P2	VF-1AL031778	supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform 1
		. 1			
2403	2403 34825_at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
T				nicity 13 (colon	
2404	2404 1640_at	ST13	U17714		putative turnor suppressor ST13
2405	2405 37745 s at	ST5	U15780	suppression of tumorigenicity 5	p82
2406	2406 37805 at	SRPUL	AF060567	sushi-repeat protein	sushi-repeat protein
				sushi-repeat-containing protein, X	
2407	2407 31855_at	SRPX	U61374		
2408	2408 31869 at	KIAA0640	AB014540	SWAP-70 protein	KIAA0640 protein
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2409	2409 40213 at	SMARCA1	M88163	subfamily a, member 1	transcription activator
				SWI/SNF related, matrix associated, actin	
		-		dependent regulator of chromatin,	
2410	2410 40961 at	SMARCA2	X72889	subfamily a, member 2	НВЯМ
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2411	2411 32579 at	SMARCA4	U29175	subfamily a, member 4	transcriptional activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2412	39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
2413	2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414	2414 41692 at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
2415	38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416	2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
					synaptosome associated protein of 23
2417	2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kU	kilodaltons, isoform A
				syndecan 2 (heparan sulfate proteoglycan	
2418	2418 39757 at	SDC2	J04621	1, cell surface-associated, fibroglycan)	_
2419	2419 32092 at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420	2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421	2421 38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
2422	38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

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2423	38774_at	STX7	U77942	syntaxin 7	syntaxin /
2424	2424 37510 at		AF036715		syntaxin 8
2425	2425 33942 s at		AF004563	nding protein 1	hUNC18b
2426	2426 37962 r at	STXBP3	D63506		unc-18homologue
				ric DNA-binding	
2427	2427 33315 at		M29204	_	chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				tor.	
2428	2428 192 at	TAF7	U18062		TFIID subunit TAFII55
				TAF9 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2429	2429 193 at	TAF9	U21858		TAFII32 precursor
				TAFII20; contains homology to histone	
				H2B; TFIID subunit; TAFII15; contains	
_				homology to histone H2B; TFIID subunit;	
				Hurnan TFIID subunits TAF20 and TAF15	
2430	2430 37620 at	TAF12: TAF2J: TAU57693	U57693		TAF20; TAF15
2431	2431 32166 at	J-LN-I	AB028950		KIAA1027 protein
2432	2432 39765 at	TLN2	AB002318	talin 2	
2433	41168 at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	2434 39779 at	TARBP1	U38847	in 1	TAR RNA loop binding protein
2435	2435 32241 at .	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	2436 39416 at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
				Tax1 (human T-cell leukemia virus type I)	
2437	2437 498 at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	
2438	2438 35279 at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	36702 at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196 at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	244134791 at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	t-complex-associated-testis-expressed t-like
				t-complex-associated-testis-expressed 1-	t-complex-associated-testis-expressed 1- t-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	

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TEG; EGRA; Homo sapiens TGPb inducible early protein and early growth response protein alpha genes, complete cds. TEG; EGRA; KLFAF050110 cds. TERF1 U40705 testis derived transcript (3 LIM domains) testis enhanced gene transcript (BAX inhibitor 1) testis enhanced gene transcript (BAX inhibitor 1) terracting 1 terraspan 3 terraspan 4 terras						1
TEG; EGRA; KLF AF050110 cds. TERF1 U40705 testis derived transcript (3 LIM domains) TES AL050162 testis derived transcript (BAX interacting) 1 TETRAN L11669 tetraspen 1 TETRAN L11669 tetraspen 1 TTC3 U46570 tetraspen 1 TIC3 D83077 tetraspen denain 3 TIEG S81439 TGFB inducible early growth response TGFB inducible early growth response and 5917-5926 may be ASN-linked and 5917-5926 may be ASN-linked glycosylation steps; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, and 5917-5926 may be ASN-linked glycosylation stes; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, indepted cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation stes; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, indepted cds. IGFBP3 M35878 complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation stes; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation stes; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.		4	80	ပ	D	n
TIEG; EGRA; KLF AF050110 cds. TERF1 U40705 testis derived transcript (3 LIM domains) TEGT X75861 inhibitor 1) TETRAN L11669 tetraspan 3 TTC1 V46570 tetraspan 3 TTC3 D83077 tetratricopeptide repeat domain 1 TGFB-induced factor (TALE family TGFB-induced factor (TALE family TGFB-induced factor (TALE family THE AS encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, Complete cds. IGFBP3 M35878 complete cds. IGFBP3 M35878 complete cds. IGFBP3 M35878 complete cds. IGFBP3 M35878 complete cds.	 				TEIG; EGRa; Homo sapiens TGFb inducible early protein and early growth	
TIEG; EGRA; KLF AF050110 cds. TERF1 U40705 interacting) 1 TES AL050162 testis derived transcript (3 LIM domains) TEGT X75861 inhibitor 1) TEGT X75861 inhibitor 1) TETRAN L11689 tetracycline transporter-like protein TTC1 U46570 tetratricopeptide repeat domain 3 TIEG S81439 TGFB inducible early growth response TGFB-induced factor (TALE family homeobox) TGFB-induced factor (TALE family homeobox) TGFB-induced by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	* .			- <u>-</u>		TGFb inducible early protein; early growth
TERF1 U40705 interacting) 1 TES AL050162 testis derived transcript (3 LIM domains) testis enhanced gene transcript (BAX 175861 inhibitor 1) TEGT X75861 inhibitor 1) TEGT W689023 tetracycline transporter-like protein tetraspan 3 tetracycline transporter-like protein tetrasporter-like protein 1 tetraspan 3 tetraticopeptide repeat domain 3 tetraticopeptide 4 tetraticopeptid	24443					response protein alpha
TES AL050162 testis derived transcript (3 LIM domains) testis enhanced gene transcript (BAX X75861 inhibitor 1) TEGT X75861 inhibitor 1) TEGT X75861 inhibitor 1) TEGT W69023 tetracycline transporter-like protein tetraspan 3 TTC1 U46570 tetratricopeptide repeat domain 1 tetratricopeptide repeat domain 3 TIEG S81439 TGFB inducible early growth response TGFB-induced factor (TALE family homeobox) TGIF X89750 homeobox) TGIF AX89750 homeobox) TGFB-induced factor (TALE family homeobox) TGFB-induced						telomeric repeat binding factor 1, isoform 2:
TES AL050162 testis derived transcript (3 LIM domains) It testis enhanced gene transcript (BAX testis enhanced gene transcript (BAX inhibitor 1) TETRAN L11669 tetracycline transporter-like protein to tetracycline transporter-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. IES AL05016 testis enhanced derived transporter-binding protein-3 precursor (IGFBP3) gene, complete cds. In Alo502 testis derived transporter-binding protein-3 precursor (IGFBP3) gene, complete cds. In Alo5016 testis enhanced transporter-binding protein-3 precursor (IGFBP3) gene, complete cds. In Alo5016 testis enhanced transporter-binding protein-3 precursor (IGFBP3) gene, complete cds.	2445					telomeric repeat binding factor 1, isoform 1
TEGT X75861 inhibitor 1) TETRAN L11669 tetracycline transporter-like protein to tetracycline transporter-like protein transporter-	2446					hypothetical protein
TEGT X75861 inhibitor 1) TETRAN L11669 tetracycline transporter-like protein to the transporter-like procursor. TIEG S81439 TGFB inducible early growth response to the transporter to the transp						testis enhanced gene transcript (BAX
TETRAN L11669 tetracycline transporter-like protein to the transporter	2447					inhibitor 1)
TSPAN-3 M69023 tetraspan 3	2448	32080_at				tetracycline transporter-like protein
TTC1 U46570 tetratricopeptide repeat domain 1 to 281439 tetratricopeptide repeat domain 3 to 281439 TGFB inducible early growth response TGFB-induced factor (TALE family homeobox) TGIF X89750 homeobox) TGFB-induced factor (TALE family homeobox) TGFB-induced factor (TALE family homeobox) TGFB-induced factor (TALE family homeobox) The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homeosapiens growth factor-binding protein-3 precursor (IGFBP3) gene, Homeosapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2449	38612_at			tetraspan 3	
TIEG S81439 TGFB inducible early growth response TGFB-induced factor (TALE family Nomeobox) TGIF X89750 homeobox) TGFB-induced factor (TALE family homeobox) TGFB-induced factor (TALE family homeobox) The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2450	37321_at	TTC1		tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
TIEG S81439 TGFB inducible early growth response TGFB-induced factor (TALE family homeobox) TGIF X89750 homeobox) The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2451	at	TTC3		tetratricopeptide repeat domain 3	TPRD
TGIF X89750 homeobox) TGIF AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2452	224 at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
TGIF X89750 homeobox) The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					TGFB-induced factor (TALE family	
The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, Complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2453			X89750	homeobox)	TGIF protein
and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. IGFBP3 M35878 complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					The AAs encoded by bases 5728-5736	
glycosylation sites; insulin-like precursor; Homo septens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo septens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					and 5917-5926 may be ASN-linked	
Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					glycosylation sites; insulin-like precursor;	-
IGFBP3 gene, Complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, IGFBP3 (M35878 complete cds.					Homo sapiens growth factor-binding	
IGFBP3 M35878 complete cds. The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					protein-3 precursor (IGFBP3) gene,	
The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	2454	37319 at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor
and 5917-5926 may be ASN-tinked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					The AAs encoded by bases 5728-5736	
glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					and 5917-5926 may be ASN-linked	
Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.					glycosylation sites; insulin-like precursor;	
protein-3 precursor (IGFBP3) gene, complete cds.					Homo sapiens growth factor-binding	
IGFBP3 M35878 complete cds.					protein-3 precursor (IGFBP3) gene,	
	2455	1586_at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor

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				ocated at second am. And ial IPPase.;	
2456		P1: M6S	1; NFD12485	pyrophosphatase, complete cus.	aso
2457 36992	36992_at	NX I	A1090080	domain-containing	hypothetical protein
267	2428 34700_ai	OGNA	ALCOCOCO		hair consessed HHCPA78 homolog VOUP1
2459	2459 31508_at	TXNIP	S73591	thioredoxin interacting protein	thioredoxin reductase (NADPH)
2460	2460 39425_at	LXNHUI	A5124/		thioredoxin-like protein
2461	2461 32214_at	TABS	AFUGSSS M63180	ase	threonyl-tRNA synthetase
2463	2463659 g at	THBS2	L12350		thrombospondin 2
2464	2464 658 at	THBS2	L12350		thrombospondin 2
					G/T mismatch-specific thymine DNA
2465	2465 40865 at	TMCBAY	U51166 M17733	thymosin beta 4. X chromosome	thymosin, beta 4
3		N. Committee		ating	
2467	2467 32654_g_at	SMAP	AW020536		1
2468	2468 39699_at	TRIP12	D28476		thyroid normone receptor interactor 12
2469	2469 41251_at	TRIP3	L40410		thyroid receptor interactor
2470	2470 39341_at	TRIP6	AJ001902		IRIP6
2471	2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
	44.006	TDABOAD	AB01116E	thyroid hormone receptor-associated	KIAA0593 protein
2472	24/2 4 1023 at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
2/1/2	מיים			TIA1 cytotoxic granule-associated RNA	TIA1 protein, isoform 1; TIA1 protein,
2474	2474 33852 at	TIA1	M77142	binding protein	isoform 2
2475	2475 41763 g at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476	2476 36655 at	TJP2	127476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801_at	TJ6	AF112972	TJ6 protein	176

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2478 35238	5238_at	TRAFS	AB000509	ated factor 5	TRAF5
24793	2479 33243 at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
8	2480 40310_at	TLR2	AF051152		Toll/interleukin-1 receptor-like protein 4
2481	2481 1030_s_at	TOP1	U07806		DNA topoisomerase I
2482	2482 36571_at	TOP2B ·	X68060	II beta (180kD)	DNA topoisomerase II
2483	2483 32233_at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
2484	2484 32219 at	TLK1	D50927		KIAA0137 protein
2485	2485 35321 at	TLK2	AB004884		PKU-alpha
				TRAF family member-associated NFKB	
2486	2486 39742_at	TANK	U59863	activator	I-TRAF
2487 40051	40051_at	KIAA0057	D31762	TRAM-like protein	TRAM-like protein
2488	2488 1073 at	TCEA1	M81601		transcription elongation factor SII
)		transcription elongation factor A (SII)-like	
2489 38317	38317_at	TCEAL1	M99701	•	transcription elongation factor A (SII)-like 1
3	1 000	i L C	1 24507	transcription elongation factor B (SIII),	RNA polymerase II elongation factor SIII,
2430	2430 1339_at	יכנים	104507	transcription alongation factor B (SIII)	RNA polymerase II elongation factor-like
2491	41759 at	TCEB1L	247087	polypeptide 1-like	protein
				transcription elongation regulator 1	
2492	2492 39426 at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
				transcription factor 12 (HTF4, helix-loop-	
2493	2493 33348_at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
7070	1000	- L	Moteos	transcription factor 3 (E2A immunoglobulin	·
****	13/3 81	2	100 OK	transcription factor 8 (represses	
2495	2495 33440 at	TCF8	U19969	interleukin 2 expression)	ZEB
				transcription factor AP-4 (activating	
2496	2496 39638_at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497	2497 37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498	2498 32578_at	TCFL4	AW005997	transcription factor-like 4	
		i		transcription factor-like 5 (basic helix-loop-	transcription forder like 5
2499		TAPAS:	AE0012124	hancorintional adoptor 3 like	ADA3-like profein
2500	2500 35749 at	IADAGE	APU09/33	וומווזכווחווחוומו מחשטוחו היוועם	יייסיטול פעוו-סעסען

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					KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein
2501	2501 35297 at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	2
				transcriptional co-activator with PDZ-	
2502	2502 33876_at	TAZ	AL050107	binding motif (TAZ)	hypothetical protein
				transcriptional co-repressor; Human	
				roid	
				0	
2503	2503 39358_at	SMRT	U37146	cds.	hormone action
T		-		transcriptional regulator interacting with	
2504	2504 37312_at	TRIP-Br2	D50917	the PHS-bromodomain 2	KIAA0127 gene product
2505	2505 40631 at	T081	D38305	transducer of ERBB2, 1	Tob
2506	2506 32554 s at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	2507 37324 at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	2508 39344_at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
				transforming growth factor beta-stimulated	
2509	2509 39032_at	TSC22	AJ222700	protein TSC-22	TSC-22
				transforming growth factor, beta 1	transforming growth factor, beta 1 (Camurati-
2510	2510 41445 at	TGFB1	X02812	(Camurati-Engelmann disease)	Engelmann disease)
				transforming growth factor, beta receptor	
2511	2511 1815_g_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta receptor	
2512	2512 1814 at	TGFBR2	D50683	II (70-80kD)	TGF-betailR alpha
				transforming growth factor, beta-induced,	
2513	2513 1385 at	TGFBI	M77349	68kD	transforming growth factor induced protein
				transforming, acidic coiled-coil containing	
2514	2514 40841 at	TACC1	AF049910	protein 1	TACCI
				transforming, acidic coiled-coil containing	
2515	2515 38816 at	TACC2	AF095791	protein 2	TACC2 protein
2516	2516 36931 at	TAGLN	M95787	transgelin	smooth muscle protein
2517	2517 36678 at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	2518131829 r at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
				transient receptor potential cation channel	_
2519	2519 39124_r_at	TRPC1	99068X	subfamily C, member 1	TRPC1 protein
2520	2520 39123 s. at	TRPC1	X89066	transient receptor potential cation channel subfamily C, member 1	TRPC1 protein
2252	22150		2000		

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				RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of spilototessate ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirliS25197 transitional endoplasmic reticulum ATPASE endoplasmic reticulum ATPASE on mouse gil55217 (Z14044) murine valosin-containing protein; 99% identical to mouse, rat, and pig homologs; X-ray cross-complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical protein in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c (Schizosaccharomyces pombe); probable membrane protein (AL021766) [Schizosaccharomyces carevisiae) (Saccharomyces carevisiae) (Saccharomyces carevisiae) (Saccharomyces carevisiae) (AB004539) ORF YLL031c (Saccharomyces carevisiae) (Saccharomyces carevisiae) (AB004539) ORF YLL031c (Saccharomyces carevisiae) (AB004539) ORF YLL031c (Saccharomyces carevisiae) (Pypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical 29.8 kDa putative membrane protein; Most similar to hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical 20102037) (C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical 20102037) (C27A12.9 [Caenorhabditis elegans]; Hypothetical 39.8 kDa putative membrane protein; Most similar to hypothetical 20102037)	TERA_HUMAN; XRCC9; P1.11659_3; P1.11659_5
2521		XHCC9	AC004472	Casilotta forter suit homolog	GC20 protein
2522	2522 33351_at	GC20	AF064607		KIAA0741 protein
2523		IF2	AB018284	translation inflation factor in 2	NIMAN 41 Protein
2524	2524 32173 at	UK114	X95384	translational inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5
2752	32 173 at				

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2525	2525 41051_at		X95073	translin-associated factor X	Translin associated protein X
2526	2526 32831 at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527	2527 36198_at	Ē	NDIND13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
2528	2528 37050_r_at	TOMM34	A1130910	translocase of outer mitochondrial membrane 34	-
2529	2529 32853_at	TOMM70A	AB018262	translocase of outer mitochondrial membrane 70 homolog A (yeast)	KIAA0719 protein
2530	2530 34796_at	TRAM	X63679	translocating chain-associating membrane protein	TRAM protein
2531	2531 38100_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531_at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535	2535 32083_at	TM7SF1	AF027826	transmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536	2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537	2537 34307 at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538	2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37445_at	TMEMS	AB015633	transmembrane protein 5	type II membrane protein
2540	2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982 at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545	2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547	2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548	2548 36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
2549	2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

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	TPM1	224727	tropomyosin 1 (alpha)	tropomyosin isoform
	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
	WRB	Y12478	tryptophan rich basic protein	congenital heart disease 5 protein
	WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
			Tu translation elongation factor,	
	TUFM	S75463	mitochondrial	P43
	TULP3	Al028290	tubby like protein 3	
	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
	TUBB	AF035316	tubulin, beta polypeptide	
	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
2559 33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
	TBCC	U61234	tubulin-specific chaperone c	cofactor C
	TBCE	U61232	tubulin-specific chaperone e	cofactor E
2562 37007 at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
			tumor necrosis factor receptor	
2563 34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
			tumor necrosis factor receptor	
			superfamily, member 12 (transfocating	
2564 41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
			tumor necrosis factor receptor	
2565 1563_s_at	TNFRSF1A	M58286	superfamily, member 1A	tumor necrosis factor receptor
			turnor necrosis factor receptor	
2566 35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
			turnor necrosis factor receptor	
2567 37643_at	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
			tumor necrosis factor, alpha-induced	
2568 36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
			tumor necrosis factor, alpha-induced	
2569 38631_at	TNFAIP2	M92357	protein 2	B94 protein
			tumor necrosis factor, alpha-induced	
	TNFAIP3	M59465	protein 3	A20
at	TPD52L2	AF004430	tumor protein D52-like 2	hD54+ins2 isoform
	TP53BP1	U09477	tumor protein p53 binding protein, 1	p53-binding protein
2573 34822_at	TP53BP2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
2574 38568 at	TP538PL	U82939	tumor protein p53-binding protein	p53 binding protein

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2575	2575 31584_at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
2576	2576/31888 s. at	ESSU	AF001294	tumor suppressing subtransferable	<u> </u>
2577	147_at			tumor susceptibility gene 101	tumor susceptibility protein
2578	2578/40328 at	TWIST	X99268	twist homolog (acrocephalosyndactyty 3; Saethre-Chotzen syndrome) (Drosophila)	B-HLH DNA binding protein
2579	2086_s_at		D17517	TYRO3 protein tyrosine kinase	Sky
2580	2580 35246_at	TYRO3	U18934	TYRO3 protein tyrosine kinase	receptor tyrosine kinase
				tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, beta
2581	2581 32324_at	YWHAB	X57346	polypeptide	polypeptide
				tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation profein theta	
2582	2582 409_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2583	2583 32530_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, zeta	
2584	2584 1235_at	YWHAZ	M86400	polypeptide	phospholipase A2
2585	2585 32718_at	TPST1	AF038009	tyrosylprotein suffotransferase 1	tyrosylprotein sulfotransferase-1
2586	2586 35172_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587	2587 38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
				U2(RNU2) small nuclear RNA auxillary	
2588	2588 36517_at	U2AF1	M96982	factor 1	U2 snRNP auxiliary factor small subunit
2589	2589 32858_at	UBN1	Al341565	ubinuclein 1	
2590	2590 34824_at	UBQLN2	AB015344	ubiquilin 2	ubiquilin 2
2591	2591 38451 at	UOCB	T58471	ubiquinol-cytochrome c reductase (6.4kD) subunit	
	-			ubiquinol-cytochrome c reductase binding	
2592	2592 39427_at	UQCRB	T79616	protein	
2593	2593 40854_at	UQCRC2	J04973	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II

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T				ubiquinol-cytochrome c reductase hinge	
25943	36104_at	UQCRH	97	protein	
25951		UBC	M26880	ııC	ubiquitin C
2596 1367	1367_f_at	UBC	M26880		ubiquitin C
				arboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	2597 36990_at	UCHL1	X04741	(ubiquitin thiolesterase)	(ubiquitin thiolesterase)
2598 811	811_at	UFD1L	U6444	ition 1-like	ubiquitin fusion-degradation 1 like protein
7882	2599 40623_at	UBE3B	AI749193	ubiquitin protein ligase	
 -				ubiquitin protein ligase E3A (human	
				sociated protein,	E6-associated protein E6-AP/ubiquitin-
5000	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2801	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602 37683_at	USP10	D80012	ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
				ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KIAA1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	Ę	isopeptidase T
				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z72499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	:
2611	2611 32572_at	USP9X	X98296	chromosome (fat facets-like Drosophila)	ubiquitin hydrolase
				ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	UBA3
				ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
2613	2613 36579_at	UBE4A	D50916	yeast)	yeast)
				ubiquitination factor E4B (UFD2 homolog,	•
2614	2614 41339_at	UBE4B	AF043117	yeast)	ubiquitin-fusion degradation protein 2
2615	2615 36959 at	URE2V1	1.149278	UEV-1	UEV-1
3	20000	1000	212510		



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				ubiquitin-conjugating enzyme E2A (HAU6	ubiquitin-conjugating enzyme EZA (HADS
616	2616 890_at	UBE2A	M74524	homolog)	homolog)
				ubiquitin-conjugating enzyme E2D 1	
2617	2617 37826_at	UBE2D1	AF020761	(UBC4/5 homolog, yeast)	
Γ				ubiquitin-conjugating enzyme E2D 2	
2618	2618 38705_at	UBE2D2	Al310002	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2619	2619 832 at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
				ubiquitin-conjugating enzyme E2D 3	
2620	2620 39083_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
Γ				ubiquitin-conjugating enzyme E2D 3	
2621	2621 504_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2E 3	
2622	2622 34850_at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
				ubiquitin-conjugating enzyme E2G 2	,
2623	2623 32236_at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
				ubiquitin-conjugating enzyme E2I (UBC9	
2624	2624 38480_s_at	UBEZI	Nee867	homolog, yeast)	ubiquitin conjugating enzyme 9
				ubiquitin-conjugating enzyme E2I (UBC9	
2625	2625 838 s at	UBEZI	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
2626	2626 223 at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627	2627 40505 at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
				ubiquitin-conjugating enzyme E2N	
2628	2628 36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629	2629 457 s at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
2630	2630 155 s at	UBL1	U61397	ubiquitin-like 1 (sehtrin)	ubiquitin-homology domain protein PIC1
2631	2631 40839 at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632	2632 37336 at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
				UDP-Gal:betaGlcNAc beta 1,4-	
2633	2633 40960 at	B4GALT1	D29805	galactosyttransferase, polypeptide 1	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
2634	2634 34177_at	B4GALT2	AF038660	galactosyftransferase, polypeptide 2	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
2635	2635 39445_at	B4GALT3	AF038661	galactosyttransferase, polypeptide 3	beta-1,4-galactosyltransferase
3636	2636 4031E of	9091	DEORAD	UDP-glucose ceramide	ceramide alucosyttransferase
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6373	2637 35214 at	HGDH	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
					uridine diphosphoglucose
)638 <u>[3</u>	2638 37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2	pyrophosphorylase
				UDP-N-acetyl-alpha-D-	
				se 1	UDP-GalNAc:polypeptide N-
S639	2639 38041_at	GALNT1	U41514	(GaiNAc-T1)	acetylgalactosaminyftransferase
				UDP-N-aceMalucosamine-2-epimerase/N-	I.IDP-N-acelviglucosamine-2-epimerase/N-IUDP-N-acetviglucosamine-2-epimerase / N-
2640	2640 36515 at	BNE	AJ238764	acetylmannosamine kinase	acetylmannosamine kinase
	3			UDP-N-acteylglucosamine	UDP-N-acetylglucosamine
2641	2641 41242 at	UAP1	AB011004	pyrophosphorylase 1	pyrophosphorylase
2642	2642 34827 at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
				uncharacterized bone marrow protein	
2643	2643 37315 f at	BM036	A1057607	ВМозе	
				uncharacterized hypothalamus protein	
2644	2644 35750_at	HT010	AL049948	HT010	
	-			uncharacterized hypothalamus protein	
2645	2645 41058 g at	HT012	AI760162	HT012	
				uncharacterized hypothalamus protein	
2646	2646 41057 at	HT012	AI760162	HT012	
				unnamed protein product; Human gene	
2647	2647 38610 s at	KRT10; KPP	X14487	for acidic (type I) cytokeratin 10.	keratin 10
2648	2648 34402 at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
	1			upstream regulatory element binding	upstream regulatory element binding protein
2649	34372_at	UREB1	AB002310	protein 1	
2650	2650 37686 s at	ONG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
	1			uridine monophosphate synthetase	uridine monophosphate synthetase (orotate
		-		(orotate phosphoribosyl transferase and	phosphoribosyl transferase and orolldine-5 -
2651	2651 33815 at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
					dermatar/chondroitin sulfate 2-
2652	2652 41859_at	UST	AB020316	uronyi-2-sulfotransferase	Sunotransierase
				UV Radiation Resistance Associated	•
				Gene; H.sapiens mHNA; UV Hadiation	(and) possovate) Ega
2653	2653 39429_at	UVRAG	X99050	Hesistance Associated Gene.	pos piecessed rolling

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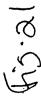
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Τ					v-abl Abelson murine leukemia viral
-					oncogene homolog 1 isoform a; v-abl
				v-abl Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654	at		X16416		homolog 1 isoform b
2655 35779	æţ	VPS45A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
Γ				VAMP (vesicle-associated membrane	
2656	2656 38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
					vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657 583	583 s at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658 1953	1953 at	VEGF	AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659	2659 36100 at		AF022375	vascular endothelial growth factor	vascular endothelial growth factor
Γ					VEGF related factor isoform VRF186
2660	2660 37268 at	VEGFB	U43368	vascular endothelial growth factor B	precursor
2661	2661 159 at	_	U43142	vascular endothelial growth factor C	vascular endothelial growth factor related protein
	m_001		75.04.0		
				VDAC protein; similar to mouse VDAC 3;	
				Homo sapiens voltage dependent anion	
2662	2662 36102_at	C3; HD-V	DA(AF038962	channel protein mRNA, complete cds.	voltage dependent anion channel protein
2663	2663 40147_at	VATI	018009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	2664 33930_at	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
				vesicle-associated membrane protein 2	
2665	2665 32254_at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VIL2	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091 s at	WI/	Z19554	vimentin	vimentin
					vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	NCL
0230	2670 20001 21	10/0	A Enzhasa	vitamin A rasponsive: cytoskeleton related JWA protein	JWA protein
2/07	03031 at		2000	whamin D (1 05, dibydroxovitemin D3)	vitamin D (1.25. dihydroxyvitamin D3)
2671	1388 g at	VDR	J03258	receptor	receptor
				v-Ki-ras2 Kirsten rat sarcoma 2 viral	
2672	2672 1940_at	KRAS2	M54968	oncogene homolog	K-ras oncogene protein
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				fibrosarcoma	
2673	2673 41504_s_at	MAF	AF055376		short form transcription factor C-MAF
				v-maf musculoaponeurotic fibrosarcoma	
2674	2674 32835_at	MAFF	AA725102	oncogene homolog F (avian)	
2675	40198 at	VDAC1	L06132	innel 1	voltage-dependent anion channel
2676	2676 37696 at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	2677 171 at	VBP1	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743_f_at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776 at	RALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2680	2680 36645 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674_at	YES1	M15990	oncogene homolog 1	homolog 1
				v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
2683	2683 1402 at	LAN	M16038	oncogene homolog	oncogene homolog
2684	2684 1058 at	WASF3	S69790	WAS protein family, member 3	
2685	2685 38736 at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
7697	2687 36009 et	Cl 683	A E091092	weakh similar to dutathione peroxidase 2	weakty similar to dutathione peroxidase 2 weakty similar to dutathione peroxidase 2
200	2688 26909 et	WEE1	X62048	WFE1+ homolog (S. pombe)	wee1 tyrosine kinase
	20202	1	WOLD TO	,	eukaryotic translation initiation factor 4H,
				Williams-Beuren syndrome chromosome	isoform 1; eukaryotic translation initiation
2689	2689 41212 r at	WBSCR1	D26068	region 1	factor 4H, isoform 2
2690	2690 41635 at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
L				wingless-type MMTV integration site	wingless-type MMTV integration site family,
2691	2691 31862_at	WNT5A	120861	family, member 5A	member 5A precursor

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T					Wolf-Hirschhorn syndrome candidate 2
2692	14225 at	WHSC2	AF101434	ndidate 2	protein
693	2693 33438 at	WBP2	AL049981	WW domain binding protein 2	
				ng protein 4 (formin	
2694	35213 at	WBP4	AF071185	binding protein 21)	formin binding protein 21
2695	s at	WWOX	U13395	ining oxidoreductase	oxidoreductase
	İ			WW domain-containing adapter with a	
19696	2696 36822 at	WAC	U51334		putative RNA binding protein RBP56
				intosum,	
. 2697	2697 1307 at	XPA	D14533	complementation group A	XPAC protein
				xeroderma pigmentosum,	
2698 1873	1873 at	XPC	D21089	complementation group C	XP-C repair complementing protein (p125)
				XPA binding protein 1; putative ATP(GTP)	
2699	2699 41756 at	NTPBP	AJ010842	binding protein	ATP(GTP)-binding protein
Γ				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	:
2700	2700 38733 at	XRCCS	M30938	80KD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	:
2701	2701 585 at	XRCC5	M30938	80kD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
			•	repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	:
2702	2702 2093 s at	XRCC5	J04977	80kD)	ATP-dependant DNA helicase II
2703	2703 35827 at	KIAA0905	AB020712	yeast Sec31p homolog '	KIAA0905 protein
2704	2704 40988 at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705	2705 891 at	W1	M77698	YY1 transcription factor	GLI-Krupple related protein
				zb29g04.s1	
				Soares_parathyroid_tumor_NbHPA Homo	
				sapiens cDNA clone IMAGE:305046 3',	
2706	2706 34887_at		N92548	mRNA sequence.	
				Zic family member 1 (odd-paired homolog,	
2707	36308_at	ZIC1	D76435	Drosophila)	Zic protein
2708	2708 35681 r at	ZFHX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein



TSGA		0	0	Ш
ZNF-U69274 U69274 ZNF-U69274 ZNF-U69274 U09412 ZNF-134 U09412 ZNF-134 U09412 ZNF-134 U09412 ZNF-134 U09412 ZNF-134 ZNF-135 Z				KIAA0742 protein
ZFP103 D76444 ZNF134 U09412 ZNF134 U09412 ZNF146 X70394 ZNF146 X70394 ZNF151 Y09723 ZNF151 Y09723 ZNF151 D28118 ZNF198 AJ224901 ZNF200 Y14443 ZNF20 ZNF20 AF062346 ZNF20 ZNF20 AF062346 ZNF20 ZNF20 AF062346 ZNF20 ZNF20 AF062346 ZNF20 ZNF294 AB018257 ZNF294 AB018257 ZNF395 AL03942 ZNF361 X79067 ZNF362 AL039314 ZNF363 AL039314 ZNF363 AL039314 ZNF363 AL039313 AF052182 ZNF364 AB023213 AL030213 AR023213 AL030213 AR023213 AR02321				zinc finger protein
at ZNF34 U09412 ZNF134 U09412 ZNF144 D13969 ZNF146 X70394 ZNF151 Y09723 ZNF151 Y09723 ZNF161 D28118 ZNF198 AJ224901 ZNF200 Y14443 ZNF200 Y14443 ZNF200 ZNF200 U47742 ZNF200 ZNF200 AB007885 ZNF200 ZN			zinc finger protein 103 homolog (mouse)	zinc finger protein 103 homolog
at ZNF144 D13969 2 ZNF144 X70394 2 ZNF151 Y09723 2 ZNF161 D28118 2 ZNF161 D28118 2 ZNF200 Y14443 2 ZNF200 Y14443 2 ZNF200 AF046001 2 ZNF201 AF062346 2 ZNF20 U47742 4 ZNF294 AB018257 4 ZNF337 AL096880 4 ZNF394 AB018257 4 ZNF361 X79067 4 ZNF362 AL050144 AB023213 4 ZNF363 AF052182 AIT ZWINT AB023213 4 ZWINT AB023213 AIT Z			Г	zinc finger protein ZNF134
ZNF146	a		zinc finger protein 144 (Mel-18)	Mel-18 protein
ZNF151	5		zinc finger protein 146	zinc finger protein
ZNF161 D28118 2 ZNF198			zinc finger protein 151 (pHZ-67)	Miz-1 protein
ZNF198			zinc finger protein 161	DB1
ZNF200		5	zinc finger protein 198	ZNF198 protein
ZNF207			zinc finger protein 200	zinc finger protein
ZNF216 AF062346 ZNF220 U47742 ZNF220 U47742 ZNF262 AB007885 ZNF294 AB018257 ZNF294 AB018257 ZNF394 AL096880 ZNF394 AL096843 ZNF361 ZNF363 AL050144 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079313 AL05182 AL052182 AL05191 AB023213 AL052182 AL05191 AB023213 AL052656 AL079334 AL079344 AL		AF046001	zinc finger protein 207	zinc finger protein 207
ZNF220 U47742 ZNF262 AB007885 ZNF262 AL096880 ZNF294 AB018257 ZNF394 AL096880 ZNF397 AL049942 ZNF361 X79067 ZFP361 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079314 ZNF364 AL079313 AL051182 AL079313 AL079313 AL079313 AL079313 AL079313 AL079313 AL0793313 AL0793313 AL0793313 AL0793313 AL0793313 AL0793313 AL07933314 AL079331314 AL079331314 AL07933314 AL079331314 AL		AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
at ZNF262 AB007885 at ZNF278 AL096880 at ZNF394 AB018257 at ZNF394 AB018257 at ZFP36 M92843 at ZFP36L1 X79067 at ZNF361 X79067 at ZNF34 AL050144 at ZNF84 AL079314 at ZNF84 AI73878 at ZDHHC3 AF052182 at ZMPSTE24 Y13834 at ZMINT AB023213 at ZWINT AF067656 at ZWINT HG4582-HT4987 t t HG2463-HT2559		U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
at ZNF278 AL096880 at ZNF294 AB018257 ZNF337 AL049942 ZFP36 M92843 ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 ZDHC3 AF052182 T ZDHC3 ZDHC3 AF052182 T ZWINT HG4582-H74987 T HG4582-H74987 HG4582-H74987		AB007885	zinc finger protein 262	zinc finger protein 262
at ZNF294 AB018257 ZNF337 AL049942 ZFP36 M92843 ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 ZDHC3 AF052182 T ZDHHC3 AF052182 T ZWINT AB023213 T ZWINT AF067656 T HG4582-HT4987 T HG4582-HT4987		AL096880	zinc finger protein 278	hypothetical protein
ZNF337 AL049942 ZFP36 M92843 ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 ZFR AI743507 ZDHHC3 AF052182 ZMPSTE24 Y13834 DZIP1 AB023213 ZWINT AF067656 HG2463-HT2559 HG2463-HT2503	at	AB018257	zinc finger protein 294	KIAA0714 protein
ZFP36 M92843 ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 ZPR AI743507 ZDHHC3 AF052182 ZMPSTE24 Y13834 ZWINT AR023213 TAMPSTE24 Y13834 HG4582-HT4987 HG4582-HT4987 HG4582-HT4987 HG1380-HT2503		AL049942	zinc finger protein 337	hypothetical protein
ZFP36 M92843 ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 ZDHC3 AF052182 T ZDHHC3 AF052182 T ZMPSTE24 Y13834 T ZWINT AR023213 T ZWINT AF067656 HG2463-HT3593 HG3463-HT3503 R HG2463-HT2503			zinc finger protein 36, C3H type, homolog	
ZFP36L1 X79067 ZNF363 AL050144 ZNF364 AL079314 ZNF84 M27878 T ZNF84 M27878 T ZDHHC3 AF052182 T ZMPSTE24 Y13834 T ZWINT AF067656 T ZWINT AF067656 T ZWINT HG4582-H74987 T ZWINT HG4582-H74987		M92843	(mouse)	zinc finger transcriptional regulator
ZNF363 AL050144 SNF364 AL079314 SNF84 M27878 SNF84 M27878 SNF84 AI743507 SNF94 AI743507 SNF952213 SWINT AB023213 AF067656 AI74987		X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
ZNF364 AL079314 ZNF84 M27878 ZNF84 M27878 ZFR AI743507 ZDHHC3 AF052182 T ZMPSTE24 Y13834 T ZWINT AF067656 HG252-HT4987 HG253-HT2559		AL050144	zinc finger protein 363	hypothetical protein
at ZNF364 AL079314 at ZNF84 M27878 at ZFR AI743507 at ZDHHC3 AF052182 at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 t HG2463-HT987 at HG2463-H7253				hypothetical protein, similar to (U06944)
at ZNF84 M27878 at ZFR AI743507 at ZDHHC3 AF052182 at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 at ZWINT HG4582-H74987 at HG2463-H72559		AL079314	zinc finger protein 364	PRAJA1 [Mus musculus]
at ZFR AI743507 at ZDHHC3 AF052182 at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 at HG2463-HT987 at HG2463-HT2559		M27878	zinc finger protein 84 (HPF2)	DNA binding protein
at ZDHHC3 AF052182 at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 at ZWINT HG4582-HT4987 at HG2463-HT2559		AI743507	zinc finger RNA binding protein	
at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 at ZWINT HG4582-HT4987 at HG2463-HT2559		AF052182	zinc finger, DHHC domain containing 3	
at ZMPSTE24 Y13834 at DZIP1 AB023213 at ZWINT AF067656 at HG4582-HT4987 at HG2463-HT2559			zinc metalloproteinase (STE24 homolog,	
at DZIP1 AB023213 at ZWINT AF067656 HG4582-HT4987 HG2463-HT2559 at HG2463-HT2559		Y13834	yeast)	farnesylated-proteins converting enzyme
at ZWINT AF067656 HG4582-HT4987 at HG2463-HT2559		AB023213	zinc-finger protein DZIP1	KIAA0996 protein
at	at	AF067656	ZW10 interactor	ZW10 interactor Zwint
at		HG4582-HT4987		
	at	HG2463-HT2559		
		HG1980-HT2023		
		HG1862-HT1897		
2740 324_f_at HG1515-HT1515	at	HG1515-HT1515		

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3															guanine nucleotide binding protein (G	protein), beta polypeptide 1	guanine nucleotide binding protein (G	protein), beta polypeptide 1
Q																		
0	HG1800-HT1823	HG2639-HT2735	HG1112-HT1112	HG3543-HT3739	HG2036-HT2090	HG162-HT3165	HG2855-HT2995	HG2855-HT2995	AL038340	HG3044-HT3742	HG4322-HT4592	HG4322-HT4592	HG1112-HT1112	HG1322-HT5143		AL031282		AL031282
8																dJ283E3.1		dJ283E3.1
A	2741 327_f_at	2742 333_s_at	2743 1840_g_at	2744 1664_at	2745 1624_at	2746 1278_at	2747 1179_at	2748 1180_g_at	2749 32243_g_at	2750 311_s_at	2751 297_g_at	2752 296_at	2753 1839_at	2754 723_s_at		2755 33300_at		2756 41249_at
Ĺ	2741	2742	2743	2744	2745	2746	2747	2748	2749	2750	2751	2752	2753	2754	L	2755	_	2756

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-	Systematic	Common	Genbank	Description	Product
				***ALU WARNING: Human Alu-Sq	
2	AFFX-hum alu at	16	U14573	subfamily consensus sequence.	
6	38820 at	15-86	3D AF051894	15 kDa selenoprotein	15 kDa selenoprotein
				26S proteasome-associated pad1	
4	33247 at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
				factor, arginine/serine-rich 7 (SFRS7)	
2	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein: Human N33 protein form	
ď	36851 n at	N33	U42360		N33 protein form 2
	70			3-hydroxy-3-methylglutaryl-Coenzyrne A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328 at	HMGCR	M11058	reductase	reductase
					succinyl CoA:3-oxoacid CoA transferase
∞	41142 at	OXCT	U62961	3-oxoacid CoA transferase	precursor
L				3'-phosphoadenosine 5'-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
은	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
=	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formytransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811 at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
	$\overline{}$			5-methyltetrahydrofolate-homocysteine	
13	38383_at	MTR	U73338	methyltransferase	methionine synthase
7	39025 at	LOC54543	AI557912	6.2 kd protein	

		_					$\overline{}$	$\overline{}$
ш	divelent cation tolerant protein Cl ITA	delta7-sterol reductase	ADAM10		metalloprotease/disintegrin/cysteine-rich protein precursor	gravin	::-	KIAA0920 protein
0	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706	7-dehydrocholesterol reductase	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein 10	A kinase (PRKA) anchor protein 1 A kinase (PRKA) anchor protein 2
ပ		AF034544	AF009615	AA142964	U41766	U81607	AA114830	AB023137
8		DHCR7	ADAM10	ADAM17	ADAM9	AKAP12	AKAP10	AKAP11 AKAP2
4		39059 at		41601 at	_			34657_at 35985_at
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Fig 21

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ш	proto-oncogene tyrosine-protein kinase	accessory proteins BAP31/BAP29	mitochondrial 3-oxoacyl-CoA thiolase	acetyl-coenzyme A transporter		acidic nuclear phosphoprotein pp32	APRIL	okadaic acid-inducible phosphoprotein	KIAA0785 protein	iron regulatory factor	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
D ABI is the cellular homolog proto-	ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; atternative splicing using alternative first exon 1b; ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; atternative splicing using exon 1a; Human proto- oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.	accessory proteins BAP31/BAP29	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	acetyl-Coenzyme A transporter	acetylserotonin O-methyltransferase-like	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	acid-inducible phosphoprotein	Ac-like transposable element	aconitase 1, soluble	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
U		X81817	D16294	D88152	AA669799	U73477	Y07969	AF069250	AB018328	Z11559	D25248	U50523
В	ABL	DXS1357E	ACAA2	ACATN	ASMTL	ANP32A	ANP32B	OA48-18	ALTE	ACO1	AFAP	ARPC2
A	1636_g_at	41724_at	41530_at	34668_at	36553_at	37034_at	38479_at	34397_at	39168_at	40077_at	37578_at	1718_at
				27								33

ľ			C		u
	A	В	٥	2	
				ted protein 2/3 complex, subunit	
36	34692 r_at	ARPC4	AF006087	4 (20 kD)	p20-Arc
1				ted protein 2/3 complex, subunit	
37	38392 at	ARPCS	AF006088		p16-Arc
Г		ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
\top	AC07/	ACTB	X00351	actin, beta	beta actin
8	AFFX-HSAC07/XACTB		X00351		beta actin
Т	32318 s at		X63432	actin, beta	mutant beta-actin (beta'-actin)
Т		_	X04098	actin, gamma 1	gamma-actin
1	39329 at	ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
T .		ACTN4	U48734	actinin, alpha 4	alpha actinin
Ąħ	38642 at	AI CAM	Y10183	activated leucocyte cell adhesion molecule MEMD protein	MEMD protein
	1 000			activated RNA polymerase II transcription	
46	36171 at	PC4	AI521453	\neg	
47	39764 at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162 s at	ACVR2	D31770	activin A receptor, type II	activin typell A receptor precursor
49	34394 at	ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
				acyl-Coenzyme A dehydrogenase,	
20	40673 at	ACADSB	U12778		acyl-CoA dehydrogenase
51	40459 at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
				adaptor-related protein complex 1, beta 1	
52	40745 at	AP1B1	L13939	subunit	beta-prime-adaptin
				adaptor-related protein complex 1,	
53	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
				adaptor-related protein complex 2, mu 1	adaptor-related protein complex 2, mu 1
54	39795_at	AP2M1	D63475	subunit	subunit
				adaptor-related protein complex 2, sigma	
55	39347 at	AP2S1	X97074	1 subunit	clathrin-associated protein
				adaptor-related protein complex 3, beta 1	
56	32039 at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
				adaptor-related protein complex 3, delta 1	
57	36172_s_at	AP3D1	AF002163	subunit	delta-adaptin
				adaptor-related protein complex 3, sigma	
58	38074_at	AP3S1	U91932	1 subunit	AP-3 complex sigma3A subunit
59	_	ADD3	D67031	adducin 3 (gamma)	adducin-like protein

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					adenosine deaminase, RNA-specífic,
					isoform ADAR-a; adenosine deaminase,
	•				RNA-specific, isoform ADAR-b; adenosine
9	38014 at	ADAR	X79448	adenosine deaminase, RNA-specific	deaminase, RNA-specific, isoform ADAR-c
т-				adenosine deaminase, RNA-specífic, B1	
9	38748 at	ADARB1	U76421	(RED1 homolog rat)	dsRNA adenosine deaminase DRADA2b
T	168 at	ADK	U50196	adenosine kinase	adenosine kinase
Т	33865 at	BS69	AA127624	adenovirus 5 E1A binding protein	
Т	33134 at	ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
П	40585 at	ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
99	33800_at	ADCY9	AF036927	adenylate cyclase 9	adenylyl cyclase type IX
29	40788 at	AK2	U84371	adenylate kinase 2	adenylate kinase 2A
T	36639_at	ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
1		CAP	L12168	adenylyl cyclase-associated protein	adenylyl cyclase-associated protein
I .	at	CAP2	N90755	adenylyl cyclase-associated protein 2	
T	at	ADFP	X97324	adipose differentiation-related protein	adipophilin
\mathbf{I}	36861_at	DKFZp56411922	AL049946	adlican	hypothetical protein
73		ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
T	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
				ADP-ribosylation factor domain protein 1.	
9/	37537_at	ARFD1	L04510	64kD	nucleotide binding protein
				ADP-ribosylation factor GTPase activating	
77	39905_i_at	ARFGAP1	AA402332	protein 1	
78	37296_at	ARL1	L28997	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
				ADP-ribosylation factor-like 6 interacting	
79	36572_r_at	ARLGIP	D31885	protein	
				ADP-ribosyltransferase (NAD+; poly (ADP-	_
8	41146_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
				ADP-ribosyltransferase (NAD+; poly (ADP	•
8	1287_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
82	34777_at	ADM	D14874	adrenomedullin	adrenomedullin precursor
				AF034176 Human mRNA (Tripodis and	
				Ragoussis) Homo sapiens cDNA clone	
83	32218_at		AF0341/6	nicons contig.	

AFG3L2		<	a	C		
34315_at AFG3L2 Y18314 AFG3ATPase family gene 3-like 2 (yeast) is 33454_at 33454_at AGRN AF016903 agin 36185_at AHNAK M80899 AHNAK nucleoprotein (desmoyokin) is 36185_at 36185_at AARS D02050 aladny-IRNA synthetase is 3247_at 36286_at ALDH1A3 U07919 member A3 aldehydrogenase 1 family. 32747_at ALDH2 X05409 (milochondrial) aldehydrogenase 2 family. 40409_at ALDH3A2 U46689 member A2 aldehydrogenase 3 family. 37331_g_at ALDH4A1 U24266 member A1 aldehydrogenase 7 family. 36132_at ALDH9A1 U34252 member A1 aldehydrogenase 7 family. 38780_at ALDH9A1 U34252 aldo-keto reductase family 1, member A1 aldo-keto reductase family 1, member A1 38780_at AKR181 X15414 (aldo-keto reductase family 1, member A2 aldo-keto reductase family 1, member A2 38258_at AKR1C3 D17793 type of the reductase family 1, member A2 38225_at			2	•		
33454_at AGRN AFO16903 agrin 37027_at AHNAK M80899 AHNAK nucleoprotein (desmoyokin) 6 36186_at ALDH1A3 U07919 alanyl-RINA synthetase 1 36686_at ALDH1A3 U07919 member A3 aldehyde dehydrogenase 1 family. 6 32747_at ALDH3A2 U46689 member A3 aldehyde dehydrogenase 3 family. 6 37331_g_at ALDH3A2 U46689 member A1 aldehyde dehydrogenase 3 family. 6 37331_g_at ALDH3A1 U24266 aldehyde dehydrogenase 4 family. 6 38780_at ALDH3A1 U24266 aldehyde dehydrogenase 7 family. 6 38780_at ALDH9A1 U34252 member A1 aldehyde dehydrogenase 9 family. 6 38780_at AKR181 X15414 (aldehyde dehydrogenase 9 family. 6 38780_at AKR181 X15414 (aldehyde dehydrogenase 9 family. 6 38780_at AKR181 X15414 (aldehyde dehydrogenase 9 family. 6 38780_at		34315_at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast)	paraplegin-like protein
37027_at AHNAK M80899 AHNAK nucleoprotein (desmoyckin) 36185_at AARS D32050 alanyl-IRNA synthetase 36686_at ALDH1A3 U07919 aldehyde dehydrogenase 1 family. 32747_at ALDH2 X05409 (mitochondrial) 40409_at ALDH2 X05409 (mitochondrial) 37331_g_at ALDH3A1 U24266 Inember A2 aldehyde dehydrogenase 2 family. 37331_g_at ALDH3A1 U24266 Inember A1 aldehyde dehydrogenase 7 family. 38589_at ALDH9A1 U34252 Inember A1 aldehyde dehydrogenase 9 family. 38589_at ALDH9A1 U34252 Inember A1 aldehyde dehydrogenase 9 family. 38589_at AKR181 X15414 (aldehyde reductase family 1, member R1 alde-keto reductase family 1, member R1 alde-keto reductase family 1, member R2 alde-keto reductase family 1, member R3 38589_at AKR181 X15414 (aldehyde reductase family 1, member R3 38589_at AKR181 X15414 (aldehyde reductase family 1, member R3 38589_at AKR181 X15414 (aldehyde reductase family 1, member R3 38589_at <td>_</td> <td>33454_at</td> <td>AGRN</td> <td>AF016903</td> <td>agrin</td> <td>agrin precursor</td>	_	33454_at	AGRN	AF016903	agrin	agrin precursor
36185_at AARS D32050 alanyl-IRNA synthetase k 36686_at ALDH1A3 U07919 member A3 aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde reductase family 1, member A1 38780_at AKR181 X15414 (aldehyde reductase family 1, member A1 38589_at AKR181 X15414 (aldehyde reductase family 1, member C3 36589_at AKR181 X15414 (aldehyde reductase family 1, member C3 37299_at AKR181 X15414 (aldehyde reductase family 1, member C3 37290_at AKR1C3 D17793 type II) 32510_at AKR7A2 AF026947 (aldehyde reductase family 1, member C3 37040_at AKR7A2 AF026947 (aldehyde reductase family 1, member C3 37040_at AF1Q	_	37027_at	AHNAK	M80899		
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41136_s_at APP Y00264 (protease nexin-II, Alzheimer disease) 40148_at APBB2 U62325 binding, family B, member 2 (Fe65-like) 38471_r_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD - 40064_at ALS2CR3 AB011121 amyotrophic lateral sclerosis 2 (juvenile) 40064_at ALS2CR3 AB011121 androgen receptor (dihydrotestosterone receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy 4577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 U83508 angiopoietin 1					amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
40148_at APBB2 U62325 binding, family B, member 2 (Fe65-like) 38471_r_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 amyloid beta precursor protein 3 and 2000 (dilydrotestosterone receptor (dilydrotestosterone receptor (dilydrotestosterone receptor (dilydrotestosterone receptor (dilydrotestosterone receptor (dilydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy 3 disease) 1577_at AR AB023263 disease) 39315_at ANGPT1 D13628 angiopoietin 1 amyloid angiopoietin 1 angiopoietin 2 amyloid angiopoietin 2 amyloid amyloid amyloid angiopoietin 2 amyloid amyloid amyloid angiopoietin 2 amyloid am	110		APP	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
40148_at APBB2 U62325 binding, family B, member 2 (Fe65-like) 38471_r_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD , 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 40064_at ARS2CR3 AB011121 chromosome region, candidate 3 40067_at ARS2CR3 AB011121 ceeptor, testicular feminization, spinal 40067_at ANGPT1 D13628 angiopoietin 1 <					amyloid beta (A4) precursor protein-	
38471_r_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD , 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 4923 at ANGPT1 U83508 angiopoietin 1	111	40148	APBB2	U62325	binding, family B, member 2 (Fe65-like)	FE65-like protein
38471_r_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD , chromosome region, candidate 3 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 4923 at ANGPT1 U83508 angiopoietin 1					amyloid beta precursor protein	
38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD , chromosome region, candidate 3 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 androgen receptor (dihydrotestosterone receptor) receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 4923 at ANGPT1 U83508 angiopoietin 1	112	38471	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
38470_i_at APPBP2 D86981 (cytoplasmic tail) binding protein 2 35364_at APPBP1 U50939 protein 1, 59kD , 159kD 40064_at ALS2CR3 AB011121 amyotrophic lateral sclerosis 2 (juvenile) 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 androgen receptor (dihydrotestosterone receptor) receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1					amyloid beta precursor protein	
35364_at APPBP1 U50939 protein 1, 59kD i 40064_at ALS2CR3 AB011121 amyotrophic lateral sclerosis 2 (juvenile) 4577_at AR M23263 androgen receptor (dihydrotestosterone receptor (dihydrotestosterone receptor); kennedy 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1	113	38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
35364_at APPBP1 U50939 protein 1, 59kD , 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 40064_at ALS2CR3 AB011121 chromosome region, candidate 3 androgen receptor (dihydrotestosterone receptor (dihydrotestosterone receptor); spinal and bulbar muscular atrophy; Kennedy disease) 38842_at AMOTL2 AB023263 disease) 39315_at ANGPT1 D13628 angiopoietin 1 4923 at ANGPT1 U83508 angiopoietin 1					amyloid beta precursor protein binding	
40064_at ALS2CR3 AB011121 chromosome region, candidate 3 chromosome region, candidate 3 androgen receptor (dihydrotestosterone receptor); testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1	114	35364_at	APPBP1	U50939	protein 1, 59kD	amyloid precursor protein-binding protein 1
40064_at ALS2CR3 AB011121 chromosome region, candidate 3 androgen receptor (dihydrotestosterone receptor) androgen receptor (dihydrotestosterone receptor) 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1					amyotrophic lateral sclerosis 2 (juvenile)	
AR AB023266 andiopoietin 1	115		ALS2CR3	AB011121	chromosome region, candidate 3	KIAA0549 protein
receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy 1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1		-			androgen receptor (dihydrotestosterone	
1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1					receptor; testicular feminization; spinal	
1577_at AR M23263 disease) 38842_at AMOTL2 AB023206 angiomotin like 2 39315_at ANGPT1 D13628 angiopoietin 1 1929_at ANGPT1 U83508 angiopoietin 1					and bulbar muscular atrophy; Kennedy	
38842 at AMOTL2 AB023206 angiomotin like 2 39315 at ANGPT1 D13628 angiopoietin 1 1929 at ANGPT1 U83508 angiopoietin 1	116		AR	M23263	disease)	androgen receptor
39315_at ANGPT1 D13628 angiopoietin 1	117	_	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
1929 at ANGPT1 (U83508 angiopoietin 1	118		ANGPT1	D13628	angiopoietin 1	angiopoietin 1
	119		ANGPT1	U83508	angiopoietin 1	angiopoietin-1

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120 3	36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrin G
121 3	at at	ANXA1	X05908	annexin A1	annexin l
122 3		ANXA11	L19605	-	56K autoantigen
123 7	te at	ANXA2	D00017		lipocortin II
124 3		ANXA2P1	M62896	annexin A2 pseudogene 1	
	s at	ANXA2P3	M62895	annexin A2 pseudogene 3	
					annexin IV (placental anticoagulant protein
126 3	37374_at	ANXA4	M82809	annexin A4	(I)
127 3	37670 at	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
	41138 at	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
				nylate	
129	40506_s_at	PABPC4; APP1; A	; AU75686	binding protein mRNA, complete cds.	polyadenylate binding protein
130	34370_at	ARCN1	X81198	archain 1	archain
_				arginine-glutamic acid dipeptide (RE)	
131	32253_at	RERE	AB007927	repeats	KIAAU458 protein
132	132 549_at	RARS	S80343	arginyl-tRNA synthetase	arginyl-tHNA synthetase
133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
				ariadne homolog, ubiquitin-conjugating	
134	134 41729_at	ARIH1	AJ009771	enzyme E2 binding protein, 1 (Drosophila)	
135	36057_at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
				ARP1 actin-related protein 1 homolog A,	
136	40052_at	ACTR1A	X82206	centractin alpha (yeast)	alpha-centractin
				ARP2 actin-related protein 2 homolog	
137	35734_at	ACTR2	Al935551	(yeast)	
138	35733 at	ACTR2	AF006082	(veast)	Arp2
				ARP3 actin-related protein 3 homolog	
139	139 35271_at	ACTR3	AF006083	(yeast)	Arp3
140	140 40516_at	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141	141 36671_at	ASNS	M27396	asparagine synthetase	asparagine synthetase
142	142 41241_at	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
143	143 38703_at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144	144 34181_at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

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	A	В	3		
145	37229 at	ATR	U49844	ataxia telangiectasia and Rad3 related	FHAP-related protein
		A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379 at	APACD	AB006679	differentiation	ATP binding protein
		ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit b,	
149	149 41228 r at	ATP5F1	X60221	isoform 1	H+-ATP synthase subunit b
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	34811 at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760 at	ATP5H	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
				ATP synthase, H+ transporting,	
152	38751 i at	ATPSI	AA426364	mitochondrial F0 complex, subunit e	
				ATP synthase, H+ transporting,	
153	36107 at	ATP5J	AA845575	mitochondrial F0 complex, subunit F6	
				ATP synthase, H+ transporting,	
154	38693 at	ATP5L	AA917672	mitochondrial F0 complex, subunit g	
				ATP synthase, H+ transporting,	
_				mitochondrial F1 complex, gamma	
155	155 40115 at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791 at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790 at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, type 2C,	
158	38684 at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159		ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
160	40853	ATP10D	Al478147	ATPase, Class V, type 10D	
161		ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
	1			ATPase, Cu++ transporting, alpha	1
162	36523 at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type A I Pase
				ATPase, H+ transporting, lysosomal	
163	163 33854_at	ATP6M	AA877795	(vacuolar proton pump)	

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			. *	ATPase, H+ transporting, lysosomal	
164	37395_at	ATP6S14	D49400	(vacuolar proton pump) 14kD	vacuolar ATPase
				ATPase, H+ transporting, lysosomal	
165	36994_at	ATP6L	M62762	(vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
				ATPase, H+ transporting, lysosomal	
166	36167_at	ATP6F	D89052	(vacuolar proton pump) 21kD	proton-ATPase-like protein
				ATPase, H+ transporting, lysosomal	
167	37367 at	ATP6E	X76228	(vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
-				ATPase, H+ transporting, lysosomal	
168	37948 at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting ATPase beta-
175	32563_at	ATP1B3	U51478	polypeptide	3 subunit
				ATP-binding cassette, sub-family A	
176	35717_at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177	38261_at	ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648_at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
,		FOX &	A1 050171	ideographic	hypothetical protein DKFZp586F1122 similar to avotrophin
2	35268_al	AVOI	ALUSU171	avouopiiii	lo avoi opini

	A	Ф	၁		ע
182	35350_at	GALNAC4S-6ST	AB011170		KIAA0598 protein
_				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
183	41562 at	BM11	L13689	(mouse)	homolog
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) опсоделе
184	1728 at	BMI1	L13689		homolog
-	36578 at	BIRC2	U37547	baculoviral IAP repeat-containing 2	MIHB
	41278 at	BAF53A	AF041474		BAF53a
187	33175 at	BBS4	AA156237	Bardet-Biedl syndrome 4	
Γ				basic helix-loop-helix domain containing,	
188	40790_at	BHLHB2	AB004066		1-Dec
189	40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	190 40202_at	BTEB1	D31716		GC box binding protein
191	35055_at	BTF3	X53281	basic transcription factor 3	general transcription factor
192	192 38364 at	BCE-1	AF068197		BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein .
				B-cell translocation gene 1, anti-	
194	37294 at	BTG1	X61123	proliferative	B-cell translocation protein 1
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060_at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010 at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436_at	BNIP3L	AF079221	protein 3-like	protein 3a
				-	glucocortoid receptor-associated protein
198	34798_at	BAG1	Z35491	BCL2-associated athanogene	RAP46
199	35291 at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
200	36463 at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
Š	38050 at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
	38101 at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	٠
				beta subunit; Human pyruvate	
204	204 (39160 at	PDHB	D90086	dene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta
	15-00100	2::2			

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	∢	8	S	0	
205 3	34644_at	BZM	AB021288	7	beta 2-microglobulin
	40601 at	88P	Al057115	beta-amyloid binding protein precursor	
T				beta-hexosaminidase alpha chain; Human	
				beta-hexosaminidase alpha chain (HEXA)	•
207	39340 at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
208	38126 at	BGN	J04599	biglycan	biglycan preproprotein
		BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
210	37074 at	P. C.	AF018631	sapiens biotindase (B i D) gene, exons 2, 3, and 4 and complete cds.	biotinidase
	, , , , , , , , , , , , , , , , , , ,			biphenyl hydrolase-like (serine hydrolase;	÷
211	40912_s_at	BPHL	X81372	antigen)	biphenyl hydrolase-related protein
+	35267 g_at	BLCAP	AL049288		bladder cancer associated protein
213	35266_at	BLCAP	AL049288	ciated protein	bladder cancer associated protein
	37700 at	BLMH	X92106	-	bleomycin hydrolase
				bone morphogenetic protein receptor, type	
215	39565 at	BMPR1A	Z22535		ALK-3
216	39551 at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607 at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
_	1			brain abundant, membrane attached	
218	32606 at	BASP1	AA135683	signal protein 1	
219	37945 at	ВАСН	U91316	hydrolase	acyl-CoA thioester hydrolase
220	37958 at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023 at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
_				branched chain keto acid dehydrogenase	
				E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683 i at	ВСКОНВ	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812 at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	protein
				brefeldin A-inhibited guanine nucleotide-	
224	224 38306_at	BIG1	AA477576	exchange protein 1	
225	225 37947 at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
				BTB and CNC homology 1, basic leucine	BTB and CNC homology 1, basic leucine
226	226 31895_at	BACH1	AB002803	zipper transcription factor 1	zipper transcription factor i

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227	36634_at	BTG2	U72649		BIGZ
_	37218 at	BTG3	D64110	BTG family, member 3	ANA
_					
229 4	41547 at	BUB3	AF047472	east)	spleen mitotic checkpoint BUB3
	,	0100	A E047479		testis mitotic checkpoint BUB3
250	34783_s_at	BUB3	AT04/4/3		
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
230	32780 at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
233	32629	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	234 39357 at	C2F	U72514	C2f protein	CZł
235	40709	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031	C9orf10	D80005	C9orf10 protein	C9orf10 protein
	33856 at	CXX1	Y13374	CAAX box 1	putative prenylated protein
	36976 at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
				cadherin 11, type 2, OB-cadherin	
239	2087 s at	CDH11	D21254	(osteoblast)	OB-cadherin-1
240	2053	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
				calcium/calmodulin-dependent protein	*
241	31670 s at	CAMK2G	U81554	kinase (CaM kinase) II gamma	CaM kinase II isoform
				calcium/calmodulin-dependent protein	
242	38716_at	CAMKK2	AB018330	kinase kinase 2, beta	KIAA0787 protein
2/3	31854 at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244	41738 at	CALD1	M64110	caldesmon 1	caldesmon
245	41739 s at	CALD1	M83216	caldesmon 1	caldesmon
				calmodulin 1 (phosphorylase kinase,	
246	41288_at	CALM1	AL036744	delta)	
L				calmodulin 2 (phosphorylase kinase,	
247	911_s_at	CALM2	M19311	delta)	calmodulin 2 (phosphorylase Kinase, delta)
248	40125_at	CANX	L10284	calnexin	cainexin
249	37001_at	CAPN2	M23254	calpain 2, (π/II) large subunit	neutral protease large subunit
250	36138_at	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

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	41257	1	D16217	calpastatin	calpastatin
252	33385 g at	CAST	U31346	calpastatin	calpastatin
253	40953 at	CNN3	S80562	calponin 3, acidic	acidic calponin
254	37345 at	CALU	AF013759	calumenin	calumein
				cAMP responsive element binding protein	cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding
255	37535_at	CREB1	M27691	-	protein 1, isoform B
256	40849 s at	CREB3	U88528	cAMP responsive element binding protein 3 (luman)	transcription factor LZIP
1	00700	200	10000	cAMP responsive element binding protein-	Gra binding protein-like 2
<u>(3)</u>	33430_al	OUEDEK	10000		cyclic AMP-responsive element modulator
258	32065_at	CREM	S68134	cAMP responsive element modulator	beta isoform
259	32067_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
300	99000	200	S69134	cAMP resonative element modulator	cyclic AMP-responsive element modulator heta isoform
3				capping protein (actin filament) muscle Z-	
261	40910 at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
L				capping protein (actin filament) muscle Z-	
262	36641_at	CAPZA2	U03851	line, alpha 2	capping protein alpha
				capping protein (actin filament) muscle Z-	
263	37012_at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
				carbohydrate (chondroitin 6)	
264		CHST3	AB017915	sulfotransferase 3	Chondrollin b-suilotransierase
265	41447_at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAAU99U protein
	_	7.TOTO	A B0003701	carbohydrate (keratan sulfate Gal-6)	keratan sulfate Gal-6-sulfotrans(erase
	41030_ai	2	100000	carbohydrate (N-acetylolucosamine-6-0)	N-acetylqlucosamine-6-O-sulfotransferase
267	137960 at	CHST2	AB014679	sulfotransferase 2	(GlcNAc6ST)
568	268 36454 at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
569	269 34876 at	CPD	U65090	carboxypeptidase D	carboxypeptidase D
270	270 36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
				Cas-Br-M (murine) ectropic retroviral	
271	35632_at	CBLB	U26710	transforming sequence b	cpl-b
272	272 40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273	273 36949_at	CSNK1D	U29171	casein kinase 1, delta	casein Kinase I delta

			C		4
	A	æ	٥		
274 3	38019_at	CSNK1E	L37043		casein Kinase I-epsilori
				containing	
275 1	1211_s_at	CRADD	U84388	adaptor with death domain	death domain containing protein CRADD
276	276 1867 at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
				caspase 4, apoptosis-related cysteine	
277	195_s_at	CASP4	U28014		cysteine protease
				caspase 8, apoptosis-related cysteine	
278	33774_at	CASP8	X98172	protease	MACH-alpha-1
				catenin (cadherin-associated protein),	
279	41156_g_at	CTNNA1	U03100	alpha 1 (102kD)	aipnaz(E)-catenin
				catenin (cadherin-associated protein),	مزسمئص (7) مراسان
780	41155_at	CTNNA1	U03100	alpha 1 (102kD)	aipnaz(E)-carenin
				catenin (cadherin-associated protein),	
281	2085_s_at	CTNNA1	D14705	alpha 1 (102kD)	numan aipna-catenin
				catenin (cadherin-associated protein),	
282	2069_s_at	CTNNA1	L23805	alpha 1 (102kD)	alpha1(E)-catenin
				catenin (cadherin-associated protein),	:
283	35331_at	CTNNAL1	U97067	alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	
284	40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
285	40444_s_at	CTNND1	AB002382	delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	стѕо	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
	339_at	CAV2	AF035752	caveolin 2	caveolin-2
				Cbp/p300-interacting transactivator, with	
291	33113_at	CITED2	U65093	Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
				CCAAT/enhancer binding protein	
292	1052_s_at	CEBPD	M83667	(C/EBP), delta	NF-IL6-beta protein
203	293 39219 at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma
3	335 13 at	25.5	2: =2=2		



	<	В	S	Ω	ш
-				CCR4-NOT transcription complex, subunit	
294	33861_at	CNOT2	AI123426	2	
				CR4-NOT transcription complex, subunit	
295	32820_at	CNOT4	U71267	4	potential transcriptional repressor NO I 4Hp
296	34819_at	CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
297	297 34699_at	CD2AP	AL050105	CD2-associated protein	hypothetical protein
				CD36 antigen (collagen type I receptor,	
				thrombospondin receptor)-like 2	
298	33823 at	CD36L2	D12676	rotein II)	85kDa human lysosomal sialoglycoprotein
				5	
299	299 2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
				CD81 antigen (target of antiproliferative	
300	35282_r_at	CD81	M33680	antibody 1)	CD81 antigen
301	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
				CDC10 cell division cycle 10 homolog (S.	
302	32175_at	CDC10	S72008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	303 40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	
304	31877_at	CDC23	AF053977	homolog)	cell division cycle protein 23
305	40690	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307	32833 at	CLK1	M59287	CDC-like kinase 1	
800	41535 at	CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
				CDP-diacylglycerol synthase	
309	41343_at	CDS2	Y16521	(phosphatidate cytidylyltransferase) 2	CDS2 protein
				CDP-diacylglycerolinositol 3-	
1				priospirational and a second s	
310	33397_at	SUPI	ALUSUSES	(phosphatidylificsito) symmase)	
31	40591_at	CDC27	S78234	cell division cycle 27	H-NUC
			v.	cell growth regulatory with ring finger	
312	450_g_at	CGR19	U66469	domain	cell growth regulator CGR19
212	36514 at	CGB19	1166469	cell growth regulatory with ring finger domain	cell growth regulator CGR19
2	1000 17 at		2000		

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	A	В	င	D	
3	35211 pt	CBEG	AF084523	cellular repressor of E1A-stimulated genes CREG	cellular repressor of E1A-stimulated genes CREG
		CENTRO	Doenea	centaurin beta 2	centaurin, beta 2
210	41333 at	CENTGO	AROSQUES	a 2	KIAA1099 protein
317	34070 at	CETN2	X72964	tein, 2	caltractin
		2011		3 (CDC31	
318	35232 f. at	CETN3	A1056696		
		CENPC1	M95724		centromere autoantigen C
320	33805_at	CAP350	AB007949	ed protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190_at	CDR2	M63256	(62kD)	major Yo paraneoplastic antigen
322	32262_at	CGI-01	AL049669		hypothetical protein
323		FOC50999	AL080084	CGI-100 protein	
324	38500_at	LOC51014	AB002450	CGI-109 protein	
325		LOC51020	AA524058	CGI-130 protein	
326	38667_at	LOC51031	AA189161	CGI-150 protein	
327	41824_at	LOC51096	A1140114	CGI-48 protein	
328	34862_at	LOC51097	AA005018	CGI-49 protein	-
329	37199_at	LOC51626	AI760932	CGI-60 protein	
330	41411_at	LOC51103	AI566877	CGI-65 protein	
33		LOC51635	AI052724	CGI-86 protein	
				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759 at	CCT2	AF026166	(beta)	homolog
L				chaperonin containing TCP1, subunit 3	
333	40774_at	CCT3	X74801	(gamma)	gamma subunit of CCT chaperonin
				chaperonin containing TCP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
				chaperonin containing TCP1, subunit 6A	
335	38416 at	CCT6A	L27706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CCT7	AF026292	(eta)	1, eta subunit
				chaperonin containing TCP1, subunit 8	chaperonin containing TCP1, subunit 8
337	7 39767_at	сств	D13627	(theta)	(theta)
338	338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	339 37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase
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ш			cholesterol 25-hydroxylase		chondroitin sulfate proteoglycan 2 (versican)		chondroitin sulfate proteoglycan 2 (versican)		chromosome-associated polypeptide		heterochromatin protein p25						uis		hypothetical protein	t protein		TGF-beta induced apotosis protein 12	vrotein		4 protein	8 protein	hypothetical protein	hypothetical protein	hypothetical protein	hypothetical protein	embryonic lung protein	GP36b glycoprotein	ein		hypothetical protein
	Icln protein		cholestero		chondroitir		chondroitir		chromoso		heterochro						Mi-2 protein		hypothetic	KIAA0584 protein		TGF-beta	C14orf3 protein	clone 22	KIAA 1064 protein	KIAA0958 protein	hypotheti	hypotheti	hypotheti	hypotheti	embryon	GP36bg	G7b protein	-	hypotheti
Q	chloride channel, nucleotide-sensitive, 1A	chloride intracellular channel 4		ycan 2		chondroitin sulfate proteoglycan 2		chondroitin sulfate proteoglycan 6	(bamacan)	chromobox homolog 1 (HP1 beta homolog	Drosophila)	chromobox homolog 3 (HP1 gamma	homolog, Drosophila)	chromobox homolog 3 (HP1 gamma	homolog, Drosophila)	chromodomain helicase DNA binding	protein 4	chromodomain protein, Y chromosome-	like	chromosome 1 open reading frame 17	chromosome 1 open reading frame 8	chromosome 12 open reading frame 22	chromosome 14 open reading frame 3	chromosome 18 open reading frame 1	chromosome 19 open reading frame 7	chromosome 21 open reading frame 80	chromosome 22 open reading frame 2	chromosome 22 open reading frame 4	chromosome 22 open reading frame 5	chromosome 3 open reading frame 4	chromosome 4 open reading frame 1	chromosome 5 open reading frame 8	chromosome 6 open reading frame 28	chromosome 6 open reading frame 34	chromosome 6 open reading frame 5
O	X91788	Al ogoet	AF059214		X15998		X15998		AF020043		U35451		AI740522		AA648295		X86691		AL050164	AB011156	Z78368	AF052105	AJ243310	AF009425	AB028987	AB023175	AL050345	AL096779	AL096879	AL080097	AF006621	U10362	AJ245416	W27949	AL050289
ď	CI NS1A	CLICA	CH25H		CSPG2		CSPG2		CSPG6		CBX1		CBX3		CBX3		CHD4		CDYL	C10rf17	Clorf8	C12orf22	C14orf3	C18orf1	C19orf7	C21orf80	C22orf2	C22orf4	C22orf5	C3orf4	C4orf1	C5orf8	C6orf28	C6orf34	C6orf5
٧	340 38732 at	i c	341 32363 at		38112 g at		38111 at		34763 at	•	37304 at		38085 at		38084 at		349 36137 at		32111 at	39550	3903	32217 at	40979 at	40045 g at	36860		33406_at	33778 at	41758 at	38690_at	36013 at	36955_at	41375_at		
	56	2 2	343	3	343		344		345		346		347		348		349		350	331	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366

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367	35193_at	CHC1L	AF060219		RCC1-like G exchanging factor RLG
368	34292 at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
369	-	cs	AF047042	citrate synthase	citrate synthase
370	41159 at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
371		OI TA	M20471	clathrin light polypeptide (Lca)	clathrin, light polypeptide A, isoform a; clathrin, light polypeptide A, isoform b
				cleavage and polyadenylation specific	
372	35743 at	CPSF4	U79569	factor 4, 30kD subunit	no arches
				cleavage stimulation factor, 3' pre-RNA,	
373	32723_at	CSTF1	L02547	subunit 1, 50kD	cleavage stimulation factor
				cleavage stimulation factor, 3' pre-RNA,	
374	41183_at	CSTF3	U15782	subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017_at	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
				clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message repressed prostate message 2,	repressed prostate message 2,
377	36780_at	CLU	M25915	2, apolipoprotein J)	apolipoprotein J)
378	378 35180_at	LOC113251	AL050205	c-Mpl binding protein	
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
380	380 38052_at	F13A1	M14539	coagulation factor XIII, A1 polypeptide	coagulation factor XIII A1 subunit precursor
381	36972_at	RNP24	X92098	coated vesicle membrane protein	transmembrane protein
382	34326_at	COPB	X82103	coatomer protein complex, subunit beta	beta-Coat protein
L				coatomer protein complex, subunit beta 2	
383	36677_at	COPB2	X70476	(beta prime)	subunit of coatomer complex
384	35205_at	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
385	36648_at	CRSP9	AF031383	activation, subunit 9 (33kD)	hMed7
386	33659_at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	-	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388		CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
390	32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
391		COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392		COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein

		prepro-alpha-1 type 3 collagen alpha (2) chain
X14420 X05610 Y14690 X15880 X52022		oro-alpha-1 type 3 collagen
X14420 X05610 Y14690 X15880 X52022		oro-alpha-1 type 3 collagen
X05610 Y14690 X15880 X52022	mal dominant)	ta (2) chain
Y14690 X15880 X52022		ייי (ב) מומייי
X15880 X52022		procollagen alpha 2(V)
X52022		alpha-1 collagen VI (AA 574-1009)
		collagen type VI, alpha 3 chain
X57527	-	alpha 1(VIII) collagen
		alpha 1 type XI collagen, isoform A
	pre	preproprotein; alpha 1 type XI collagen,
	osi	isoform B preproprotein; alpha 1 type XI
COL11A1 J04177 collagen,		collagen, isoform C preproprotein
COL16A1 M92642 collagen	collagen, type XVI, alpha 1	alpha-1 type XVI collagen
malduoo		complement component 1, q subcomponent
C1QBP M69039 subcomp	subcomponent binding protein bin	binding protein precursor
	mponent 1, r	
M14058 subcomponent		complement component 1, r subcomponent
complem	complement component 1, s	
J04080 subcomponent		complement component 1, s subcomponent
CTGF X78947 connectiv	connective tissue growth factor	connective tissue growth factor
conserve	conserved gene amplified in	
AF000152 osteosarcoma		OS-4 protein
	conserved helix-loop-helix ubiquitous	
CHUK AF009225 kinase		IKB kinase alpha subunit
1.165928	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	Jun activation domain binding protein
U51205		COP9 signalosome subunit 1 CSN1
MOV34-34KD U70735 COP9 St	COP9 subunit 6 (MOV34 homolog, 34 kD) 34 kDa Mov34 homolog	kDa Mov34 homolog
U83246	ים	copine I
AB014536		KIAA0636 protein
D16611	ohyrinogen oxidase	coproporphyrinogen oxidase
B AF001461		Krinnel-like zinc finger protein 719
	ohyrinogen oxidase phyria, harderoporphyria) noter element binding protein	שמשפורווואס בוויס יוויואסיו אייטייי בייב
AF104398 cornichon-like	ein	transcription factor

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7		1700	020021	COX11 homolog, cytochrome c oxidase	COX11 homolog
4 10	34/23 at	1 400	013610	ChG island protein: Human nested dene	80000
417	37907 at	F8A: DXS522E	M34677	protein gene, complete cds.	coagulation factor VIII-associated protein
418	38664 at	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
				CREB binding protein (Rubinstein-Taybi	
419	33831_at	CREBBP	U47741	syndrome)	CREB-binding protein
420	420 36948_at	CRI1	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421	38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	37902	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	423 40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
				CSE1 chromosome segregation 1-like	
424	38804_at	CSE1L	AF053641	(yeast)	cellular apoptosis susceptibility protein
425	425 1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
456	426 41309 g at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	427 40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	428 39723_at	CUL1	AF062536	cullin 1	cullin 1
429	429 40141 at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
				cut-like 1, CCAAT displacement protein	
430	31823_at	CUTL1	M74099	(Drosophila)	cut-like 1, CCAAT displacement protein
431	36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
				cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
432	432 41808_at	DMTF1	AF052102	factor 1	
				cyclin D1 (PRAD1: parathyroid	
433	38418_at	CCND1	X59798	adenomatosis 1)	cyclin
				cyclin D1 (PRAD1: parathyroid	
434	2020_at	CCND1	M73554	adenomatosis 1)	bcl-1
435	36650_at	CCND2	D13639	cyclin D2	cyclin D2
436	40225	GAK	D88435	cyclin G associated kinase	HsGAK
437	37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439		CCNH	U11791	cyclin H	cyclin H
440		CCN	D50310	cyclin 1	cyclin I
144	1792_g_at	CDK2	M68520	cyclin-dependent kinase 2	cdc2-related protein kinase

Fig 2)

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\vdash				cyclin-dependent kinase 7 (MO15	
				homolog, Xenopus laevis, cdk-activating	
442 3	33317_at	CDK7	L20320		protein serine/threonine kinase
				cyclin-dependent kinase 7 (MO15	
-				homolog, Xenopus laevis, cdk-activating	
443	1969_s_at	CDK7	X77743	kinase)	CDK activating kinase
444	35140 at	CDK8	R59697	cyclin-dependent kinase 8	
_				cyclin-dependent kinase inhibitor 1A (p21,	
445	2031_s_at	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
				cyclin-dependent kinase inhibitor 1B (p27,	
446	33847_s_at	CDKN1B	Al304854	Kip1)	
Γ				cyclin-dependent kinase inhibitor 2C (p18,	
447	447 36053_at	CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent Kinase Innibitor
448	38700_at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
449	449 41401 at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
85	450 40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
451	38772 at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
452	40408 at	CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
				cytidine monophosphate-N-	
		-		acetylneuraminic acid hydroxylase (CMP-	
453	39317 at	CMAH	D86324	N-acetylneuraminate monooxygenase)	CMP-N-acetylneuraminic acid hydroxylase
				cytochrome b5 outer mitochondrial	
454	34340_at	CYB5-M	AA173896	membrane precursor	
455	35818_at	HCS	D00265	cytochrome c	cytochrome c
		COX5B	AI526089	cytochrome c oxidase subunit Vb	
				cytochrome c oxidase subunit Vla	
457	41206_r_at	COX6A1	AI540925	polypeptide 1	
458	36165 at	coxec	W51774	cytochrome c oxidase subunit VIc	
				cytochrome c oxidase subunit VIIa	
459	39031_at	COX7A1	AA152406	polypeptide 1 (muscle)	
				cytochrome c oxidase subunit VIIa	
460	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
				cytochrome c oxidase subunit VIIa	
461	34330_at	COX7A2L	AB007618	polypeptide 2 like	COX7RP
462	462 34381_at	COX7C	AI708889	cytochrome c oxidase subunit VIIc	

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	∢	В		D	Ш
463	38080_at	COXB	AI525665	cytochrome c oxidase subunit VIII	
_	35819 at	CYC1	X06994	cytochrome c-1	cytochrome c-1
				cytochrome P450, 51 (lanosterol 14-alpha-	
465	33389_at	CYP51	U23942	demethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
466	466 859_at	CYP1B1	U03688	primary infantile)	cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
467	467 40071 at	CYP1B1	U03688	primary infantile)	cytochrome P450
468	at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469		KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
	:			cytoplasmic; Human Ser/Thr protein	
470	1706 at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	471 34338 at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	472 32529 at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	473 40282 s at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877 s at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	1243 at	DDB2	U18300	(48kD)	DDBb p48
476	36616 at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
477	37663 at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent HNA helicase #46
L				DEAD/H (Asp-Glu-Ala-Asp/His) box	-
479	40490_at	DDX21	U41387	polypeptide 21	Gu protein
L				DEAD/H (Asp-Glu-Ala-Asp/His) box	
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, A Isolorm
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDXS	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
	_			DEAD/H (Asp-Glu-Ala-Asp/His) box	
				polypeptide 9 (RNA helicase A, nuclear	
485	482 36153_at	6XQQ	L13848	DNA helicase II; leukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

DAP3 DAP4 DAP5 DAP7 DAD1 DAT1 DAT1 DAT1 DAT1 DAT1 DAT2 DAT2 DAT2 DAT2 DAT2 DAT2 DAT3		4	8	O	Q	ш
39114_at DEPP AB022718 of 38413_at DOCK1 D50857 of 38413_at DAD1 D15057 of 38224_at DAD1 DEGS AF039704 32337_at DEGS AF039704 33337_at DEGS AF035119 33791_at DLC1 AF035119 33791_at DLC1 AF035119 33791_at DLC1 AF035119 38629_at DSIP1 AI635895 38629_at DSIP1 AI635895 38629_at DSIP1 AI635895 39641_at DSIP1 AI635895 39641_at DSIP1 AI635895 39641_at DGKD D73409 39641_at DGKD D73409 39641_at DGKZ U94905 339041_at DGKZ U94905 339041_at DGKZ U94905 339041_at DGKZ U94905 339041_at DGKZ U94905 33920_at DGKZ U94905 340607_at DGKZ U94905 36149_at DFYSL2 U97105 36149_at DFYSL3 D78014 38220_at DPYSL49128 AA176780	484	1356 a	l	U18321	death associated protein 3	ionizing radiation resistance conferring protein
39114_at DEPP AB022718 of 39638_at DOCK1 D50857 of 38413_at DAD1 D15057 of 38413_at DAD1 D15057 of 38224_at CLN2 AF039704 32337_at DEGS AF039704 33337_at DEGS AF035119 33791_at DLC1 AF035119 33791_at DLC1 AF035119 33629_at DLC1 AF035119 36629_at DLC1 AF035119 36629_at DLC1 AF035119 36629_at DLC1 AF035138 38003_s_at DCKD D73409 39044_s_at DGKZ U94905 339041_at DLAT AF051782 339041_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 38220_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL4 AB06713						
37638_at DOCK1 D50857 38413_at DAD1 D15057 32824_at CLN2 AF039704 33337_at DEGS AF035139 38992_at DLC1 AF035139 37951_at DLC1 AF035139 38791_at DLC1 AF03519 37951_at DLC1 AF03519 38794_at DSIPI AF03519 38744_at DSS1 N95406 38744_at DSS1 N95406 38744_at DSIPI AF03519 38744_at DSS1 N95406 38744_at DSIPI AF03538 38344_at DSIPI AF03538 38385_at DGKD D73409 38044_at DGKD D73409 38003_s_at DIAPH1 AF051782 38041_at DLAT Y00978 3649_at DPYSL2 U97105 38503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 <t< th=""><th>485</th><th>39114_at</th><th>DEPP</th><th>AB022718</th><th></th><th>ОЕРР</th></t<>	485	39114_at	DEPP	AB022718		ОЕРР
38413_at DAD1 D15057 32824_at CLN2 AF039704 32824_at CLN2 AF039704 38992_at DEK X64229 38791_at DLC1 AF035119 33791_at DLC1 AF035119 33791_at DLC1 AF03513 38744_at DSS1 N95406 36629_at DSIP1 AI635895 38744_at DSS1 N95406 38041_at DSIP1 AI635895 38385_at DSTN S65738 38044_at DSTN S65738 38044_at DGKD D73409 38044_at DGKD D73409 38044_at DGKD D73409 3804_as_at DIAPH1 AF051782 3804_at_at DLAT Y00978 40607_at DPYSL2 U97105 3820_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL2 U20938	486	37638_at	DOCK1	D50857	1	DOCK180 protein
32824_at CLN2 AF039704 33337_at DEGS AF002668 38992_at DEK X64229 337951_at DLC1 AF035119 337951_at DLC1 AF035119 337951_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIP1 AF034603 38385_at DSIP1 AF03409 39044_at DDEF2 AB007860 39044_at DDEF2 AB007860 39041_at DGKD DAF2 AF051782 33920_at DGKZ U94905 33920_at DGKZ U97309 339041_at DCAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL4 AB006713	487	38413	DAD1	D15057		DAD-1
32824_at CLN2 AF039704 33337_at DEGS AF02668 38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIPI AF036895 35814_at GA17 AF03409 39044_s_at DEF2 AB007860 39044_s_at DGKD D73409 339041_at DGKD DAF2 339041_at DGKD DAF2 339041_at DGKD DPYSL2 339041_at DGKD DPYSL2 339041_at DDYSL2 U97105 34667_at DPYSL2 U97105 36149_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL4 AB06713					deficient in late-infantile neuronal ceroid	
32824_at CLN2 AF039704 33337_at DEGS AF002668 38992_at DEK X64229 337951_at DLC1 AF035119 33791_at DLC1 AF035119 38744_at DSS1 N95406 36629_at DSIPI AF064603 35814_at DSTN S65738 39044_s_at DGKD DFF2 AB007860 39044_s_at DGKD DATO D73409 33920_at DDAPH1 AF051782 33920_at DDAPH1 AF051782 33920_at DDAPH1 AF051782 33920_at DDYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB066713 38220_at DPYSL4 AB066713					lipofuscinosis; Homo sapiens lysosomal	
32824_at CLN2 AF039704 33337_at DEGS AF002668 38992_at DEK X64229 33791_at DLC1 AF035119 33791_at DLC1 AF035119 33791_at DLC1 AF035119 38744_at DSS1 N95406 36629_at DSIPI AF064603 35814_at GA17 AF064603 39044_at DGKD DEF2 AB007860 39044_at DGKD DATA S65738 39041_at DGKZ U94905 33920_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 33920_at DDYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB066713					pepstatin insensitive protease (CLN2)	
3337_at DEGS AF002668 38992_at DEK X64229 38992_at DLC1 AF035119 33791_at DLC1 Y15227 3874_at DSS1 N95406 36629_at DSIPI AF064603 35814_at GA17 AF064603 39385_at DSTN S65738 39041_at DDEF2 AB007860 38003_s_at DGKD D73409 33920_at DIAPH1 AF051782 37692_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 37692_at DBI AI557240 37692_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780	488		CLN2	AF039704	gene, complete cds.	lysosomal pepstatin insensitive protease
3337_at DEGS AF002668 38992_at DEK X64229 38992_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 3629_at DSIPI AI635895 35814_at GA17 AF064603 39385_at DSTN S65738 39041_at DDEF2 AB007860 38003_s_at DGKD D73409 33920_at DIAPH1 AF051782 37692_at DIAPH1 AI557240 37692_at DBI AI557240 37692_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYD U20938 40485_at HSA249128 AA176780					degenerative spermatocyte homolog, lipid	
38992_at DEK X64229 37951_at DLC1 AF035119 38791_at DLEU1 Y15227 38744_at DSS1 N95406 35814_at DSS1 AR054603 35814_at GA17 AF064603 38385_at DSTN S65738 390410_at DDEF2 AB007860 38003_s_at DGKD D73409 33920_at DGKD D73409 33920_at DGKZ U94905 37692_at DBI AI557240 37692_at DBI AI557240 37692_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL2 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780	489	33337	DEGS	AF002668	desaturase (Drosophila)	MLD
37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIPI AF064603 35814_at GA17 AF064603 38385_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 39042_at DGKZ U94905 33920_at DIAPH1 AF051782 36067_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780	490		DEK	X64229	DEK oncogene (DNA binding)	putative oncogene
33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIPI AF064603 35814_at GA17 AF064603 38385_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 39003_s_at DGKZ U94905 37692_at DIAPH1 AF051782 3607_at DBI AI557240 37692_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780			DLC1	AF035119	deleted in liver cancer 1	deleted in liver cancer-1
38744_at DSS1 N95406 36629_at DSIPI AI635895 35814_at GA17 AF064603 38365_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 3607_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780			DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
36629_at DSIPI AI635895 35814_at GA17 AF064603 38385_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 3607_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780	493	38744	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
36629_at DSIPI AI635895 35814_at GA17 AF064603 38385_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 37692_at DBI AI557240 39041_at DLAT Y00978 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780					delta sleep inducing peptide,	*
35814_at GA17 AF064603 38385_at DSTN S65738 39044_s_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 37692_at DBI AI557240 37692_at DBYSL2 U97105 36149_at DPYSL2 U97105 39503_s_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL4 AB006713 38220_at DPYSL4 AA006713	494	36629_at	DSIPI	AI635895	immunoreactor	
38385_at DSTN S65738 39410_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF651782 37692_at DIAPH1 AF57240 37692_at DBI AI557240 39041_at DPYSL2 U97105 36149_at DPYSL2 U97105 39503_s_at DPYSL3 D78014 38220_at DPYSL4 AB006713 38220_at DPYD U20938 40485_at HSA249128 AA176780	495		GA17	AF064603	dendritic cell protein	GA17 protein
39410_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 39041_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 38220_at DPYD 'U20938 40485_at HSA249128 AA176780	496		DSTN	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
39410_at DDEF2 AB007860 factor 2 39044_s_at DGKD D73409 diacylglycerol kinase, delta (130kD) 38003_s_at DGKZ U94905 diacylglycerol kinase, zela (104kD) 33920_at DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) 33920_at DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) 37692_at DBI AI557240 binding protein) 37692_at DBI AI557240 dihydrolipoamide S-acetyltransferase (E2 39041_at DLAT Y00978 component of pyruvate dehydrogenase 36149_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL3 D78014 dihydropyrimidinase-like 3 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	L				development and differentiation enhancing	development- and differentiation-enhancing
39044_s_at DGKD D73409 diacylglycerol kinase, delta (130KD) 38003_s_at DGKZ U94905 diacylglycerol kinase, zeta (104kD) 33920_at DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) 37692_at DBI AI557240 binding protein) 37692_at DBI AI557240 binding protein) 40607_at DLAT Y00978 component of pyruvate dehydrogenase 39041_at DPYSL2 U97105 dihydropyrimidinase-like 2 36149_at DPYSL3 D78014 dihydropyrimidinase-like 3 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	497	39410_at	DDEF2	AB007860	factor 2	factor 2
at DGKZ U94905 Idiacylglycerol kinase, zeta (104kD) DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) diazepam binding inhtbitor (GABA receptor modulator, acyl-Coenzyme A receptor modulator, acyl-Coenzyme A pinding protein) A1557240 DBI A1557240 binding protein) DLAT Y00978 component of pyruvate dehydrogenase DPYSL2 U97105 dihydropyrimidinase-like 2 DPYSL3 D78014 dihydropyrimidinase-like 3 at DPYSL4 AB006713 dihydropyrimidinase-like 4 DPYD U20938 dihydropyrimidine dehydrogenase HSA249128 AA176780 DIPB protein	498	39044_s_at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
DIAPH1 AF051782 diaphanous homolog 1 (Drosophila)	499	38003_s_at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
Als57240 DBI Als57240 DBI Als57240 DBI Als57240 DINDING CONTROL DBI Als57240 DINDING DINDI	200	33920_at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
37692_at DBI A1557240 binding protein) 39041_at DLAT Y00978 component of pyruvate dehydrogenase 39503_s_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein					diazepam binding inhibitor (GABA	
37692_at DBI AI557240 binding protein) 39041_at DLAT Y00978 component of pyruvate dehydrogenase 39041_at DLAT Y00978 complex) 40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein					receptor modulator, acyl-Coenzyme A	
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase component of pyruvate dehydrogenase complex) DPYSL2	501	37692	DBI	AI557240	binding protein)	
DLAT Y00978 component of pyruvate dehydrogenase DPYSL2 U97105 dihydropyrimidinase-like 2 DPYSL3 D78014 dihydropyrimidinase-like 3 DPYSL4 AB006713 dihydropyrimidinase-like 4 DPYD U20938 dihydropyrimidine dehydrogenase HSA249128 AA176780 DIPB protein					dihydrolipoamide S-acetyltransferase (E2	
DLAT Y00978 complex) DPYSL2 U97105 dihydropyrimidinase-like 2 DPYSL3 D78014 dihydropyrimidinase-like 3 DPYSL4 AB006713 dihydropyrimidinase-like 4 DPYD U20938 dihydropyrimidine dehydrogenase HSA249128 AA176780 DIPB protein		-		_	component of pyruvate dehydrogenase	
DPYSL2U97105dihydropyrimidinase-like 2DPYSL3D78014dihydropyrimidinase-like 3DPYSL4AB006713dihydropyrimidinase-like 4DPYDU20938dihydropyrimidine dehydrogenaseHSA249128IAA176780DIPB protein	505	39041_at	DLAT	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
DPYSL3 D78014 dihydropyrimidinase-like 3 DPYSL4 AB006713 dihydropyrimidine 4 DPYD U20938 dihydropyrimidine dehydrogenase HSA249128 IAA176780 DIPB protein	503	40607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
DPYSL4AB006713dihydropyrimidinase-like 4DPYD'U20938dihydropyrimidine dehydrogenaseHSA249128IAA176780DIPB protein	504	36149 at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
DPYD 'U20938 dihydropyrimidine dehydrogenase HSA249128 AA176780 DIPB protein	505	39503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
HSA249128 AA176780	206	38220_at		:U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
The state of the s	507	40485_at		AA176780	DIPB protein	

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				disabled homolog 2, mitogen-responsive	
508	479_at	DAB2	U53446	phosphoprotein (Drosophila)	DOC-2
				discoidin domain receptor family, member	
509	36643_at	DDR1	L20817	-	tyrosine protein kinase
510	510 40575 at	DLG5	AB011155	discs, large (Drosophila) homolog 5	KIAA0583 protein
				dishevelled associated activator of	
511	33753_at	DAAM1	AB014566	morphogenesis 1	KIAA0666 protein
512	33150 at	SAS10	Al126004	disrupter of silencing 10	
				dJ635G19.1 (LAMR1 (Laminin Receptor 1	
				(67kD) (RPSA, 40S Ribosomal Protein	
				SA, P40)) pseudogene); match: cDNAs:	
				Em:X15005 Em:J03799 Em:X61156	
				Em:M64923 Em:X06406 Em:AF140348	
				Em:J02870 Em:L16589 Em:Z22749	
				Em:D25224 Em:M14199 Em:M27798;	
513	513 40916_at	dJ635G19.1	AL035494	match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
L					
				dJ734P14.1 (KRAB box and C2H2 Zinc	
				finger domain protein pseudogene) match:	
				cDNAs: Em:M27878 Em:M29580	
				Em:U27186 Em:D31763 Em:AB007872	
				Em:U09366 Em:U09413 Em:X17617	
				Em:AF011573 Em:AF020591 Em:X78925	
				match: proteins: Sw:P52736 Sw:Q06730	
		-		Sw:P51523 Tr:Q14585 Sw:P15620	
				Sw:Q02386 Sw:P51786 Sw:Q99676	
			,	Tr:O60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (small nuclear
514	514 38456_s_at	dJ734P14.1	AL049650	Tr:Q61116 Tr:Q64247	ribonucleoprotein particle) protein B)

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	٥	B	O	<u>Q</u>	Ш
515	38455	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:U09366 Em:U09413 Em:X17617 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:Q02386 Sw:C014585 Sw:Q099676 Tr:C060792 Sw:Q03923 Sw:Q75820 Tr:C061116 Tr:C064247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)
516	516 35809 q at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:D21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:P21590 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serinerich 6 (SRP55-2)(isoform 2))
				dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O77485 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P652818 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O65082 Sw:O13418 Sw:O9324 Sw:O63743 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Contains and RPL15 (60S	
518	518 32433_at	dJ90L6.1	297353	Protein L15) pseudogette, E318, 3138 and GSSs, complete sequence.	

Fig 21

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- 1	A	┪			ш
(C)	34183_at	DKFZP434C171 /	AL080169		hypothetical protein
◂	520 40801_at	DKFZP434C212 /	AA643063	DKFZP434C212 protein	
10)	38400_at	DKFZP434D1335 /	A1920820	DKFZP434D1335 protein	
522 3	33392_at	DKFZP434J154 /	AL080155	DKFZP434J154 protein	hypothetical protein
ניזן	523 39411_at	DKFZP434J214 /	AL080156	DKFZP434J214 protein	hypothetical protein
┰	524 40564_at	DKFZP564A043	N42007		
(7)			AL035304	DKFZP564B167 protein	hypothetical protein
16.)	526 33433 at	DKFZP564F0522	2 AL049943	DKFZP564F0522 protein	hypothetical protein
14	527 41437_at	DKFZP564F1123 AL080118	AL080118		hypothetical protein
(۲)	528 39442_at	DKFZP564G0222	AL080115	DKFZP564G0222 protein	hypothetical protein
14	529 40437_at	DKFZP564G2022 AL049944	AL049944	DKFZP564G2022 protein	hypothetical protein
157	530 36456_at	DKFZP5641052	AL080063	DKFZP5641052 protein	hypothetical protein
۳		DKFZP564M1416	16 AL049934	DKFZP564M1416 protein	hypothetical protein
1		DKFZP56400423	123 AL080120	DKFZP56400423 protein	hypothetical protein
Ë	533 38256_s_at	DKFZP5640092	W21827	DKFZP5640092 protein	
Ë	534 39034_at	m	AL080122	DKFZP564O123 protein	hypothetical protein
٠.٠	535 41662 at	m	AL050272	DKFZP566B183 protein	hypothetical protein
536	32807_at		AF004292	DKFZP566C134 protein	
ΙĆ	537 38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
٦	538 33776 at		AL050062	DKFZP566K023 protein	hypothetical protein
٦	539 41335_at		AL050084	DKFZP56601646 protein	hypothetical protein
T	540 36961_at	DKFZP586A011	AL050286		hypothetical protein
ť	541 38717 at	DKFZP586A0522	22 AL050159	DKFZP586A0522 protein	hypothetical protein
À	542 40831_at	DKFZP586B0923	23 AL050190		hypothetical protein
lm	543 34821_at	DKFZP586D0623 AL050197	AL050197		hypothetical protein
T.	544 39986_at	DKFZP586D0919 AL050100	AL050100		hypothetical protein
10	545 34269 at	DKFZp586F1019	19 AL050102	DKFZp586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918	18 AL050091	,	hypothetical protein
1	547 40832_s_at	DKFZP586G011	AL050126		hypothetical protein
8	548 36007_at	DKFZP586L151	AL050137		hypothetical protein
549	34833_at	DKFZP58600120	20 AL050157	DKFZP586O0120 protein	hypothetical protein
		DNMT1	X63692	DNA (cytosine-5-)-methyltransferase 1	DNA (cytosine-5-)-methyltransferase
				DNA segment on chromosome X (unique)	
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
2	552 34215 at	DXYS155E	L03426	DNA segment on chromosome X and Y (unique) 155 expressed sequence	DNA segment on chromosome X and Y (unique) 155 expressed sequence
1					

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	A	В	၁	Q	Ţ
553	1252 at	D5S346	M73547	DNA segment, single copy probe LNS- CAI/LNS-CAII (deleted in polyposis	polyposis locus-encoded protein
-				H4	DNA segment, single copy, probe pH4
554	37162 at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
_				DnaJ (Hsp40) homolog, subfamily A,	
555	39118_at	DNAJA1	690807	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily A,	
556	276_at	DNAJA1	L08069	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
557	41233_at	DNAJB6	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	
559	36166_at	DNAJC8	AF083190	member 8	SPF31
				docking protein 1, 62kD (downstream of	
560	816 g at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
				docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
				dolichyl-phosphate mannosyltransferase	
562	34879_at	DPM1	AF007875	polypeptide 1, catalytic subunit	dolichol monophosphate mannose synthase
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	32168	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565		DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
266	_	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
567	32621_at	DR1	M97388	binding (negative cofactor 2)	phosphoprotein
568	37981 at	DBN1	D17530	drebrin 1	drebrin E
				dual specific protein; Homo sapiens	
				tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570	39727_at	DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
				dual specificity phosphatase 3 (vaccinia	
572	572 41225_at	DUSP3	AL049417	virus phosphatase VH1-related)	

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	<	8	၁	O	2
573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DUSP6
574	36946 at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
575	1512_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
578	760 21	DVRK2	Y09216	dual-specificity tyrosine-(Y)- phosphorvlation regulated kinase 2	dual-specificity tyrosine-(Y)-phosphorylation requlated kinase 2 isoform 1
577	39931 at	DYRK3	Y12735	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 3	Dyrk3 protein
578		DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579		DCTN2	U50733	dynactin 2 (p50)	dynamitin
580		NIA	AI540958	dynein, cytoplasmic, light polypeptide	
581	34829_at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
582	32234 at	DYT1	AF007871	dystonia 1, torsion (autosomal dominant; torsin A)	torsinA
				dystroglycan 1 (dystrophin-associated	
583	36989_at	DAG1	L19711	glycoprotein 1)	dystroglycan
				dystrophin (muscular dystrophy,	
584	584 40488_at	DMD	M18533	Duchenne and Becker types)	dystrophin
585	585 40106_at	E1B-AP5	AJ007509	E18-55kDa-associated protein 5	E18-55KJa-associated protein
586	586 33354_at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	587 40375 at	EGR3	X63741	early growth response 3	transcription factor
588	588 36135 at	EBNA1BP2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730 at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
290	33254_at	EVIS	AF008915	ecotropic viral integration site 5	EVI-5 homolog
				ectodermal-neural cortex (with BTB-like	
591	39542_at	ENC1	AF059611	domain)	nuclear matrix protein NHP/B
				ectonucleotide	
592	41124 r at	ENPP2	L35594	pyropnospnatase/phosphodiesterase z (autotaxin)	autotaxin
				ectonucleotide	
				pyrophosphatase/phosphodiesterase 2	
593	41123_s_at	ENPP2	L35594	(autotaxin)	autotaxin
594	594 32551 at	FFFMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein
3	10000 I				

	¥	6	ပ		Π
595	36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
596	40509 at	ETFA	J04058	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	electron transfer flavoprotein, alpha polypeptide
	7000	C L	V21100	oeta	electron transfer flavonrofein beta subunit
297	36881_at	EITB	A/1129	polypeptide	deciron named mayor con con construction
				elongation factor Er-1-alpha; numan elongation factor EF-1-alpha gene.	eukaryotic translation elongation factor 1
598	598 1288 s at	EEF1A	J04617		alpha 1
599	31853 at	EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
				squamous cell carcinoma-associated	
009	39861_at	EMS1	M98343	(p80/85 src substrate)	amplaxin
				end of last exon based on GENSCAN	
				prediction presumably this gene and	
				dJ477H23.2 are part of the same gene	
601	41478_at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	603 37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	604 39010_at	ENSA	AI658639	endosulfine alpha	
				endothelial differentiation,	
			,	lysophosphatidic acid G-protein-coupled	nolomod reference biog sibitadassodassod
605	605 40387_at	EDG2	U80811	receptor, 2	ואצטטווסצטוושנוחוכ מכוח ובכבטומו ווסוווסוסא
202	40074 24	1 1 1	A IONESEO	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
	1001			enhancer of rudimentary homolog	human protein homologous to DROER
607	607 39079_at	ERH	D85758	(Drosophila)	protein
808	608 2035 s at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609	609 34335 at	EFNB2	AI765533	ephrin-B2	
				epidermal growth factor receptor pathway	epidermal growth factor receptor pathway
610	37731_at	EPS15	Z29064	substrate 15	substrate 15
L				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
611	1467_at	EPS8	U12535	substrate 8	substrate
612	37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	39631 at	EMP2	U52100	epithelial membrane protein 2	XMP

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	מ	ن ا	D FPM1 disease gene: cysteine protease	ш .
<u>_</u>	cystatin B	U46692	inhibitor, Human cystatin B gene, complete cds.	cystatin B
	EPB41L2	AF027299	erythrocyte membrane protein band 4.1- like 2	protein 4.1-G
_	ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
			estrogen receptor binding site associated,	0 0 0 U
	EBAG9	AB00/619	antigen, 9	EDAGS
1		WZ8948	FOLS	
		N30151	ESIS	
-	C1S	W28612	ESTs	-
Ì	ATP6S1	AI400326	ESTs	
Г		Al808712	ESTs	
		AA890010	ESTs	
			ESTs, Highly similar to RS21_HUMAN	
			40S RIBOSOMAL PROTEIN S21	
	RPS21	AI526078	[H.sapiens]	
			ESTs, Moderately similar to	
			ALUB_HUMAN ALU SUBFAMILY SX	
			SEQUENCE CONTAMINATION	
		W61005	WARNING ENTRY [H.sapiens]	
			ESTs, Moderately similar to	1
			GLK5_HUMAN GLUTAMATE	
		_	RECEPTOR, IONOTROPIC KAINATE 5	
		AA977136	PRECURSOR [H.sapiens]	
			ESTs, Moderately similar to T46365	
			hypothetical protein DKFZp434A1518.1	-
		Al986201	[H.sapiens]	
			ESTs, Weakly similar to 0903209A	
		AL042729	peptide PD,basic Pro rich [H.sapiens]	
			ESTs, Weakly similar to N-WASP	
		AL046940	[H.sapiens]	
	PIG8	AF010313	etoposide-induced mRNA	Pig8
			eukaryotic translation elongation factor 1	
	EEF1A1	W28170	alpha 1	

Fig 21

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	A	В	၁	Ŋ	U
				eukaryotic translation elongation factor 1	
632	35175_f_at	EEF1A2	X70940		elongation factor 1 alpha-2
				eukaryotic translation elongation factor 1	
633	35748_at	EEF182	X60489	beta 2	elongation factor-1-beta
				eukaryotic translation elongation factor 1	
				delta (guanine nucleotide exchange	
634	41256_at	EEF1D	Z21507	protein)	human elongation factor-1-delta
				eukaryotic translation elongation factor 1	
635	1676_s_at	EEF1G	M55409	gamma	pancreatic tumor-related protein
000	To do	G L L	711600	2 rotic formalation along factor 2	himan elongation factor 2
200	3038/_al	בברג	76017		
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	638 34278 at	EIE1A	L18960	eukarvotic translation initiation factor 1A	protein synthesis factor
3				eukarvotic translation initiation factor 2.	eukaryotic translation initiation factor 2,
639	1154 at	EIF2S1	J02645	subunit 1 (alpha, 35kD)	subunit 1 (alpha, 35kD)
				eukaryotic translation initiation factor 28,	eukaryotic translation initiation factor 2B,
640	40515 at	EIF2B2	AF035280	subunit 2 (beta, 39kD)	subunit 2 (beta, 39kD)
				eukaryotic translation initiation factor 3,	
641	1644_at	EIF3S2	U36764	subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
				eukaryotic translation initiation factor 3,	
642	35327_at	EIF3S3	U54559	subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
				eukaryotic translation initiation factor 3,	
643	32576_at	EIF3S5	U94855	subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
				eukaryotic translation initiation factor 3,	murine mammary tumor integration site 6
644	38681_at	EIF3S6	U62962	subunit 6 (48kD)	(oncogene homolog)
				eukaryotic translation initiation factor 3,	
645	35298_at	EIF3S7	U54558	subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
				eukaryotic translation initiation factor 3,	
646	35323_at	EIF3S9	U78525	subunit 9 (eta, 116kD)	eukaryotic translation initiation factor
L				eukaryotic translation initiation factor 4	
647	41785_at	EIF4G2	U73824	gamma, 2	p97
				eukaryotic translation initiation factor 4	
648	648 33907_at	ElF4G3	AF012072	gamma, 3	elF4GI

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	A	8	O	Q	ш
649	1420 s_at	EIF4A2	D30655	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic initiation factor 4AII
650	37752 at	EIF4E	M15353		cap-binding protein
-				ation initiation factor 4E	
	35263_at	EIF4EBP2	N73769		and the state of t
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318_at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
				excision repair cross-complementing	excision repair cross-complementing rodent
				ation	repair deficiency, complementation group 3
					(xeroderma pigmentosum group B
654	1885 at	ERCC3 .	M31899	B complementing)	complementing)
				excision repair cross-complementing	
			•	rodent repair deficiency, complementation	
	Arren			group 5 (xeroderma pigmentosum,	
				complementation group G (Cockayne	
655	2063_at	ERCC5	L20046	syndrome))	excision repair protein
		!		exons 1-4 beyond this clone; match:	dJ434O14.1 (Hydroxysteroid (11-beta)
929	33734_at	HSD11B1	AL022398	proteins P28845 P50172 P51975 Q29608 Denydrogenase 1 (EC 1.1.1.146))	Denydrogenase 1 (EC 1.1.1.146))
657	222_at	EXT1	829639	exostoses (multiple) 1	exostoses (multiple) 1
658	658 36526 at	EXTL2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
629	659 38809_s_at	EXTL3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
99	660 37729_at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
				exportin, tRNA (nuclear export receptor for	
661	38753_at	XPOT	AF039022	(tRNAs)	exportin t
				extracellular matrix protein 2, female	
662	662 39673_i_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
				extracellular matrix protein 2, female	
663	39674_r_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
664	664 35226_at	EYA2	U71207	eyes absent homotog 2 (Drosophila)	Eab1
			00000	family with sequence similarity 8, member	
ဂ္ဂ	38318_at	FAIMBA	ALUSUIZO		
999	666 31879 at	FUBP3	U69127	far upstream element (FUSE) binding protein 3	FUSE binding protein 3

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\dagger	C			larnesyl diphosphate synthase (famesyl	farnesyl diphosphate synthase (farnesyl
					pyrophosphate synthetase,
				,e,	dimethylallyltranstransferase,
667 3	37325 at	FDPS	D14697		geranyltranstransferase)
+				nesyltransferase	
58	668 34848 at	FDFT1	X69141		farnesyl-diphosphate farnesyltransferase
١		FNTA	L10413	farnesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
+					
670	38755 at	FADD	X84709	\neg	mediator of receptor induced toxicity
	1			fasciculation and elongation protein zeta 1	
671	37743 at	FEZ1	U60060	_	FEZ1
T				fasciculation and elongation protein zeta 2	
672	38651 at	FEZ2	U60061	\rightarrow	FEZ2
T				or suppressor homolog 1	
73	673 40454 at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
T				fatty-acid-Coenzyme A ligase, long-chain	
74	674 40082 at	FACL2	D10040		long-chain acyl-CoA synthetase
Γ				fatty-acid-Coenzyme A ligase, long-chain	•
675	33880 at	FACL3	D89053	3	Acyl-CoA synthetase 3
				fatty-acid-Coenzyme A ligase, long-chain	
9/9	33881 at	FACL3	AA977580	3	
677	33360 at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA 1004 protein
	37205 at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
679	32854 at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
989	32169 at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBX07	AL050254	F-box only protein 7	hypothetical protein
				FBRNP; heterogeneous ribonucleoprotein	
				homolog; This sequence comes from Fig.	
				3; D10S102=FBRNP [human, fetal brain,	
382	33817_at	D10S102	S63912	mRNA, 3043 nt].	FBRNP
683		Hill	HG1103-HT1103		dinitrogenase reductase
684	34678	FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
				FERM, RhoGEF (ARHGEF) and pleckstrin	
882	685 32148_at	FARP1	A1/01049	מסונומונו הנסופונו ו (כווסוומוסכאופ-מפוואפת)	

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A	В	L.	၁	D	ш
FTH1 L20941	L20941		ē	ferritin, heavy polypeptide 1	ferritin heavy chain
at FALZ U05237	U05237		fetal	fetal Alzheimer antigen	fetal Alzheimer antigen
at FBN1 X63556	X63556		fibril	fibrillin 1 (Marfan syndrome)	fibrillin
FAP U09278	U09278		fibro		fibroblast activation protein
FGF7 M60828	7 M60828		fibro grov	fibroblast growth factor 7 (keratinocyte growth factor)	keratinocyte growth factor
					precursor; fibroblast growth factor receptor
					1, isoform 2 precursor; tibroblast growth
					fibroblast growth factor receptor 1, isoform 4
					precursor; fibroblast growth factor receptor
					1, isoform 5 precursor; fibroblast growth
	_				factor receptor 1, isoform 6 precursor;
			<u> </u>		fibroblast growth factor receptor 1, isoform 7
(ibrob	fibrob	fibrob	fibrob	fibroblast growth factor receptor 1 (fms-	precursor; libroblast growth factor receptor
relate	relate	relate	relate	related tyrosine kinase 2, Pfeiffer	1, isotorm 8 precursor; libroblast grown
2057 g at FGFR1 M34641 syndrome)	M34641		syndre	ome)	factor receptor 1, isotorm 9 precursor
					fibronectin 1, isoform 1 preproprotein;
692 31720 s at FN1 M10905 (fibro	M10905		fibro	fibronectin 1	fibronectin 1, isoform 2 preproprotein
31719 at FN1 X02761	X02761		fibro	fibronectin 1	fibronectin precursor
		fibro	fibro	fibronectin leucine rich transmembrane	fibronectin leucine rich transmembrane
34853_at FLRT2 AB007865	AB007865		prot	protein 2	protein 2
695 38026 at FBLN1 U01244 (fibulin 1	U01244		nqıj	lin 1	fibulin-1D
39038_at FBLN5 AF093118	AF093118		fibu	fibulin 5	UP50
697 38078 at FLNB AF042166 filar	AF042166		filar	filamin B, beta (actin binding protein 278)	beta-filamin
38761 s at FKBP9 AA487755	AA487755		꿏	FK506 binding protein 9 (63 kD)	
at FMO3 M83772	M83772		fla	flavin containing monooxygenase 3	flavoprotein
FLN29 AB007447	AB007447	47	뜨	FLN29 gene product	Fln29
			<u>ō</u>	follistatin precursor, Human follistatin	follistatin isoform FST317 precursor;
701 38356 at FST M19481 ge	M19481		<u>6</u>	gene, exon 6.	follistatin isoform FST344 precursor

Fig 21

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				forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like	
	702 41027 at	FKHI 7	AF078096		forkhead/winged helix-like transcription factor 7
1152	703 36319_at	*	U13220	F2	forkhead protein FREAC-2
ı 🕸	40570 at	FOX01A	AF032885	forkhead box O1A (rhabdomyosarcoma)	forkhead protein
12	34740_at	FOX03A .	AF032886	forkhead box O3A	forkhead protein
121	32542_at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
12	38422_s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
12	708 41649_at	FHX	AF038177	FOXJ2 forkhead factor	
14	34997_r_at	FZD5	U43318	frizzled homolog 5 (Drosophila)	transmembrane receptor
14	472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
ĭάl	222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
Ιĕ	38923_at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
ĺά	38139_at	FPGT	AF017445	fucose-1-phosphate guanylyttransferase	GDP-L-fucose pyrophosphorylase
١ ٠٠	41814_at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
l				Fukuyama type congenital muscular	
Õ	715 40022_at	FCMD	AB008226	dystrophy (fukutin)	fukutin
N	716 32546_at	FH	U59309	fumarate hydratase	fumarase precursor
9	36145_at	SIAHBP1	U51586	fuse-binding protein-interacting repressor siah binding protein 1	siah binding protein 1
1 0	40.480 s. at	N	M14333	EYN oncodene related to SBC. FGB. YES	FYN oncodene related to SBC, FGB, YES FYN oncodene related to SRC, FGR, YES
)	100 P				
9	2039_s_at	FYN	M14333	FYN oncogene related to SHC, FGH, YES	FYN oncogene related to SAC, FGH, TES FTN oncogene related to SAC, FGH, TES
4	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
	37308_at	GPR107	A1888084	G protein-coupled receptor 107	
12	37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
Į U	2E70E of	F Idvavava	M/28281	GABA(A) receptor-associated protein like	
21		יין ויין ויין ויין	1150501	GABA(A) recentor-associated protein-like	
ູເຕ	35767_at	GABARAPL2	A1565760	2	
IZ.	37825_at	GALK2	M84443	galactokinase 2	galactokinase
1	742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

	4	B .	၁	D	LL.
				lase,	
727	37263_at	ВВН	U55206		human gamma-glutamyi hydrolase
				orotein, alpha 1, 43kD	
728	32531_at	GJA1	X52947		connexin 43
				GCN1 general control of amino-acid	
729	36603_at	GCN1L1	D86973	synthesis 1-like 1 (yeast)	
730	35307_at	GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811		coding sequence
				riants near HD	gene with multiple splice variants near HD
732	32180_s_at	RES4-22	AB000461	locus on 4p16.3	locus on 4p16.3
					Bruton's tyrosine kinase-associated protein-
733	466_at	GTF2I	U77948	general transcription factor II, i	135
734		GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010_at	GTF2A2	AI203737	subunit)	
				general transcription factor IIA, 2 (12kD	
736	869_at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kD)	TFIIE-alpha
				general transcription factor IIE,	
738	37295_at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kD)	TFIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
				general transcription factor IIH,	
740	40754_at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 kD subunit
741	36188 at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742		GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	763 at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793 at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	
745	745 32643_at	GBE1	L07956	1V)	1,4-alpha-glucan branching enzyme
746	746 34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

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				glucosaminyl (N-acetyl) transferase 1,	
747 3	38218_at (GCNT1	M97347	(beta-1,6-N-acetylglucosaminyltransferase
748 3	39122 at	GPI	K03515		neuroleukin
	at	GRP58	Z49835	glucose regulated protein, 58kD	protein disulfide isomerase
750	je	GePD	X03674	enase	glucose-6-phosphate dehydrogenase
751 3	at	GUSB	M15182		glucuronidase, beta
752			M20867	enase 1	glutamate dehydrogenase 1
753	at		X80818	tropic 4	metabotropic glutamate receptor type 4
				glutamate-ammonia ligase (glutamine	
754 4	40522_at	GLUL	X59834	synthase)	glutamateammonia ligase
Γ				glutamate-cysteine ligase, catalytic	
755	31850_at	GCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
Γ				glutamic-oxaloacetic transaminase 1,	
757	35343 at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
				glutamic-oxaloacetic transaminase 2,	
				mitochondrial (aspartate aminotransferase	
758	758 40764 at	GOT2	M22632	2)	aspartate aminotransferase 2 precursor
759	34719 at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
260	32626 at	GFPT1	M90516	transaminase 1	amidotransferase
				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640 at	GFPT2	AB016789	transaminase 2	amidotransferase
762	35300 at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutaminyl-tRNA synthetase
763	34311 at	GLRX	X76648	glutaredoxin (thioltransferase)	glutaredoxin
764	37033 s at	GPX1	X13710	glutathione peroxidase 1	
765	40508 at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
	38386 r at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824 at	GSTTLp28	U90313	transferase omega	glutathione-S-transferase homolog
				glyceraldehyde-3-phosphate	
768	AFFX-HUMGAP(GAPD	(GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
				glyceraldehyde-3-phosphate	
769	35905_s_at	GAPD	U34995	dehydrogenase	

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1			10000	glyceraldehyde-3-phosphate	ahraraldehvde-3-nhosphate dehvdrogenase
श	AFFX-HUMGAPIGAPU	IGARU	W35187	nenyungenase	Silver and a property of the p
77.1	30302 at	GNPAT	A.1002190	alyceronephosphate O-acyltransferase	dihydroxyacetone phosphate acyttransferase
_				glycine cleavage system protein H	glycine cleavage system protein H
772	37357 at	GCSH	D00723	(aminomethyl carrier)	(aminomethyl carrier)
773	773 39665 at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774	40645 at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775	775 40876 at	GYG	U31525	glycogenin	glycogenin
776	76 35334 at	GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777	38379_at	GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
778	778 37251_s_at	GPM6B	AF016004	glycoprotein M6B	
779	33126 at	AD-017	L13435	glycosyltransferase AD-017	
780	780 36582 q at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
781	781 36581 at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	36201 at	GL01	D13315	glyoxalase I	lactoyl glutathione lyase
				glyoxylate reductase/hydroxypyruvate	
783	783 40133 s at	GRHPR	W28944	reductase	
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
				-	polypeptide 1, isoform XL-alpha-s; guanine
					nucleotide binding protein (G protein), alpha
					stimulating activity polypeptide 1, isoform
784	37449 i at	GNAS	X04409	GNAS complex locus	alpha-s-1
785	785 37448 s at	GNAS	X56009	GNAS complex locus	alpha subunit of GsGTP binding protein

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786	786 37450 r at	GNAS	X04409		guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1
787	37959 at	GGA3	D63876	golgi associated, gamma adaptin ear containing, ARF binding protein 3	ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long
788	788 32713_at	GOLGA1	U51587	уa,	Golgi complex autoantigen golgin-97
789	789 32150_at	GOLGA4	X82834	golgi autoantigen, golgin subfamily a, 4	256 kD golgin
28	36827_at	GOLPH1	AF020762	golgi phosphoprotein 1	unknown protein
791	38620 at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
792	34737 at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	putative 13 S Golgi transport complex 90kD subunit brain-specific isoform
793	793 41767 r at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950_at	HSGP25L2G	X90872	gp25L2 protein	
795	36035 at	GPAA1	AB002135	GPAA1P anchor attachment protein 1 homolog (yeast)	glycosylphosphatidylinositol anchor attachment 1 (GPAA1)
96/	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
797	39822 s at	GADD45B	AF078077	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible protein GADD45beta
700	20001 0 00	GADDAEB	Nostica	growth arrest and DNA-damage-inducible,	
799		GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
88	41839 at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
8	37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802		GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
804	804 41752_at	GHITM	W28190	growth hormone inducible transmembrane protein	

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_	A	B	د	0	
805	160030_at	GHR	X06562	growth hormone receptor	growth hormone receptor
908	806 40113_at	GS3955	D87119	GS3955 protein	GS3955
				otein overexpressed in	
807	37279_at	GEM	010550		Celli
				guanine nucleotide binding protein (G protein), albha inhibiting activity	
808	33809 at	GNAI1	AL049933	polypeptide 1	hypothetical protein
				guanine nucleotide binding protein (G	guanine nucleotide binding protein (G
				protein), alpha inhibiting activity	protein), alpha inhibiting activity polypeptide
808	37307_at	GNAI2	X04828	polypeptide 2	2
				guanine nucleotide binding protein (G	
810	34608_at	GNB2L1	M24194	protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	35272_at	GNG5	AI541042	protein), gamma 5	
812	812 37735_at	0	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	35735_at	GBP1	M55542	inducible, 67kD	guanylate binding protein isoform I
814	814 905_at	GUK1	L76200	guanylate kinase 1	guanylate kinase
815	815 32249_at		M65292	H factor (complement)-like 1	factor H homologue
816	32250_at	王	X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	817 420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	818 31673_s_at	sion re	gu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003 at	CD63; MLA1; ME4	E4X62654	H.sapiens gene for Me491/CD63 antigen. ME491 /CD63 antigen	ME491 /CD63 antigen
820	820 38076 at	P1 dene for c subu	70669X)qr	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
821	35125 at		X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822		mS7	225749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	823 31510_s_at	hH3.3B	248950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

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824 33820 g_at IdhB 825 33819 at IdhB 826 34787 at ORF1 827 36012 at Itre 829 40471 at PXF 830 37038 at PXMP1 831 31583 at PXMP1 832 1685 at SPHAR 833 38127 at SPHAR 834 37310 at UPA 835 34308 at H2AFL 836 39337 at H2AFL 836 39337 at H2AFL 836 39337 at H2AFC 837 33458 r at H2BFL 838 40818 at HAFG 839 254 at HAFG 839 254 at HAFG 839 254 at HAFG 839 3353 at HAFG 839 3353 at HAFG 839 3353 at HAFG	O .	0	ш
33820_g_al h 33819_al h 34787_al G 34787_al G 340471_al h 40471_al h 31583_al h 37310_al h 38127_al h 38121_al h 3651_al h 37720_al h		Construction of the constr	
33820 g al la sa		H.sapiens lactate denydrogenase o gene	
33820_g_al li 33819_at li 34787_at (34787_at (40471_at li 37038_at (1685_at (1685_at		1 and 2 (EC 1.1.1.27) (and joined	
33819_at	X13794	一	lactate dehydrogenase B
33819_at		H.sapiens lactate dehydrogenase B gene	
34787_at		exon 1 and 2 (EC 1.1.1.27) (and joined	
34787_at (0 36012_at t 40471_at t 40471_at t 40471_at t 37038_at t 1685_at t 38127_at t 38127_at t 37310_at t 334308_at t 33458_r_at t 40818_at t 254_at t 39969_at t 39591_at t 35215_at t 35215_at t 35251_at t	X13794		lactate dehydrogenase B
36012_at 1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
31526 f at tt 40471 at 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		H.sapiens mRNA for PIBF1 protein,	
at it	Y09631	complete.	PIBF1 protein
at it		H.sapiens mRNA for tre oncogene (clone	
at a	X63547	213).	oncogene
at a	Y09048	H.sapiens PxF gene.	PxF protein
31583_at 1685_at 1685_at 38127_at 37310_at 34308_at 39337_at 40818_at 40818_at 39359_at 39969_at 39969_at 39969_at 39969_at 39969_at 39969_at 39969_at 39969_at 39969_at		H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
31583_at 1685_at 38127_at 37310_at 34308_at 34308_at 34368_r_at 40818_at 254_at 33959_at 32591_at 32591_at 32591_at 35215_at 35515_at	X83467	joined CDS).	protein
31583_at 1685_at 38127_at 37310_at 34308_at 39337_at 40818_at 40818_at 254_at 39969_at 39969_at 35215_at 35215_at 35215_at 35215_at		H.sapiens rpS8 gene for ribosomal protein	
38127_at 37310_at 37310_at 34308_at 39337_at 40818_at 40818_at 254_at 39969_at 39969_at 35215_at 35215_at	X67247	S8.	ribosomal protein S8
38127_at 37310_at 34308_at 39337_at 39337_at 40818_at 254_at 254_at 39969_at 392591_at 35215_at 35215_at 35215_at		H.sapiens SPHAR gene for cyclin-related	:
38127_at 37310_at 34308_at 39337_at 33458_r_at 40818_at 254_at 39969_at 39969_at 35215_at 35215_at 35215_at	X82554	protein.	S-phase response (cyclin-related)
38127_at 37310_at 34308_at 39337_at 33458_r_at 40818_at 254_at 39969_at 39669_at 32591_at 32591_at 32591_at 32591_at 35215_at			: : : : : : : : : : : : : : : : : : : :
37310_at 34308_at 39337_at 33458_r_at 40818_at 254_at 39969_at 39969_at 32591_at 32591_at 37215_at 35215_at	in-1 Z48199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
34308_at	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
39337_at 33458_r_at 40818_at 254_at 39969_at 32591_at 32591_at 37215_at 39353_at	U90551	H2A histone family, member L	histone 2A-like protein
33458 r at 40818 at 254 at 39969 at 32591 at 35215 at 39353 at 37720 at	M37583	H2A histone family, member Z	H2A histone family, member Z
40818 at 254 at 39969 at 32591 at 35215 at 37720 at 37720 at 36614 at	AI688098	H2B histone family, member L	
254_at	580 D14041	H-2K binding factor-2	H-2K binding factor-2
39969_at 32591_at 35215_at 39353_at 37720_at	M11353	H3 histone, family 3A	H3 histone, family 3A
32591_at 35215_at 39353_at 37720_at	AA255502	H4 histone family, member G	
35215_at 39353_at 37720_at	AI494623	HCDI protein	
39353_at 37720_at 36614_at	418P AL049996	HDCMA18P protein	hypothetical protein
		heat shock 10kD protein 1 (chaperonin	
	AI912041	10)	
	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
		heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
	X87949	regulated protein, 78kD)	regulated protein, 78kU)
HSPAGB	B 15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
1			

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847	32316 s at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
_	33984	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
070	21006 at	невр.	A FOR8754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
Î	31300_at	-			tumor necrosis factor type 1 receptor
850	1468_at	TRAP1	U12595	heat shock protein 75	associated protein
851		HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
				hepatoma-derived growth factor (high-	!
852	38779_r_at	HDGF	D16431	mobility group protein 1-like)	hepatoma-derived GF
853	35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
				heterogeneous nuclear ribonucleoprotein	
854	38094_at	HNRPAB	M65028	A/B	hnRNP type A/B protein
·				heterogeneous nuclear ribonucleoprotein	
855	37334_at	HNRPAO	U23803	AO	heterogeneous ribonucleoprotein A0
				heterogeneous nuclear ribonucleoprotein	
856	34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
		-		heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857	36654 s at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
					heterogeneous nuclear ribonucleoprotein C,
				heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
828	33666_at	HNRPC	M16342	C (C1/C2)	ribonucleoprotein C, isoform a
				heterogeneous nuclear ribonucleoprotein	
_				D (AU-rich element RNA binding protein 1,	
859	38016_at	HNRPD	M94630	37kD)	DNA-binding protein
				heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
				heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
					heterogeneous nuclear ribonucleoprotein
083	41083 34	HNBDH3	AE052131	heterogeneous nuclear ribonucleoprotein H3 (2H9)	H3, Isolorm a; neterogeneous nuclear ribonucleoprotein H3, isoform b
				heterogeneous nuclear ribonucleoprotein	
863	40836_s_at	HNRPH3	W26677	НЗ (2Н9)	

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864	39415	HNRPK	X72727	heterogeneous nuclear ribonucleoprotein K	transformation upregulated nuclear protein
				heterogeneous nuclear ribonucleoprotein	
865	35201 at	HNRPL	X16135		heterogeneous nuclear ribonucleoprotein L
				terogeneous nuclear ribonucleoprotein	Si constant
998	37717_at	HNHFM	L03532	十	WIT DIOCEIL
867	. te 00208	HNRPR	AF000364	heterogeneous nuclear ribonucleoprotein R	heterogeneous nuclear ribonucleoprotein R
3					
				eoprotein	
868	38654_at	HNRPU	X65488		nnHink U protein
869	869 32818_at	HXB	X78565	, cytotactin)	human tenascin-C
870	870 39827 at	RTP801	AA522530	HIF-1 responsive RTP801	
				high density lipoprotein binding protein	
871	31504_at	HOLBP	M64098	(vigilin)	high density lipoprotein binding protein
				high-mobility group (nonhistone	
872	32220_at	HMG1	D63874	chromosomal) protein 1	HMG-1
				high-mobility group (nonhistone	high-mobility group (nonhistone
873	306_s_at	HMG14	J02621	chromosomal) protein 14	chromosomal) protein 14
				high-mobility group (nonhistone	
874	35738_at	HMG17L3	AI347088	chromosomal) protein 17-like 3	-
				high-mobility group (nonhistone	high-mobility group (nonhistone
875	38065_at	HMG2	X62534	chromosomal) protein 2	chromosomal) protein 2
876	38843_at	HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877	35693_at	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009 at	HIN11	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231 at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
880	41855	HAT1	AF030424	histone acetyltransferase 1	histone acetyltransferase 1
881	38771 at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882		HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883		HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	1 39046_at	H2AV	AL049324	histone H2A.F/Z variant	
885	5 39092_at	H2AV	AW007731	histone H2A.F/Z variant	
886		HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
88/	7 40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein



	A	89	ပ	O	Щ
888	39809_at	HBP1	AF019214	HMG-box containing protein 1	HMG box containing protein 1
				HMG-domain containing protein which is	
				the 57 kd subunit within SWI/SNF-related	
				BAF complexes; contains a proline-rich N-	
				terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
				sapiens BAF57 (BAF57) gene, complete	
889	33828 at	BAF57	AF035262		BAF57
				HMT1 hnRNP methyltransferase-like 1 (S.	
890	890 39348 at	HRMT1L1	X99209	cerevisiae)	arginine methyltransferase
				HMT1 hnRNP methyttransferase-like 2 (S.	
891	32825 at	HRMT1L2	Y10805	cerevisiae)	arginine methyltransferase
				HNRNP Core Protein A1 LIKE	
				pseudogene; match: proteins P04256	
				Q28521 P49312 P09651 P51991 P51992	
892	892 31463_s_at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787	heme-lyase)	holocytochrome c-type synthetase
894	39610_at	HOXB2	X16665	homeo box B2	homeo box B2
895	40674 s at	НОХСЕ	S82986	homeo box C6	homeo box C6
896	38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	homer-3
				Homo sapiens (clone 11/252) ubiquinoi	
			-	cytochrome c reductase Rieske Iron-	
897	897 34401_at	UQCRFS1	L32977	sulphur protein (UUCHFS1) gene, exon 2. Hieske Fe-5 protein	Hieske re-5 protein
				Homo sapiens (clone FFE-7) type II	
				inosine monophosphate dehydrogenase	
				(IMPDH2) gene, exons 1-13, complete	inosine monophosphate dehydrogenase type
898	36624_at	IMPDH2	L33842	cds.	
				Homo canione aldebyda oxidasa (AOX1)	
800	37599 at	AOX1	AF017060	gene, exon 35 and complete cds.	aldehyde oxidase
				Homo canions alpha NAC mRNA	
900	39740 g at	NACA	AF054187	complete cds.	alpha NAC

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901 39739_at NACA 902 41154_r_at CTNNA1 903 41153_f_at CTNNA1 904 39324_at 905 35310_at 906 35754_at 907 33325_at 909 41253_s_at 910 39162_at 911 41807_at	AF054187 AF102803 AF102803 AL050078 D45288		alpha NAC alphaE-catenin alphaE-catenin
41154_r_at 41153_f_at 41153_f_at 39324_at 35754_at 35754_at 41253_s_at 41253_s_at 41253_s_at 41253_s_at 39162_at		s alphaE-catenin (CTNNA1) 3 and complete cds. s alphaE-catenin (CTNNA1) 9 and complete cds. c DNA FLJ10784 fis, clone 48, highly similar to Homo A; cDNA DKFZp566G0746	alphaE-catenin alphaE-catenin
	AF102803 AF102803 AL050078 D45288	TNNA1) TNNA1) is, clone Homo	alphaE-catenin alphaE-catenin
	AF102803 AL050078 D45288	TNNA1) is, clone Homo SG0746	alphaE-catenin
39324_at 35310_at 35754_at 35754_at 3102_at 41253_s_at 41253_s_at 41807_at	AF102803 AL050078 D45288		alphaE-catenin
	AL050078 D45288	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	
	AL050078 D45288	NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	
	AL050078 D45288	sapiens mRNA; cDNA DKFZp566G0746	
	D45288	THE PERSON OF TH	
	D45288	Homo sapiens cUNA FLJ1326/ 11s, clone	
		OVARC1000964	
		Homo sapiens cDNA FLJ13553 fis, clone	
907 33325_at 908 38102_at 909 41253_s_at 910 39162_at 911 41807_at 912 38643_at	L40391	PLACE1007454	
907 33325_at 908 38102_at 909 41253_s_at 910 39162_at 911 41807_at		Homo sapiens cDNA FLJ14821 fis, clone	
907 33325_at 908 38102_at 909 41253_s_at 910 39162_at 911 41807_at		OVARC1000556, highly similar to	
907 33325_at 908 38102_at 909 41253_s_at 910 39162_at 911 41807_at		RIBOSOMAL PROTEIN S6 KINASE II	
908 38102_at 909 41253_s_at 910 39162_at 911 41807_at 912 38643_at	W26667	ALPHA 2 (EC 2.7.1)	
908 38102_at 909 41253_s_at 910 39162_at 911 41807_at 912 38643_at		Homo sapiens cDNA FLJ25016 fis, clone	
909 41253_s_at 910 39162_at 911 41807_at 912 38643_at	W28575	CBL01574	
		Homo sapiens cDNA FLJ30436 fis, clone	
	A1983043	BRACE2009037	
910 39162_at 911 41807_at 912 38643_at		Homo sapiens cDNA FLJ30544 fis, clone	
911 41807_at 912 38643_at	AA156987	BRAWH2001412	
911 41807_at 912 38643_at		Homo sapiens cDNA FLJ31959 fis, clone	
912 38643_at	AL040137	NT2RP7007422	
912 38643_at		Homo sapiens cDNA FLJ33151 fis, clone	
	W87466	UTERU2000263	
		Homo sapiens cDNA: FLJ21175 fis, clone	
913 34246_at	AA418437	CAS11071	
		Homo sapiens cDNA: FLJ21243 fis, clone	
914 40813 at	AI768188	COL01164	

Fig 21

	A	8	၁	O	ш
				Homo sapiens cDNA: FLJ21449 fis, clone	
				COL04483, highly similar to AF010235	
				Homo sapiens mRNA from chromosome	
915	915 40923_at		AA290994	5q31-33 region	
				Homo sapiens cDNA: FLJ21904 fis, clone	
916	916 38993_r_at		W27522	HEP03585	
				Homo sapiens cDNA; FLJ21927 fis, clone	
				HEP04178, highly similar to HSU90909	
917	917 38093_at		O30309	Human clone 23722 mRNA sequence	
				Homo sapiens cDNA: FLJ22642 fis, clone	
918	918 34840_at		AI700633	HSI06970	
				Homo sapiens cDNA: FLJ23324 fis, clone	
				HEP12482, highly similar to	
	_			HUMMYOHCB Human nonmuscle myosin smooth musc	cle myosin heavy chain isoform
919	919 32838_at	smooth muscle my S67247	S67247	heavy chain-B (MYH10) mRNA SMemb	
				Homo sapiens cervical cancer suppressor-	
920	920 33737 f at	,	AI871359	1 mRNA, complete cds	
				Homo sapiens clone 23570 mRNA	
921	41663_at		AF038202	sednence	
				Homo sapiens clone 23700 mRNA	
922	36815_at	-	AF038185	sednence	
			-	Homo sapiens clone 23718 mRNA	
923	923 41841_at		AF052138	sednence	
				Homo sapiens clone 23903 mRNA	
924	924 37794_at		AF035281	sednence	
				Homo sapiens clone 23938 mRNA	
925	925 38764_at		AF007142	sednence	
				Homo sapiens clone 24416 mRNA	
956	35342_at		AF052159	sednence	
				Homo sapiens clone 24630 mRNA	
927	31867_at		AF052174	sednence	
				Homo sapiens clone 24674 mRNA	
928	928 36758_at		AF070578	sednence	
				Homo sapiens clone 24790 mRNA	
929	929 41864_at		AF052181	sednence	

Γ	۷	8	0	Q	ш
				Homo sapiens clone FBD3 Cri-du-chat	
930	38070_at		AL080234	critical region mRNA	
				Homo sapiens cofactor A protein mRNA,	
931	34773_at	TBCA /	AF038952		cofactor A protein
				Homo sapiens cytochrome c oxidase	
				subunit IV precursor (COX4) gene,	
				<u>a</u>	
932	932 39027 at	COX4	AF017115		cytochrome c oxidase subunit IV precursor
				Homo sapiens D15F37 pseudogene, S4	
933	933 40878_f_at	D15F37	AF041081	allele, mRNA sequence.	
				Homo sapiens deoxycytidylate deaminase	
934	631 g at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
				ycytidylate deaminase	
935	630_at	DCTD	L39874		deoxycytidylate deaminase
				Homo sapiens DNA for	
				exon 17 and	
936	33936_at	GALC	D86181		galactocerebrosidase
				Homo sapiens F1Fo-ATPase synthase f	
937	40134_at	ATP5J2; ATP5JL; AF047436	AF047436		F1Fo-ATPase synthase f subunit
				Homo sapiens gene for LD78 alpha	
938	36103_at	SCYA3; LD78ALP	ALP D90144	precursor, complete cds.	LD78 alpha precursor
				Homo sapiens GOS28/P28 protein	
939	40725_at	GOSR1; P28; GS2AF047438	AF047438	mRNA, complete cds.	GOS28/P28 protein
				Homo sapiens GTP binding protein	
940	38708_at	RAN; TC4; ARA24AF054183	AF054183	mRNA, complete cds.	GTP binding protein
				Homo sapiens H beta 58 homolog mRNA,	
941	35790_at	VPS26; HB58; HB	HB AF054179	complete cds.	H beta 58 homolog
				Homo sapiens histone macroH2A1.2	
942	942 36576_at	H2AFY; H2A.y; H4AF054174	AF054174	mRNA, complete cds.	histone macroH2A1.2
				Homo sapiens insulin induced protein 1	
943	943 35303_at	INSIG1	N96876	(iNSIG1) gene, complete cds.	insulin induced protein 1
				Homo sapiens interferon-gamma receptor	
				alpha chain gene, exon 7 and complete	
944	944 1038_s_at	interferon-gamma U19247	U19247	cds.	interferon-gamma receptor alpha chain

	A	В	ပ	O	T I
945	895 at	MIF	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. macrophage migration inhibitory factor	macrophage migration inhibitory factor
	-			Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene	
946	38967 at	C14orf2; MP68; P	P AF054175	encoding mitochondrial protein, complete cds.	mitochondrial proteolipid 68MP homolog
7,70	31881 at		Y14155	Homo sapiens mRNA for Hmob33 protein, 3' untranslated region	
948		1132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
040	"		AL079279	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114	
				Homo sapiens mRNA; cDNA	
950	950 33418 at		AL096752	DKFZp434A012)	
				Homo sapiens mRNA; cDNA	
951	38630 at		AL080192	DKFZp434B102)	
				Homo sapiens mRNA; cDNA	
,	1 00 00 00 00 00 00 00 00 00 00 00 00 00		W72230	DKFZp434M162 (from clone DKFZp434M162)	
705	41529_g_al		207711	Homo caniane mRNA: cDNA	
				DKFZp434M245 (from clone	
953	36451 at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
730	26021 21	DKEZP5644026	41 050367	DKFZp564A026 (from,clone DKFZp564A026)	hypothetical protein
5	2005	220000000000000000000000000000000000000		Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366 at		AL049969	DKFZp564A072)	
L				Homo sapiens mRNA; cDNA	
				DKFZp564B222 (from clone	
956	39506_at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
- 1	170		A1 050021	DKFZp564D016 (from clone DKFZp564D016)	
ŝ	39/40 at		ALCOURT !	DIN EPOS 120'S	

Fig 21

	A	В	ပ	
T				Homo sapiens mRNA; cDNA
				DKFZp564D156 (from clone
958	38357_at		AL049321	DKFZp564D156)
T				Homo sapiens mRNA; cDNA
				DKFZp564E122 (from clone
959	33716 at		N95443	OKFZp564E122)
				Homo sapiens mRNA; cDNA
	- 4			DKFZp564E2222 (from clone
096	35301 at		AL049941	DKFZp564E2222)
3				Homo sapiens mRNA; cDNA
				DKFZp564F053 (from clone
196	35842 at		AL049265	DKFZp564F053)
				Homo sapiens mRNA; cDNA
				DKFZp564F112 (from clone
362	962 40552 s at		AL049987	DKFZp564F112)
				Homo sapiens mRNA; cDNA
				DKFZp564J0323 (from clone
963	39170 at		AL049957	DKFZp564J0323)
				Homo sapiens mRNA; cDNA
				DKFZp564L0822 (from clone
964	34303 at		AL049949	DKFZp564L0822)
				Homo sapiens mRNA; cDNA
				DKFZp564L222 (from clone
965	36509 at		AL049998	DKFZp564L222)
				Homo sapiens mRNA; cDNA
				DKFZp564P0823 (from clone
996	40353 at		AL049962	DKFZp564P0823)
				Homo sapiens mRNA; cDNA
				DKFZp566J2146 (from clone
296	35290 at		AL050081	DKFZp566J2146)
	_			Homo sapiens mRNA; cDNA
				DKFZp586B0918 (from clone
896	38079 at		AL049367	DKFZp586B0918)
				Homo sapiens mRNA; cDNA
				DKFZp586B1922 (from clone
696	969 32195 at		AL049450	DKFZp586B1922)

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				Homo sapiens mRNA; cDNA	
				DKFZp586C1019 (from clone	
970	970 39379_at		AL049397	DKFZp586C1019)	
				Homo sapiens mRNA; cDNA	
				DKFZp586C1723 (from clone	
971	37575_at		AL050192	DKFZp586C1723)	
				Homo sapiens mRNA; cDNA	
				DKFZp586F071 (from clone	-
972	972 34283 at		AL050125	DKFZp586F071)	
				Homo sapiens mRNA; cDNA	
_				DKFZp586G1922 (from clone	
973	39600_at		AL080110	DKFZp586G1922)	
Γ				Homo sapiens mRNA; cDNA	
				DKFZp586G2222 (from clone	
974	974 34752_at		AL080111	DKFZp586G2222)	
Γ				Homo sapiens mRNA; cDNA	-
				DKFZp58610523 (from clone	
975	39103 s at		H98552	DKFZp586l0523)	
				Homo sapiens mRNA; cDNA	
				DKFZp58611823 (from clone	
926	36092 at		AL080213	DKFZp586l1823)	
				Homo sapiens mRNA; cDNA	
				DKFZp586K1123 (from clone	
977	35187_at		AL080216	DKFZp586K1123)	
				Homo sapiens mRNA; cDNA	
				DKFZp586K2322 (from clone	
978	35363_at	DDX17	AL080113	DKFZp586K2322)	
				Homo sapiens mRNA; cDNA	
				DKFZp586M2022 (from clone	
979	41013_at		AL080114	DKFZp586M2022)	
				Homo sapiens mRNA; cDNA	
				DKFZp586N012 (from clone	
980	41690_at		AL049471	DKFZp586N012)	
				Homo sapiens mRNA; cDNA	
•				DKFZp586N1720 (from clone	
981	981 40349_at		AL049442	DKFZp586N1720)	

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	∢	80	C	ח	
Γ				Homo sapiens mRNA; cDNA	
				DKFZp586N1918 (from clone	
982	32672 at		AL049387	DKFZp586N1918)	
				me b5	
983	36668 at	DIA1	M28713	reductase (b5R) gene, exon 9.	NADH-cytochrome b5 reductase
Γ				Homo sapiens nucleophosmin	
				phosphoprotein (NPM) gene, 3' flanking	
984	38542 at		U89322	sequence.	
				Homo sapiens p18 protein mRNA,	
985	40587 s at	EEF1E1; P18	AF054186		p18 protein
	1			Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	41448 at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
				Homo sapiens prion protein (PrP) gene,	
987	36159 s at	PrP	U29185	complete cds.	prion protein
				Homo sapiens putative dienoyl-CoA	
				isomerase (ECH1) gene, exons 7-10, and	
988	32756 at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
989	35824 at	RP58	AJ223321	CDS.	RP58 protein
				Homo sapiens Sec61 gamma mRNA,	
990	39169 at	SEC61G	AF054184	complete cds.	Sec61 gamma
				Homo sapiens signal transducer and	
				activator of transcription 6 (STAT6) gene,	signal transducer and activator of
991	41222_at	STATE	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	
992	38817_at	SPAG7; ACRP; F\$AF047437	AF047437	mRNA, complete cds.	sperm acrosomal protein
				Homo sapiens splicing factor,	
		~	00000		
993	36033_at		AL049309	complete cus	
				Homo sapiens thymosin beta-10 gene,	Ot stort aircoming
994	31481_s_at	UMSB10	MYZSKS	sena.	intylliosin bota- 10
	,	j		Homo sapiens TIMP gene for tissue	in this form of material constraints
995	995 1693_s_at	TIMP	1011139	inhibitor of metalloproteinases, partial cus. Jussue illinibitor of illetalloproteinases	ussue illibitol of illetaliopioteniases

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Γ	•	α	C	Q	IJ
	3			Homo sapiens transaldolase-related	
				protein gene, exons 3-8 and complete	
966	37311 at	TALDO1; TAL-H; AF010400	AF010400	cds.	transaldolase-related protein
				Homo sapiens translation initiation factor	
997	32229 at	EIF4EL3, 4EHP; 4 AF038957	AF038957	4e mRNA, complete cds.	translation initiation factor 4e
		UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
999	at		U49869	Homo sapiens ubiquitin gene.	ubiquitin
1000	1000 38372 at	-	U66042	Homo sapiens unknown mRNA	
				Homo sapiens vacuolar H(+)-ATPase	
1001	1001 38814 at	ATP6V1G1; ATP6	FP6 AF038954	subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
				Homo sapiens vesicle trafficking protein	
1002	1002 41597 s_at	SEC22L1; SEC22	AF047442	sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003	1003 34957_at	X5L Y18504	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662_at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312 at		AL050002	mRNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388 at		AL080223	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4132509,	
1001	1007 38676_at		AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
1008	1008 40238 at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
1009	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
1010	1010 38650 at	IGFBP5	L27560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4183312,	
101	1011 1396_at	IGFBP5	L27560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	
1012	1012 40432_at		AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	-
		L, F	70000	related protein, clone MGC:9246	
101	1013 36130_f_at	MIIE	1492331	וואואמביספקלאוי ווועואי רסוווקופים רחפ	

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T	\ \ \	a	O	Q	Ţ
1	₹			Homo sapiens, Similar to serine (or	
			_ _	cysteine) proteinase inhibitor, clade E	
				(nexin, plasminogen activator inhibitor	
				type 1), member 2, clone MGC:23129	
7	1014/4124E at		AI743134	IMAGE:4578406, mRNA, complete cds	
3	41240	-		Homo sapiens, similar to unknown, clone	
				MGC:39325 IMAGE:5440447, mRNA,	
1	4045 44500 04		U79298		
2	41332 at			-inducible, endoplasmic	homocysteine-inducible, endoplasmic
				e	reticulum stress-inducible, ubiquitin-like
240	1016 20722 24	HERPI JO1	AF055001		domain member.1
2				homolog of yeast mutL gene; Human	
				homolog of yeast mutL (hPMS1) gene,	,
7.0		PDMS1	U13695	complete cds.	postmeiotic segregation 1
2	1017 323 9 at			homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
	40	1	119535	cds	ras suppressor protein 1
2	1018 32345 L at	1-000	2001	homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
Š	1010 20E44 c at	BSIL1	1,12535	cds.	ras suppressor protein 1
	32344 3 at	LAY4	IRASER	HS1 binding protein	HAX-1
	1020 39800_s_at	I VAL	2000	Human 2.4-dienovl-CoA reductase gene,	
Ç	20 100 100 1	DECRI- NADPH	U78302	exon 10 and complete cds.	2,4-dienoyl-CoA reductase
22	30104_at			Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
-	to 1 90770 000+	ADHS	M81118	complete cds.	alcohol dehydrogenase
200				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
103	1003 37707 i at	ADHS	M81118	complete cds.	alcohol denydrogenase
٤				Human alpha-1 collagen type IV gene,	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
102	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collageri
5	1005 38417 at	AMPD2	M91029	Human AMP deaminase (AMPD2) mRNA	Human AMP deaminase (AMPD2) mRNA. AMP deaminase isoform L splicing variant
<u> </u>					
102	1026 37747_at	ANX5	U05770	Human annexin V (ANX5) gene, exon 13. Jannexin V	lannexin v

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Human calmodulin (2,3,4,5 and 6, and c Human calhepsin D 8, and 9. Human cellular onc sequence). Human c-jun proto complete cds, clon Human Complete complete cds, clon deany complete cds, clon Human Complete		,				ш
Human calmodulin (CALM1) gene, exons of 2,3,4,5 and 6, and complete cds. 2,3,4,5 and 6, and complete cds. Human calthepsin D (calD) gene, exons 7, Human cellular oncogene c-fos (complete cds. Human cellular oncogene (JUN), Complete cds. Comple	1	Α	В	٥	ם	
CTSD M63138 Human cathepsin D (calD) gene, exons 7, and 9.	ì				e, exons	almodulin
CTSD M63138 8, and 9. Human cellular oncogene c-fos (complete bluman cellular oncogene c-fos (complete celos complete celos V01512 Human c-lun proto oncogene (JUN), JUN J04111 Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cels, clone hCJ-1. Human clone A9A2BRB5 (CAC)r/(GTG)n Human clone cels. Human clone cels. Human clone cels. Human clone cels. Human DNA sequence from clone 73H22 Human DNA sequence from clone 73H22 Human DNA sequence from clone 73H22 Human COS2 protein gene complete cels Human GOS2 protein gene. complete cels Human	71				, exons 7,	
C-los V01512 Human cellular oncogene c-los (complete sequence). V01512 Human cellular oncogene c-los (complete sequence). V01512 Human c-lun proto oncogene (JUN), Complete cds, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cds, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cds, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cds, clone hCJ-1. Human c-lun proto oncogene (JUN), Complete cds, clone hCJ-1. Human clone 23589 mRNA sequence Human clone 23589 mRNA sequence CCC CCCC CCCC CCCC CCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	0					athepsin D
t c-los V01512 Sequence). 1)				Human cellular oncogene c-tos (complete ly	ncogene homolog
Complete cds, clone hCJ-1. Human c-jun proto oncogene (JUN).	-1	·			Human cellular oncodene c-fos (complete	-fos FBJ murine osteosarcoma viral
Human c-jun proto oncogene (JUN), Complete cds, clone hCJ-1.	_ T				sequence).	pincogene homolog
JUN JO4111 Complete cds, clone hCJ-1.	: I			104444		opiniavian salcoma viico
at JUN J04111 complete cds, clone hCJ-1. http 4_att U79297 Human clone 23589 mRNA sequence 5_at L00946 repeat-containing mRNA repeat-containing repeat containing repeat repeat-containing repe	201	583_at		11100	ne (JUN),	/-jun avian sarcoma virus 17 oncogene
Human clone 23589 mriva sequence Human clone 23589 mriva sequence Human clone 23589 mriva sequence	~	95 at		J04111	,	homolog
Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA repeated repea		604 at		U79297	Human clone 23589 mriva sequence	
PPIA X52851 (EC 5.2.1.8).					Human clone A9A2BRB5 (CAC)n/(GTG)n	
PPIA X52851 (EC 5.2.1.8). Human cyclophilin gene for cyclophilin gene for cyclophilin (EC 5.2.1.8). (EC 5.2.1.8). (EC 5.2.1.8). Human cytochrome b5 (CYB5) gene, exon tax		10 10		U00946	repeat-containing mRNA	
CYB5	VII	100 81			Human cyclophilin gene for cyclophilin	peptidylprolyl isomerase
CYB5		3667_at	PPIA	X52851	(EC 5.2.1.8).	
g_at CYB5 L39945 Human cytochrome b5 (CYB5) gene, exon Human cytochrome b5 (CYB5) gene, exon Human cytochrome b5 (CYB5) gene, exon b4. at DLD; E3; LAD; DL L13761 gene, exon 14. s_at YWHAH; YWHAI D78577 exon2 and complete cds. exon2 and complete cds. Human DNA sequence from clone 73H22 on chromosome 6q23, complete cds. at dJ73H22.1 AL035699 at ENO2 X51956 (gamma) enolase. at GOS2 M69199 Human GOS2 protein gene, complete cds. at TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).				1 2004	Furnan cytochione 55 (51.55) generally and complete cds.	cytochrome b5
at CYB5 L39945 6 and complete cds. at DLD; E3; LAD; DL L13761 Human dihydrolipoamide dehydrogenase gene, exon 14. s_at YWHAH; YWHAI D78577 Human DNA for 14.3-3 protein eta chain, exon2 and complete cds. at dJ73H22.1 AL035699 sequence. at ENO2 X51956 Human G0S2 gene for neuron specific (gamma) enolase. tat TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	==	8459_g_at	CYBS	L39943	Human cytochrome b5 (CYB5) gene, exon	•
at DLD; E3; LAD; DL L13761 gene, exon 14. DLD; E3; LAD; DL L13761 gene, exon 14.		8458 at	CYBS	L39945	6 and complete cds.	cytochrome b5
DLD; E3; LAD; DLL13761 Gene, excit 14.3-3 protein eta chain, Human DNA for 14.3-3 protein eta chain, Human DNA sequence from clone 73H22 on chromosome 6q23, complete con chromosome 6	- I	10000			Human dihydrolipoamide dehydrogenase	dihydrolipoamide dehydrogenase
YWHAH; YWHAI D78577 exon2 and complete cds. Human DNA sequence from clone 73H22 Human DNA sequence from clone 73H22 Human DNA sequence from clone 73H22 on chromosome 6q23, complete sequence. Human ENO2 gene for neuron specific Human ENO2 gene for neuron specific (gamma) enolase. Human GOS2 protein gene, complete cds. TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	~~	6163_at		L13761	gene, exon 14.3.3 protein eta chain.	
at GOS2 M69199 Human GoS2 protein gene, complete cds. Human gene for alpha-tubulin (b alpha 1).		40 A CA		D78577	exon2 and complete cds.	14-3-3 protein eta chain
dJ73H22.1 AL035699 sequence. r ENO2 K51956 (gamma) enolase. r GOS2 M69199 Human GOS2 protein gene, complete cds. r TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	انت				Human DNA sequence from clone 73H22	
dJ73H22.1 AL035699 sequence. Human ENO2 gene for neuron specific Human ENO2 gene for neuron specific R (gamma) enolase. M69199 Human GOS2 protein gene, complete cds. Human gene for alpha-tubulin (b alpha 1).					on chromosome 6q23, complete	(TBP-like profein)
ENO2 X51956 (gamma) enolase. t G0S2 M69199 Human G0S2 protein gene, complete cds. t TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	r	1707	d 173H22 1	AL035699	sequence.	מז/פעליו (ופר יוואס אומיםיו)
ENO2 X51956 (gamma) enolase. G0S2 M69199 Human G0S2 protein gene, complete cds. TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	וני	1/9/_al			Human ENO2 gene for neuron specific	036 040 044
GOS2 M69199 Human GOS2 protein gene, complete cds. TUBA3; FLJ25113 X01703 Human gene for alpha-tubulin (b alpha 1).	7	10193 at	ENO2	X51956	(gamma) enolase.	numan gamma enorace
TUBA3; FLJ25113X01703	, ,	10000	6069	M69199	Human GOS2 protein gene, complete cds	G0S2 protein
TUBA3; FLJ25113 X01703	1	3832b_at	9000			:
		40567 at	_	13 X01703	Human gene for alpha-tubulin (b alpha 1)	alpha-tubulin

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	V	В	ပ		IJ
1040	1044 39775 at	5	N X54486		C1 inhibitor
	3			ase B (EC	G Cooking College
1045	1045 40862 i_at	CKB; CKBB	X15334	7	creatine Kinase D
·_				microtubular aggregate protein p44, exon h	nepatitis C-associated microtubular
1046	1046 37641 at	IF144: p44: MTAP4	P4D28915	$\overline{}$	aggregate protein p44
	3-110			Human gene for heterogeneous nuclear	
1047	1047 40211 at	HNRPA1: HNRNP	NPX12671		hnrnp a1 protein
	, 1771			Human gene for melanoma growth	melanoma growth stimulatory activity
1048	1048 408 at	MGSA	X54489		preprotein
				Human gene for ornithine decarboxylase	
1049	1049 36203 at	ODC1	X16277	\neg	ornithine decarboxylase (ODC)
				Human gene for very low density	
1050	1050 36873 at	VLDLR	D16532		very low density lipoprotein receptor
551	1051 34759 at		U68494	Human hbc647 mRNA sequence	
1052	1052 32805 at	AKR1C1; DD1; DD	DI U05861	dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
				Human HMG-17 gene for non-histone	
1053	1053 41231 f at	HMG17: MGC562	62 X13546		put. HMG-17 protein
3				Human HOX 5.1 gene for HOX 5.1	
1054	1054 38294 at	HOXD4; HOX4; HX17360	X17360	protein.	hox 5.1 protein
				Human hsc70 gene for 71 kd heat shock	
1055	1055 40637_at	HSP73 HSC70 HS	HSY00371	cognate protein.	71 Kd heat shock cognate protein
1056	1056 232 at	I AMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
				Human lipoprotein-associated coagulation	
				inhibitor (LACI) gene, exon 9 and	
1057	1057 40767 at	TFPI	M59499	complete cds.	lipoprotein-associated coagulation inhibitor
,	1 10000	<u>></u>	16805	Hirman lysyl oxidase (LOX) gene. exon 7. lysyl oxidase	lysyl oxidase
3	1030 30037 at	100		Human medium-chain acvl-CoA	
1050	1059 37532 at	MCAD	M91432	dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA dehydrogenase
		1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7,0007	Human metallothionein-III gene, complete	metallothionein-III
1060	1060 870_f_at	MT3; GIF; GIFB	M93311	cus.	

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	4	В	ပ	O	u
				Human metaxin (MTX) gene, complete	
1061	1061 40890 at	MTX	U46920		metaxın
				Human mRNA for erythrocyte adducin	
1062	1062 32145 at	ADD1	X58141	alpha subunit.	erythrocyte alpha adducin
1				Human mRNA for general transcription	
1063	37381 g at	TF2B	X59268	factor IIB.	IIB protein
1064	1064 33683 at	TI-227H	D50525	Human mRNA for TI-227H.	
	1			Human myocyte-specific enhancer factor	myocyte-specific enhancer factor 2A, C9
		3		2A (MEF2A) gene, last coding exon, and	form; myocyte-specific enhancer factor 2A,
1065	1065 41747 s at	MEF2A	U49020	complete cds.	C4 form
				Human NAD(P)H:quinone oxireductase	
1066	1066 38066 at	NOON	M81600	gene, exon 6.	NAD(P)H:quinone oxireductase
				Human natural killer cell enhancing factor	
1067	1067 39729_at	NKEFB	L19185	(NKEFB) mRNA, complete cds.	enhancer protein
				•	# 1
				Human nonmuscle/smooth muscle alkali	non-muscie myosin light chain; smooth
1068	1068 33994 g at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
				Human nucleic acid binding protein gene,	
1069	1069 32841_at	ZNF9; DM2; CNB	JB(U19765	complete cds.	nucleic acid binding protein
1070		NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1071 1782 s at	Op 18	M31303	complete cds.	oncoprotein 18
				Human prostaglandin D2 synthase gene,	
1072	1072 216_at	PTGDS	M98539	exon 7.	prostaglandin D2 synthase (21kD, brain)
			-	Human protein phosphatase 2A catalytic	protein phosphatase-2A catalytic subunit-
1073	1073 237 s at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
	!			Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1074	1074 812 at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
	+			Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1075	1075 33180_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
1 6	90 0000		W.21884	Human putative ribosomal protein S1	
	1076 35356 at		144 2 1004	CARTILL	

	A	В	၁	Q	Ш
				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1077	1077 491_at	PTPRG	U46116	complete cds.	receptor tyrosine phosphatase gamma
				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1078	1078 492 q at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human red cell-type low molecular weight	
				acid phosphatase (ACP1) gene, exon 6	red cell-type fow molecular weight acid
1079	1079 36611 at	ACP1	U25849	and 7, complete cds.	phosphatase
				Human SH3 domain-containing protein	
1080	1080 174 s at	SH3P18	U61167	SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
				Human spermidine synthase gene,	
1081	1081 241 g at	SRM	M64231	complete cds.	spermidine synthase
				Human sterol carrier protein-X/sterol	
				carrier protein-2 (SCP-X/SCP-2) gene,	
1082	1082 36688_at	SCP-X/SCP-2	U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	1083 32587 at	ZFP36L2; BRF2; 1007802	U07802	Human Tis11d gene, complete cds.	Tis11d .
1084	1084 31680 at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
				Human transformation-related protein	
1085	1085 36446 s at	HMG1L2	L24521	mRNA, 3' end	transformation-related protein
				Human transmembrane protein (CD59)	
1086	1086 39351_at	CD59	M84349	gene, exon 4.	CD59 protein
1087	1087 38727 at	THE	M23161	Human transposon-like element mRNA	
				Human vascular cell adhesion molecule-1	
1088	1088 41433_at	VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1089	40121 at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
1090	35973 at	НУРН	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	1091 40196_at	HYA22	D88153	HYA22 protein	HYA22
	·			hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
				thiolase/enoyl-Coenzyme A hydratase	dehydrogenase alpha-subunit of trifunctional
1092	1092 36952_at	HADHA	D16480	(trifunctional protein), alpha subunit	protein

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	ō	. 00	HUMAN;	
	ta-subunit	drogenas		
ш	hiolase be	teroid deh	C269730_	
	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein	17beta-hydroxys	BC269730_1; BC269730_2; FEN1_HUMAN;	BC269730_4
		a) dehydrogenase 4	unknown function; otein; Hypothetical ty to motifs found in urase, a te b5 containing otetical proteins [13F2.1] and [270271) litis elegans]; DNA nunclease FEN1; SE-1; DNA topothetical human hyp relatedprotein; extends ORF of trial coding acular dystrophy i536); Homo 11, BAC CIT-HSP-ntaining the hFEN1	псе.
O	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (281122) T13F2.1 [Caenorhabditis elegans] and (270271) W08D2-4 [Caenorhabditis elegans] DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy relatedprotein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1	gene, complete sequence.
C	D16481	X87176		AC004770
В	НАОНВ	HSD17B4		FEN1
A	093 39741 at	1094 36626_at		1095 41583_at
-	10933	10943		1095

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ш	BC269730 1: BC269730 2: FEN1 HUMAN:	BC269730_4	hypothetical protein CG018	hypothetical protein AF038182
O	Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein (AF038536); Homo sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-11-28, 1-28, RC2563730) containing the hFEN 1-1-28.		hypothetical gene CG018	hypothetical gene supported by AF038182; BC009203
ပ		AC004770	U50527	AF038182
8		FEN1	CG018	LOC90355
A		096 34224_at	097 1527 s at	1098 33466_at
		109	60	109

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ш	R32184_3		hypothetical protein, similar to (AC007017) putative RNA helicase A [Arabidopsis thaliana]			
Q	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (AL021106) from Drosophila melanogaster: Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRAIL_predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) T01C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C- terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against [R32184_3; R32184_3;	hypothetical protein		hypothetical protein	hypothetical protein 23851	hypothetical protein 24636
0	φ	AA015605	AL079292	AF007130	AF035313	A 651368
α	7 SEA	Ft.120811	1 OC54505	LOC54104	LOC56007	LOC55977
V		1100 38440 s at	∯ ≅		103 39517 at	1104 41561_s_at
			5	12	읃	=



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	V	2	د		
1105	105 41128_at	LOC92703	AF070537	hypothetical protein BC0130/3	
1106	106 38972 at	LOC115207	AF052169	hypothetical protein BC013764	
1107	и .	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108	108 39960 at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109	1109 38837 at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110	1110 35142 at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
1111	34830	DKFZP564K0822 W25986	W25986	hypothetical protein DKFZp564K0822	
1112	31852 at	DKFZP5640043	AL050390	hypothetical protein DKFZp5640043	
1113	1113 33895_at	DKFZP586F1318 AL050373	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114	1114 39692 at	DKFZP586F2423	F2423 AL080209	hypothetical protein DKFZp586F2423	
1115		FLB6421	Al133727	hypothetical protein FLB6421	
1116	1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117	1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118	1118 36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119	1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120	1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
1121	1121 33173 q at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122	1122 39923 at	FLJ10971	A1935420	hypothetical protein FLJ10971	
				hypothetical protein FLJ11021 similar to	
1123	1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	
1124	1124 33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125	1125 35709 at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126	1126 38141 at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127	1127 40859 at	FLJ11806	AI561196	hypothetical protein FLJ11806	
1128	1128 41177 at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129	1129 41434 at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130	1130 36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131	1131 32222 at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132	1132 38710 at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133	1133 38652 at	FLJ20154	AF070644	hypothetical protein FLJ20154	
138	1134 40868 at	FLJ20274	AA442799	hypothetical protein FLJ20274	
138	1135 34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
113	1136 34857_at	FLJ20986	Z24724	hypothetical protein FLJ20986	
113,	1137 32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138	1138 40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
133	1139 33915 at	FLJ23027	W22655	hypothetical protein FLJ23027	

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11403	1140 35198_at	LOC57146		4796	hypothetical protein from clone 24796
11413	1141 38483 at	HSA011916	AJ011916		hypothetical protein
11424	11236_at	HSU79252	U79252		hypothetical protein HSU79252
1143	1143 38443 at	MGC14433	U79291	hypothetical protein MGC14433	
1144	1144 39811_at	MGC2749	AA402538	hypothetical protein MGC2749	
				hypothetical protein MGC2840 similar to a	
1145	1145 32051_at	MGC2840	AJ224875	putative glucosyltransferase	glucosyltransferase
1146 35219	35219_at	MGC3047	AL050202	hypothetical protein MGC3047	
11474	1147 41696_at	MGC3077	AI620381	$\neg 1$	
				hypothetical protein MGC4276 similar to	hypothetical protein MGC4276 similar to
1148	1148 41147_at	MGC4276	AF038186	CG8198	CG8198
1149	1149 37242_at	MGC5149	U79260	hypothetical protein MGC5149	-
1150	1150 36975 at	MGC8721	W26659	hypothetical protein MGC8721	
1151	35677_at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	1152 32504 at	MY014	AW024812	hypothetical protein My014	
1153	1153 38106 at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
1154	1154 37640 at	HPRT1	M31642	hypoxanthine phosphoribosyttansferase 1. (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyltransferase 1
1155 1039	1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
				Incremental processing processing and the processing decorate processing protein-4 (IGEBP4)	
1156	1156 39781 at	IGFBP4	U20982	gene, promoter and complete cds.	insulin-like growth factor binding protein-4
1157	1157 38046 at	ᆂ	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	1158 218_at	X	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	37690 at	ILVBL	U61263	iNB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160	1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161	1161 1237 at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	1162 34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1 alpha 4 protein	alpha 4 protein

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				perfamily containing	
1163	38636_at	ISLR	AB003184		ISLH
	1			IMP (inosine monophosphate)	IMP (inosine monophosphate)
1164	1164 40695 at	IMPDH1	J05272	dehydrogenase 1	dehydrogenase 1
1165		IBTK	AL050018	inhibitor of Bruton's tyrsoine kinase	hypothetical protein
	1			nant	inhibitor of DNA binding 1, dominant
1166	1166 36617 at		X77956		negative helix-loop-helix protein
				inhibitor of DNA binding 2, dominant	
1167	1167 41215 s at	ID2	D13891		Id-2H
				inhibitor of kappa light polypeptide gene	
1168	1168 34344 at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169[37659 at	IMMI	L42572		transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
11170	1170 755 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
11171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
1172	1172 36154 at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
	1				lithium-sensitive myo-inositol
11173	1173 32697 at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
1174	1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2 myo-inositol monophosphatase 2	myo-inositol monophosphatase 2
1175	1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176	1176 41049 at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177	1177 851_s_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
				insulin-like growth factor 1 (somatomedin	
1178	1178 38737 at	IGF1	X57025	(5)	insulin-like growth factor I
				insulin-like growth factor 1 (somatomedin	
11175	1179 1501 at	IGF1	X57025	(0)	insulin-like growth factor I
1180	0 160027 s at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
				insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2 insulin-like growth factor binding protein 2
118	1181 40422_at	IGFBP2	X16302	(36kD)	(36kD)
,	1024	700101	MEDAGS	ine like growth factor hinding protein 4	insulin-like growth factor binding protein 4 linsulin-like growth factor binding protein 4
2	1182 1737_s_at	l'arbr4	INIOZ403	manufacture grown lactor and grown	

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1183	OOR9 at	IGFRP7	119182	insulin-like growth factor binding protein 7	
3	1100 2002		10000	integral mombrone protein 1	integral membrane protein 1
1184	37991_at	LMI	138861	megral memorane protein i	megla memorano process
				integral membrane protein; swiss-prot	
1185	1185 37326 at	A4	U93305	differentiation in intestinal epithelium	LIM domain only 6
1186	1186 41163 at	48	AL109672	integral type I protein	p24B protein
					integrin beta 1 isoform 1A precursor; integrin
					beta 1 isoform 1B precursor; integrin beta 1
					isoform 1C-1 precursor; integrin beta 1
				integrin beta 1 subunit precursor; Human	isoform 1D precursor; integrin beta 1 isoform
1187	1187 32808 at	ITGB1; CD29; FN	FN(X07979	mRNA for integrin beta 1 subunit.	1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	1188 1195_s_at	ICAP-1A	AF012024	protein 1	protein
1189	1189 120 at	ITGA1	X68742	integrin, alpha 1	
1190	1190 37484 at	ITGA1	X68742	integrin, alpha 1	
1191	1191 36892 at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
				integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071_at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	1193 39754 at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058 s at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
				integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681 at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	1196 35365 at	I.K	U40282	integrin-linked kinasė	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; afternatively translated;	
				long form; interacts with adenovirus E3-	_
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				alternatively translated; short form; Homo	
				sapiens FIP2 alternatively translated	
1197	1197 41743_i_at	OPTN; NRP; FIP2/AF061034	2AF061034	mHNA, complete cds.	FIFZ

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T				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated,	
				long form; interacts with adenovirus E3-	
-				14.7KDa, a TNF-alpha cytolysis	
_				antagonist; leucine zipper protein;	
				alternatively translated; short form; Homo	
				sapiens FIP2 alternatively translated	
198	1198 41742 s at	OPTN; NRP; FIP2	P2/AF061034	mRNA, complete cds.	FIP2
T				interferon induced transmembrane protein i	interferon induced transmembrane protein interferon induced transmembrane protein 1
199	1199 676 g at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675 at	IFITM1	J04164	1 (9-27)	(9-27)
	1			interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745 at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202	1202 1456 s at	IF116	M63838		interferon-gamma induced protein
1203	II	IFI30	J03909		interferon, gamma-inducible protein 30
1204	1204 39728 at	IFI30	103909		interferon, gamma-inducible protein 30
					interferon-induced protein with
1205	1205 32814 at	IFIT1	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679 at	IFRD1	Y10313		PC4 protein
1207	1207 1368 at	IL1R1	M27492	interleukin 1 receptor, type l	interleukin 1 receptor, type I
1208	1208 33228 q at	IL10RB	AI984234	interleukin 10 receptor, beta	
1209	1209 33227 at	IL10RB	Al984234	interleukin 10 receptor, beta	
1210	1210 38969 at	IL27	A1828168	interleukin 27	
1211	1211 38299 at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r at	11.8	M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	36189 at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030 at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776 at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431 at	S	AB023153	intestinal cell kinase	KIAA0936 protein
				IQ motif containing GTPase activating	CTDscs activation like protein
1217	1217 1825 at	IGGAP1	L330/5	protein i	las a i rase-activating-line protein

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_	∢	В	٥	(TOUVIN) L SOUSSESSIPHING TO THE	
218	1218 39023 at	IDH1	AF020038		NADP-dependent isocitrate dehydrogenase
	20000			NAD+) beta	
1219	1219 40112_at	ПРНЗВ	AA522698	Isocillate deligal ogenese o (1915)	NAD+-specific isocitrate dehydrogenase
- 000	4000 40111 0 at	IDH3B	U49283	la	beta precursor
221	a la	KIAA1162	AL021396	$\overline{}$	hypothetical protein
201		dJ196E23.1	Z97632	isoform 2 match: protein Q99991	Coloned 4DNA synthetese
1223		IARS	U04953	isoleucine-tRNA synthetase	Isoleucyl-think sylmitetase
1004	1224 36985 at	IDI	X17025	isopentenyl-diphosphate delta isomerase isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
7		H	A E064084	isoprenylcysteine carboxyl methyltransferase	prenylcysteine carboxyl methyltransferase
1225	1225 41775_at	2			
1226	1226 34877_at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine Kinase)	IMA protein
1227	1227 34318 at	JM4	AJ005896	JM4 protein	SINIA PIOCEIII
122R	1228 40957 at	JJAZ1	D63881	joined to JAZF1	וסווופם וס שאבר ו
1229	1229 41250 at	JTV1	U24169	JTV1 gene	- N I O
1230	1230 41483 s at	ONOC	X56681	jun D proto-oncogene	June protein
1231	1231 1612 s at	ONOC	X56681	jun D proto-oncogene	Jund protein
1232	1232 40464 g at	KPNB2	U70322	karyopherin (importin) beta 2	Transporting Profession 5
1233	1233 39028 at	KPNB3	Y08890	karyopherin (importin) beta 3	hall of the billion of the state of the stat
1234	1234 35725 at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	Karyophenn anipir o
15.5	1235 32487 s at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	
	2 22			katanin p60 (ATPase-containing) subunit	
1236	1236 32708 g at	KATNA1	AI191768	A1	
	-6-2-			KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1237	1237 37386_i_at	KDELR1	X55885	reticulum protein retention receptor 1	NOEL receptor
			277	KDEL (Lys-Asp-Giu-Leu) endoplasmic	KDEL receptor 2
1238	1238 39080_at	KDELHZ	WI88458	KDEL (Lvs-Asp-Glu-Leu) endoplasmic	
100	1000000	KDFI R3	AL035081	reticulum protein retention receptor 3	hypothetical protein
Š Š	1239 33402 at	AB026190	AB026190	Kelch motif containing protein	Kelch motif containing protein
124	1241 32329 at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type II intermediate mament of mair Kerami
		KUDDBK1	M88108	KH domain containing, KNA binding, signal transduction associated 1	p62
124	1242[39346_at	I SQUOUN	20100111		

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et KIAA0009 D13634 KIAA0002 gene product K et KIAA0022 D14664 KIAA0022 gene product K et KIAA0022 D26067 KIAA0022 gene product K et KIAA0033 Protein K et KIAA0062 D31887 KIAA0036 protein et KIAA0096 D43636 KIAA0097 gene product et KIAA0096 D43948 KIAA0097 gene product et KIAA0097 D43948 KIAA0098 las a sequence of KIAA0098 las product Is kIAA0098 Is kIAA0099 Is kIAA0099 Is kIAA0099 Is kIAA0099 Is kIAA0199 Is kIAA0199 Is a kIAA0199	_	∢	8	ပ	U	IJ
### KIAA0022 D14664 KIAA0022 gene product ### KIAA0033 D28667 KIAA0033 protein ### KIAA0033 D28657 KIAA0033 protein ### KIAA0062 D038531 KIAA0035 protein ### KIAA0096 D43936 KIAA0097 gene product ### KIAA0097 D43948 KIAA0098 is a human counterpart of ### MO3850 D43938 KIAA0097 gene product ### KIAA0098 D43950 mANA for KIAA0098 - Homo sapiens ### KIAA0102 D14658 KIAA0100 gene product ### KIAA0121 D50911 KIAA0110 gene product ### KIAA0121 D50911 KIAA0111 gene product ### KIAA0121 D50911 KIAA0112 gene product ### KIAA0121 D50911 KIAA0113 protein ### KIAA0122 D63986 KIAA013 protein ### KIAA0132 D83996 KIAA013 protein ### KIAA0132 D83996 KIAA013 protein ### KIAA0139 D80001 KIAA013 protein ### KIAA0139 D80001 KIAA013 protein ### KIAA0139 D80006 KIAA0139 gene product ### KIAA0139 D80006 KIAA0139 protein ### KIAA0139 D80006 KIAA0139 gene product #### KIAA0139 D80006 KIAA0139 gene product ### KIAA0139 D80006 KIAA0139 gene product #### KIAA0139 D80006 KIAA	1243	32679 at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
KIAA0033 D26067 KIAA0033 protein KIAA0062 D31887 KIAA0062 protein KIAA0096 D43636 KIAA0096 protein KIAA0097 D43636 KIAA0096 protein KIAA0097 D43638 KIAA0098 protein KIAA0097 D43848 KIAA0098 protein KIAA0097 D43848 KIAA0098 protein KIAA0097 D43848 KIAA0098 protein KIAA0098 D43947 KIAA0098 protein KIAA0102 D14658 KIAA0100 gene product KIAA0111 D21853 KIAA0110 gene product KIAA0112 D21853 KIAA0110 gene product KIAA0113 D6091 KIAA0112 gene product KIAA0113 D60926 KIAA0113 gene product KIAA0113 D60926 KIAA0130 gene product KIAA01143 D65928 KIAA0130 gene product KIAA0115 D63926 KIAA0130 gene product KIAA0116 D73994 KIAA0130 gene product KIAA0117 D73994 KIAA0170 gene product KIAA0119	1244	34760 at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
KIAA0062 D31887 KIAA0062 protein KIAA0077 D38521 KIAA0097 protein KIAA0096 D43636 KIAA0097 gene product M KIAA0097 D43948 KIAA0097 gene product M KIAA0097 D43948 KIAA0097 gene product M KIAA0098 D43950 MRNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098; Horno saptiens KIAA0110 D43947 KIAA0102 gene product M KIAA0111 D50911 KIAA0102 gene product M KIAA0132 D50926 KIAA0112 gene product M KIAA0133 D50926 KIAA0112 gene product M KIAA0136 D50926 KIAA0112 gene product M KIAA0137 D50926 KIAA0112 gene product M KIAA0136 D50926 KIAA0132 gene product M KIAA0143 D50926 KIAA0132 gene product M KIAA0157 D50926 KIAA0132 gene product M KIAA0157 D63877 KIAA0137 protein KIAA0140	1245		KIAA0033	D26067	KIAA0033 protein	
KIAA0077 D38521 KIAA0077 protein KIAA0096 D43636 KIAA0096 protein KIAA0097 D43948 KIAA0097 gene product KIAA0097 D43948 KIAA0098 js a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is rot identified. MAD121 B43950 MRNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098; Homo saptens mRNA for KIAA0098 protein, partial cds. I KIAA0111 MRAA0102 KIAA0112 D43947 KIAA0102 gene product I KIAA0114 KIAA0111 D50926 KIAA0102 gene product I KIAA0118 KIAA0113 D50926 KIAA0118 gene product I KIAA0119 KIAA0138 D50928 KIAA0138 gene product I KIAA0119 KIAA0112 D63477 KIAA0138 gene product I KIAA0119 KIAA0113 D63477 KIAA0118 gene product I KIAA0118 KIAA0112 D79996 KIAA01172 protein KIAA0119 KIAA0114 D80001 KIAA01172 protein KIAA0119 KIAA0195 D80001 KIAA0119 protein KIAA0196 D83776 KIAA0196 gene product <td>1246</td> <td></td> <td>KIAA0062</td> <td>D31887</td> <td>KIAA0062 protein</td> <td></td>	1246		KIAA0062	D31887	KIAA0062 protein	
KIAA0096 D43636 KIAA0096 protein KIAA0097 D43948 KIAA0097 gene product KIAA0097 D43948 KIAA0097 gene product KIAA0097 RAPA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098; Homo sapiens KIAA0102 D143950 MRNA 61 KIAA0098; Homo sapiens KIAA0102 D14658 KIAA0102 gene product KIAA011 D21853 KIAA0111 gene product KIAA012 D50911 KIAA0132 gene product KIAA013 D50928 KIAA0132 gene product KIAA0143 D50928 KIAA0132 gene product KIAA0150 D50928 KIAA0132 gene product KIAA0150 D50928 KIAA0132 gene product KIAA0150 D79994 KIAA0152 protein KIAA0170 D79995 KIAA0172 gene product KIAA0171 D79994 KIAA0172 gene product KIAA0172 D89001 KIAA0174 gene product KIAA0173 D89001 KIAA0174 gene product KIAA0173	1247		KIAA0077	D38521	KIAA0077 protein	
KIAA0097 D43948 KIAA0097 gene product MAA0097 MAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. had1413 CDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098 protein, partial cds. It KIAA0102 D43950 MAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. had1413 contained to KIAA0102 MAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. had1413 contained to KIAA0102 MAA0098 is a human counterpart of the mouse chaperon of KIAA0102 gene product MAA0098 is a human counterpart of the mouse chaperon of KIAA0113 gene product MAA0102 is a manual contained to the mouse chaperon of the m	1248	37718 at	KIAA0096	D43636	KIAA0096 protein	
KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. hao1413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098 i. Homo sapiens KIAA0100 D43947	1249	37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
Mouse chaperonin containing TCP-1 gene. Start codon is not identified.					KIAA0098 is a human counterpart of	
May		-			TCP-1	
Being Start Codon is not identified.			_			
Carrier of the cape in the c					gene. Start codort is not identified.	
RIAA0098					MAD 14 13 COINT CIOILE IOI NICASOSO IIAS A	
KIAA0098 D43950 mRNA for KIAA0098; Homo sapiens KIAA0100 D43947 KIAA0100 gene product KIAA0102 D14658 KIAA0102 gene product KIAA0102 D14658 KIAA0102 gene product KIAA0121 D21853 KIAA0111 gene product KIAA0121 D50911 KIAA0111 gene product KIAA0136 D50926 KIAA0121 gene product KIAA0138 D50928 KIAA0138 gene product KIAA0143 D63477 KIAA0138 gene product KIAA0152 D63877 KIAA0172 gene product KIAA0170 D79994 KIAA0172 gene product KIAA0174 D79996 KIAA0174 gene product KIAA0179 D80001 KIAA0179 gene product KIAA0191 D80006 KIAA0179 gene product KIAA0191 D83776 KIAA0199 gene product KIAA0199 D83777 KIAA0199 gene product KIAA0199 D83779 KIAA0199 gene product KIAA0199 D83779 KIAA0199 gene product KIAA0199 D83779 KIAA0199 gene produ					2-bp insertion between 736-737 of the	
KIAA0098 D43950 mRNA for KIAA0098 protein, partial cds. KIAA0100 KIAA0102 D14658 KIAA0102 gene product H KIAA0121 D21853 KIAA0111 gene product H KIAA0121 D50911 KIAA0121 gene product H KIAA0138 D50926 KIAA0138 gene product H KIAA0143 D63477 KIAA0138 gene product H KIAA0152 D63486 KIAA0132 gene product H KIAA0152 D63486 KIAA0152 gene product H KIAA0157 D79992 KIAA0172 protein H KIAA0172 D79994 KIAA0172 protein H KIAA0174 D79996 KIAA0174 gene product H KIAA0179 D80000 KIAA0179 protein KIAA0184 protein KIAA0184 D80006 KIAA0191 protein KIAA0195 KIAA0195 D83776 KIAA0195 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202					sequence of KIAA0098.; Homo sapiens	
KIAA0100 D43947 KIAA0100 gene product KIAA0102 D14658 KIAA0102 gene product KIAA0121 D21853 KIAA0111 gene product KIAA0121 D50911 KIAA0121 gene product KIAA0138 D50926 KIAA0138 gene product KIAA0143 D63477 KIAA0138 gene product KIAA0152 D63486 KIAA0143 protein KIAA0152 D63486 KIAA0152 gene product KIAA0157 D79992 KIAA0172 protein KIAA0172 D79994 KIAA0172 protein KIAA0174 D79996 KIAA0174 gene product KIAA0179 D80000 KIAA0179 protein KIAA0191 D80006 KIAA0194 protein KIAA0193 D83776 KIAA0195 gene product KIAA0195 D83779 KIAA0195 gene product KIAA0196 D83779 KIAA0196 gene product KIAA0196 D83779 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0202 D86971 KIAA022 protein	1250		KIAA0098	D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
KIAA0102 D14658 KIAA0102 gene product KIAA0111 D21853 KIAA0111 gene product KIAA0121 D50911 KIAA0121 gene product KIAA0138 D50926 KIAA0138 gene product KIAA0143 D63477 KIAA0138 gene product KIAA0152 D63486 KIAA0132 gene product KIAA0157 D63877 KIAA0152 gene product KIAA0170 D79992 KIAA0172 protein KIAA0172 D79994 KIAA0172 protein KIAA0174 D79996 KIAA0174 gene product KIAA0179 D800001 KIAA0179 protein KIAA0191 D80006 KIAA0194 protein KIAA0191 D83776 KIAA0195 gene product KIAA0195 D83779 KIAA0195 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein	1251	39783 at	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
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It KIAA0170 D79992 KIAA0170 gene product KIAA0172 D79994 KIAA0172 protein KIAA0174 D79996 KIAA0174 gene product KIAA0179 D80001 KIAA0179 protein KIAA0184 D80006 KIAA0184 protein KIAA0191 D83776 KIAA0191 protein KIAA0195 D83777 KIAA0193 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0205 D86957 KIAA0205 protein KIAA0205 DR6971 KIAA0205 protein	1259	37642 at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
KIAA0172 D79994 KIAA0172 protein KIAA0174 D79996 KIAA0174 gene product KIAA0179 D80001 KIAA0179 protein KIAA0184 D80006 KIAA0184 protein KIAA0191 D83776 KIAA0191 protein KIAA0195 D83777 KIAA0193 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0205 protein KIAA0255 protein KIAA0255 protein	1260	32661 s at	KIAA0170	D79992	KIAA0170 gene product	KIAA0170 gene product
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KIAA0179 D80001 KIAA0179 protein KIAA0184 D80006 KIAA0184 protein KIAA0191 D83776 KIAA0191 protein KIAA0193 D83777 KIAA0193 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0255 D86971 KIAA0225 protein	1262	36942 at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
KIAA0184 D80006 KIAA0184 protein KIAA0191 D83776 KIAA0191 protein KIAA0193 D83777 KIAA0193 gene product KIAA0196 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0255 D86978 KIAA0225 protein	1263	31863 at	KIAA0179	D80001	KIAA0179 protein	
KIAA0191 D83776 KIAA0191 protein KIAA0193 D83777 KIAA0193 gene product KIAA0195 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0225 D86978 KIAA0227 protein	1264	37734 at	KIAA0184	D80006	KIAA0184 protein	
KIAA0193 D83777 KIAA0193 gene product KIAA0195 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0225 D86978 KIAA0227 protein	1265	41669 at	KIAA0191	D83776	KIAA0191 protein	
KIAA0195 D83779 KIAA0195 gene product KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0225 D86971 KIAA0217 protein	1266	36192 at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
KIAA0196 D83780 KIAA0196 gene product KIAA0202 D86957 KIAA0202 protein KIAA0217 D86971 KIAA0217 protein KIAA0225 D86978 KIAA0227 protein	1267	38056 at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
KIAA0202 D86957 KIAA0217 D86971	1268	38419 at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
KIAA0217 D86971	1269	38067 at	KIAA0202	D86957	KIAA0202 protein	
SATOR ST KIAANSSK INSEATR	1270	32586 at	KIAA0217	D86971	KIAA0217 protein	
	1271	38728	KIAA0225	D86978	KIAA0225 protein	

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1272 4	40971_at	KIAA0229	D86982	KIAA0229 protein	
2733	1273 37748 at	KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
2743	1274 38892 at	KIAA0240	D87077	KIAA0240 protein	
1275 40765	0765 at	KIAA0251	D87438	KIAA0251 protein	
2764	1276 41634 at	KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
12773	36971_at	KIAA0257	D87446	KIAA0257 protein	
1278 32237	2237 at	KIAA0265	D87454	KIAA0265 protein	
1279 39405	9405 at	KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
2803	17	KIAA0276	D87466	KIAA0276 protein	
1281 38592	8592 s at	KIAA0284	A1828210	KIAA0284 protein	
1282 41381	1381_at	KIAA0308	AB002306	KIAA0308 protein	
1283 37943	17943_at	KIAA0321	AB002319	KIAA0321 protein	-
2843	1284 32592 at	KIAA0323	AB002321	KIAA0323 protein	
1285 39797	19797 at	KIAA0349	AB002347	KIAA0349 protein	
1286 34661		KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
287	1287 32208 at	KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
288	1288 32223 at	KIAA0365	AB002363	KIAA0365 gene product	
1289	1289 33442 at	KIAA0367	AB002365	KIAA0367 protein	
1290	1290 35830 at	KIAA0370	AB002368	KIAA0370 protein	
1291	1291 40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
1292	1292 34837 at	KIAA0376	AB002374	KIAA0376 protein	
1293	1293 41457 at	KIAA0423	AB007883	KIAA0423 protein	
1294	1294 35167 at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
1295	1295 33340 at	KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
1296	1296 40805 at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
1297	1297 32091 at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
1298	1298 41243 at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
1299	1299 32206 at	KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
380	1300 36069 at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
1301	1301 37230 at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
1302	1302 33893 r at	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
1303	1303 34445 at	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
1304	1304 35318 at	KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
1305	1305 35786_at	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
1306	1306 35762_at	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
1307	1307 41830_at	KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

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조조조	B KIAA0514 KIAA0515 KIAA0532	C AB011086 AB011087 AB011104	KIAA0514 gene product KIAA0515 protein KIAA0532 protein	KIAA0514 protein KIAA0515 protein KIAA0532 protein
KIAA0537 KIAA0546 KIAA0564		AB011109 AB011118 AB011136	KIAA0537 gene product KIAA0546 protein KIAA0564 protein	KIAA0537 protein KIAA0546 protein KIAA0564 protein
KIAA0592	1 1	AB011164	KIAA0592 protein	KIAA0592 protein KIAA0594 protein
KIAA0605		AB011177	KIAA0605 gene product	KIAA0605 protein
KIAA0610 KIAA0618		AB011182 AL080109	KIAA0610 protein KIAA0618 gene product	NAAUS IU protein hypothetical protein
KIAA0625		AB014525	KIAA0625 protein	KIAA0625 protein
KIAA0626	1	AB014526 AB014530	KIAAU626 gene product KIAA0630 protein	KIAA0630 protein
KIAA0648	1 1	AB014548	KIAA0648 protein	KIAA0648 protein
KIAA0650		AB014550	KIAA0650 protein	KIAA0650 protein
KIAA0662 KIAA0663	\neg	AB014562 AB014563	KIAA0662 gene product KIAA0663 gene product	KIAA0663 protein
KIAA0674	Т	AB014574	KIAA0674 protein	KIAA0674 protein
KIAA0678		AB014578	KIAA0678 protein	KIAA0678 protein
KIAA0692		AB014592	KIAA0692 protein	KIAAU692 protein
KIAA0700	T	AB014600	KIAA0700 protein	KIAA0700 protein
KIAA0716	I	AB018259	KIAA0716 gene product	KIAA0716 protein
KIAA0721		AB018264	KIAA0721 protein	KIAA0721 protein
KIAA0725 KIAA0729	1	AB018268 AR018272	KiAA0725 protein KIAA0729 protein	KIAA0725 protein KIAA0729 protein
KIAA0738		AB018281	KIAA0738 gene product	KIAA0738 protein
KIAA0740		AB018283	KIAA0740 gene product	KIAA0740 protein
KIAA0746		AB018289	KIAA0746 protein	KIAA0746 protein
KIAA0747		AB018290	KIAA0747 protein	KIAA0747 protein
KIAA0750		AB018293	KIAA0750 gene product	KIAA0750 protein
KIAA0769		AB018312	KIAA0769 gene product	KIAA0769 protein
KIAA0776		AB018319	KIAA0776 protein	KIAA0776 protein
KIAA0779		AB018322	KIAA0779 protein	KIAA0779 protein
KIAA0781	•	AB018324	KIAA0781 protein	KiAAU/81 protein

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1344 41224 at	KIAA0788	AB018331	KIAA0788 protein	KIAA0788 protein
15	KIAA0795	AB018338	KIAA0795 protein	KIAA0795 protein
1346 39614 at	KIAA0802	AB018345	KIAA0802 protein	KIAA0802 protein
1347 36588 at		AB018353	KIAA0810 protein	KIAA0810 protein
		AB020633	KIAA0826 protein	KIAA0826 protein
1349 40455 at		AB020637	KIAA0830 protein	KIAA0830 protein
1350 41372 at		AB020638	KIAA0831 protein	KIAA0831 protein
1351 36888 at		AB020648	KIAA0841 protein	KIAA0841 protein
1352 39597 at		AB020650	KIAA0843 protein	KIAA0843 protein
1353 41503 at		AB020661	KiAA0854 protein	KIAA0854 protein
1354 38730 at		AB020671	KIAA0864 protein	KIAA0864 protein
1355 39021 at		AB020684	KIAA0877 protein	KIAA0877 protein
1356 32215) te	AB020685	KIAA0878 protein	KIAA0878 protein
		AB020689	KIAA0882 protein	KIAA0882 protein
1358 35720 at		AB020700	KIAA0893 protein	KIAA0893 protein
1359 40423 at		AB020710	KIAA0903 protein	KIAA0903 protein
1360 41421 at		AB020716	KIAA0909 protein	KIAA0909 protein
1361 41498 al		AB020718	KIAA0911 protein	KIAA0911 protein
1362 39777 at		AF075587	KIAA0916 protein	protein associated with Myc
1363 32735 at		AB023148	KIAA0931 protein	KIAA0931 protein
33408		AB023151	KIAA0934 protein	KIAA0934 protein
35369	t KIAA0937	AB023154	KIAA0937 protein	KIAA0937 protein
3323	I KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
32740	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
1368 35794 at		AB023159	KIAA0942 protein	KIAA0942 protein
1369 41595 at	II KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
1370 38649 at	t KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
1371 34396_at		AB023195	KIAA0978 protein	KIAA0978 protein
1372 32085 at	It KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
35199	It KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
32769	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
1375 34751 at	KIAA0997	Al970189	KIAA0997 protein	
H I	at KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
1377 33193_at		AW052084	KIAA1001 protein	
1378 36002_at		AB023229	KIAA1012 protein	KIAA 1012 protein
1379 35802_e	at KIAA1014	AB023231	KIAA1014 protein	KIAA1014 protein

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1	A	a	٠	1	VIA 8 4000 - 100
1380 39615	9615_at	KIAA1026	AB028949	KIAA1026 protein	NIAA IOZO PIOIGIII
13813	381 34089_at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
1382 41651	1651 at	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
13834		KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
13843	1384 35163_at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
13853	1385 38778_at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
13864	1386 41268 g at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
1387 4	1387 40855 at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
13883	1388 39400_at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
1389 33877	13877 s at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
13903	1390 34688 at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
13913	1391 33924 at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
13923	1392 32508 at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
13934	1393 41179 at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394 34839	34839_at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395 33457	33457 at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396 36814	36814_at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397 34274	34274 at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398 37617	37617 at	KIAA1128	U90912	KIAA1128 protein	
1399		KIAA1157	W29087	KIAA1157 protein	
14007	1400 40308_at	KIAA1240	A1830496	KIAA1240 protein	
1401 33811	33811_at	KIAA1254	AI761567	KIAA1254 protein	
1402	1402 38674 at	KIAA1354	AA115140	KIAA1354 protein	
1403	1403 32730 at	KIAA1750	AL080059	KIAA1750 protein	
1404	1404 32171_at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	1405 39897 at	KIAA1966	N36997	KIAA1966 protein	
1406	1406 32846 s at	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
1407	1407 39057 at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408;	1408 32079 at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	1409 33345_at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	1410 34294 at	KIFC3	AL041493	kinesin family member C3	
141	1411 41474 at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412	1412 40779 at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	1413 34216 at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
7,7	1414 38768 of	НАПНЯС	X96752	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	3-hydroxyacyl-CoA dehydrogenase
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14154	41485_at	LDHA	X02152	enase A	lactate dellydlogeriase A
14162	1416 288 s_at	LBR	L25931		lamin B receptor
-				laminin receptor 1 (67kD, ribosomal	
1417 256 s	56 s at	LAMR1	M14199	protein SA)	laminin receptor 1
1418 37671	17671 at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419 581	81 at	LAMB1	M61916	laminin, beta 1	aminin B1
	t			lic synthetase component C-	
1420 39441	9441 at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
				ing growth factor beta	latent transforming growth factor beta
1421	1421 1495 at	LTBP1	M34057		binding protein 1 precursor
				latent transforming growth factor beta	
1422 3	1422 37906 at	LTBP2	237976		LTBP-2 precursor
				lectin, galactoside-binding, soluble, 1	
1423	1423 33412 at	LGALS1	A1535946	(galectin 1)	
				lectin, galactoside-binding, soluble, 3	
1424 35367	35367 at	LGALS3	AB006780	(galectin 3)	galectin-3
				lectin, galactoside-binding, soluble, 3	
1425	1425 37754 at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
				lectin, galactoside-binding, soluble, 8	
1426 1846	1846 at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
1427	1427 34267 r at	LEPR	U50748	leptin receptor	leptin receptor
1428	1428 33830 at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	1429 33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
4 4 30	1430 38085 21	EPROTI 1	AFORSEOR	lentin receptor overlapping transcript-like 1 brain mv047 protein	brain mv047 protein
				leucine rich repeat (in FLII) interacting	
1431	1431 41320_s_at	LRRFIP1	0969A	protein 1	transcription repressor
1432	1432 39967_at	LDOC1	AB019527	leucine zipper, down-regulated in cancer 1 LDOC1 protein	LUCC1 protein
1433	1433 41754 at	LRPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
1434	1434 37470_at	LAIR1	AF013249	leukocyte-associated Ig-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	1435 38081 at	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	1436 36062_at	LPXN	AF062075	leupaxin	leupaxin
1437	1427 35078 21	RPS29	A 541542	libtest16.A02.r bvnorm Homo sapiens cDNA 5' mRNA sequence.	
2007		111 OEV	A1524873	like mouse brain profein F46	
1438	1438 3968/_at	E40L	M324013	וואם וווסמסם בומוון בוסנסווי ביס	

in E46 hypothetical protein hase D-interacting hypothetical protein nase D-interacting e suppressors of KIAA0671 protein se TC10-alpha ce TPR-containing, brotein has a variant n CSTF-64 KIAA0689 protein old istacking protein limitigen-like breast tumor autoan kIAA0430 protein cid, cholesterol hysosomal acid lipase presease) hypothetical lipase presease) hypothetic						L
E46L AL050282 like mouse brain protein E46 https://doi.org/10.000282 like mouse brain protein E46 https://doi.org/10.00000000000000000000000000000000000	T	Φ	8	O	O	IJ
E46L AL050282 like mouse brain protein E46 https://doi.org/10.1018/220 W27233 substance of 220 kDa likely ortholog of rat kinase D-interacting substance of 220 kDa likely ortholog of mouse suppressors of k AL043108 likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein likely ortholog of mouse arrient LIMS1 AB014589 likely ortholog of mouse variant LIMS1 LIMS2 LIM and senescent cell antigen-like LIM and SH3 protein 1 LIMS4 LIMS4 LIM and SH3 protein 1 LIMS4 LIMS6 LIM domain kinase 2 LIM and SH3 protein 1 LIMS4 LIMS5 LIM domain winase 2 LIM domain winase 2 LIM domain winase 3 LIM domain winase 4 LIM domain winase 6 LIM domain winase 7 LIM domain winase 8 LIM domain winase 9 LIM do	i c	20686 g at		AL050282		lypothetical protein
KIDINS220 W27233 Substance of 220 kDa SOCS5 AB014571 Cytokine signalling 5 Cytokine signalling 6 Cytokine	60	33000 g at	1011	A1 050282		ypothetical protein
KIDINS220 W27233 Substance of 220 kDa SOCS5 AB014571 Cytokine signalling 5 Coton TC10 AL043108 Iikely ortholog of mouse TC10-alpha TC10 AL043108 Iikely ortholog of mouse TRR-containing, TC10 AL043108 Iikely ortholog of mouse TRR-containing, TC10 AL043108 Iikely ortholog of mouse TRR-containing, TC10 AB014589 Iikely ortholog of mouse variant CSTF2T AB014589 Polyadenylation protein CSTF-64 Iikely ortholog of rat golgi stacking protein IIMS1 U09284 LIM and SH3 protein 1 LIM and SH	4 5	39685_at	E40L	ALUSUEUE)-interacting	
SOCS5 AB014571 cytokine signalling 5 SOCS5 AB014571 cytokine signalling 5 TC10 AL043108 likely ortholog of mouse TC10-alpha likely ortholog of mouse TFR-containing, SH2-binding phosphoprotein likely ortholog of mouse variant polyadenylation protein CSTF-64 CSTF2T AB014589 polyadenylation protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein homolog GRASP55 LIM and senescent cell antigen-like likely ortholog of rat golgi stacking protein likely orthologo likely orthologo limikain bt LIMA AB007890 limikain bt LIMA AB007890 limikain bt LIPA AB007890 limikain bt LIPA AB007890 lipin 1 lipin 1 at LIPL2 D86961 lipin 1 lipin 2 lipoma HMGIC fusion partner-like 2 lipoprotein lipase LIV-1 lipin lipin 1 lipin 1 lipin 1 lipin 1 lipin 1 lipin 1 lipin 2 lipoma HMGIC lusion partner-like 2 lipoprotein lipase complete cds.		20162 24	OSSNICIX:	W27233	substance of 220 kDa	
SOCS5 AB014571 Cytokine signalling 5 KI	-	03 100 at	יאוסוויים וואסויים		e suppressors of	
TC10	1442	32669 at	SOCS5	AB014571		(IAA0671 protein
Ilkely ortholog of mouse TPR-containing, SH2-binding phosphoprotein SH2-binding phosphorylase SH2	443	40555 at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
TSBP D63875 SH2-binding phosphoprotein Kikely ortholog of mouse variant polyadenylation protein CSTF-64 ikely ortholog of rat golgi stacking protein GRASP55 AA447263 homolog GRASP55 LIM and senescent cell antigen-like to LASP1 X82456 LIM and SH3 protein 1 LIMK2 D45906 LIM domains 1 LIMO4 D45906 LIM domain kinase 2 LIM AB007890 limkain b1 linkain b1 limkain b1 limkain b1 l	2					
CSTF2T AB014589 polyadenylation protein CSTF-64 polyadenylation protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein bordon call antigen-like to LIM and senescent cell antigen-like domains 1 LMS1 U09284 domains 1 LMS1 D4596 LIM and SH3 protein 1 LMO4 U24576 LIM domain kinase 2 LIM domain call antigen-like bordon call LIM domain call cholesterol limbain b1 limbain b1 limbain b1 limbain b1 limbain b1 limbain call cholesterol call LIPA X76488 esterase (Wolman disease) call LIPA X76488 esterase (Wolman disease) call LIPA LIPL D80010 lipin 1 lipona HMGIC fusion partner-like 2 lipona to LIV-1 protein, estrogen regulated libase liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	1444	40844 at	TSBP	D63875		KIAA0155 gene product
CSTF2T AB014589 polyadenylation protein CSTF-64 Ikely ortholog of rat golgi stacking protein		3-1				
Ikely ortholog of rat golgi stacking protein Ikely ortholog GRASP55 AA447263 homolog GRASP55 LIM and senescent cell antigen-like LIM and senescent cell antigen-like LIM and senescent cell antigen-like LIM and SH3 protein 1 LIMS1 DA5906 LIM domain kinase 2 LIM domain only 4 LIMO4 U24576 LIM domain only 4 LIMO4 AB007890 limkain b1 LIMAP AB007890 limkain b1 LIPA X76488 esterase (Wolman disease) LIM LIPA X76488 esterase (Wolman disease) LIM LIPA D80010 lipin 1 LIPA D80010 lipin 1 LIPA D86961 lipoma HMGIC fusion partner-like 2 LIV-1 U41060 LIV-1 protein, estrogen regulated LIV-1 LIV-1 protein, estrogen esterase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	1445	41248 at	CSTF2T	AB014589		KIAA0689 protein
GRASP55 AA447263 homolog GRASP55	2	20111			likely ortholog of rat golgi stacking protein	
LIMS1 U09284 domains 1 LIMS1 U09284 domains 1 LIMK2 D45906 LIM and SH3 protein 1 LIMC4 U24576 LIM domain kinase 2 LIMO4 U24576 LIM domain nolly 4 LIMO4 LIMO4 LIM domain nolly 4 LIMO4 LIMO5900 limkain b1 LIMO5000000000000000000000000000000000000	1446	35805 at	GRASP55	AA447263	homolog GRASP55	
LIMS1 U09284 domains 1 LIMS1 LIMS1 X82456 LIM and SH3 protein 1 LIMK2 D45906 LIM domain kinase 2 LIM domain only 4 LIMO4 U24576 LIM domain only 4 LIMO50000 LIM domain only 4 LIMO5000000000000000000000000000000000000	2				LIM and senescent cell antigen-like	
LASP1	1447	39232 at	LIMS1	U09284	domains 1	PINCH protein
LIMK2 D45906 LIM domain kinase 2 LIMO4 U24576 LIM domain only 4 LMO4 U24576 LIM domain only 4 LMO4 AB007890 limkain b1 LPA X76488 esterase (Wolman disease) R LPIN1 D80010 lipin 1 LPL D86961 lipoma HMGIC fusion partner-like 2 LIV-1 U41060 LIV-1 protein, estrogen regulated LIV-1 U41060 LIV-1 protein, estrogen glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	1440	36181 at	I ASP1	X82456		LIM and SH3 domain protein
LMO4		20101	LIMKS	D45906		LIMK-2
at LKAP AB007890 limkain b1 at LIPA X76488 esterase (Wolman disease) at LPA X76488 esterase (Wolman disease) at LPPL2 D86961 lipin 1 at LPL M15856 lipoprotein lipase t LIV-1 U41060 LIV-1 protein, estrogen regulated t LIV-1 U41060 LIV-1 protein, estrogen regulated phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	2442	30017 at	MOM	1124576		breast turnor autoantigen
LIPA X76488 esterase (Wolman disease) LPIN1 D80010 lipin 1 LPIN1 D80961 lipin 1 lipoma HMGIC fusion partner-like 2 LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	450	1432 at	KAP	AR007890		KIAA0430 protein
LIPA X76488 esterase (Wolman disease) LPIN1 D80010 lipin 1 LHFPL2 D86961 lipoma HMGIC fusion partner-like 2 LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL)	2	31300 a at	3		lipase A, lysosomal acid, cholesterol	
LPIN1 D80010 lipin 1 LHFPL2 D86961 lipoma HMGIC fusion partner-like 2 LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL)	1452	38745 at	LIPA	X76488	esterase (Wolman disease)	lysosomal acid lipase
CHFPL2 D86961 Ilpoma HMGIC fusion partner-like 2 LPL M15856 Ilpoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated Iliver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	1453	38098 at	LPIN1	D80010	lipin 1	
LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and pyGL AF046798 complete cds.	1454	37542 at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	145	41209 at	LPL	M15856	lipoprotein lipase	Ilpoprotein lipase precursor
liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	145	1798 at	LIV-1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.					liver form; Homo sapiens glycogen	
PYGL AF046798 complete cds.			•		phosphorylase (PYGL) gene, exon 20 and	
	1457	37215 at	PYGL	AF046798	complete cds.	glycogen phosphorylase

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				long tailed isoform; individual exons 6-14	
				are alternative exons any of which can be	
				spliced out of the mMNA.; putative; long	
				tailed isoform; putative; long tailed	
				isoform; hemopoietic variant; putative;	
				long tailed isoform; epithelial form;	
				putative; Human cell surface glycoprotein	
				CD44 (CD44) gene, 3' end of long tailed	
1458	1458 40493_at	CD44	L05424		cell surface glycoprotein CD44
				low density lipoprotein-related protein-	
				associated protein 1 (alpha-2-	
				macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated	alpha-2-macroglobulin receptor-associated
1459	1459 36194 at	LRPAP1	M63959	1)	protein
				low molecular mass ubiquinone-binding	
1460	1460 34400_at	aP-c	AI540957	protein (9.5kD)	
1461	1461 37025 at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462	1462 39017 at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463	1463 38038 at	LUM	U21128		lumican
1464	1464 38115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465	1465 39428 at	LNK	AF055581	otein	adaptor protein Lnk
1466	1466 39396 at	LYPLA1	AF081281		lysophospholipase
1467	1467 33788 at	LYSAL1	AB002390	-like 1	lysosomal apyrase-like 1
			04100	1. The second of the second se	lycocomal membrane alyconrolein-1
1468	1468 39758_I_at	LAIMIP	204102	iyadadillar-associated illeliiblarie protein	Jacob de la companya
1469	1469 38403_at	LAMP2	X77196	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2
1470	1470 38402 at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2b
				lysosomal-associated protein	lysosomal-associated protein
1471	1471 39019 at	LAPTM4A	D14696	transmembrane 4 alpha	transmembrane 4 alpha
1472	33127 at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473	1473 34336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474	1474 32832_at	MAEA	AF084928	macrophage erythroblast attacher	erythroblast macrophage protein EMP
1 7	147E 26174 of	MACMABCKS	A20328	macrophage myristoylated alanine-rich C	macrophage myristoylated alanine-rich C kinase substrate
*	301/4 at	CYICLUCINICAINI	V10020		

ш	legic mad protein homolog	legic	mad protein homolog		mad protein nomolog		Dpc4		Smad5	legic	Smad6		MAD-related gene SMAD7		HLA-A26		HLA-DMB	_	HLA-DPB1		HLA-DPB1		DR alpha precursor	class II,			MHC class I-related protein 1 isotorm D			protein 'A', isoform 1		oluble) cytosolic malate dehydrogenase
MAD, mothers against decapentaplegic	homolog 2 (Urosopnila)	MAD, mothers against decapentaplegic	homolog 3 (Drosophila)	MAD, mothers against decapentaplegic	homolog 3 (Drosophila)	MAD, mothers against decapentaplegic	homolog 4 (Drosophila)	MAD, mothers against decapentaplegic	homolog 5 (Drosophila)	MAD, mothers against decapentaplegic	homolog 6 (Drosophila)	MAD, mothers against decapentaplegic	homolog 7 (Drosophila)	major histocompatibility complex, class 1,	A	major histocompatibility complex, class II,	DM beta	major histocompatibility complex, class II,	DP beta 1	major histocompatibility complex, class II,	DP beta 1	major histocompatibility complex, class II,	DR alpha	major histocompatibility complex, class II,	DR beta 1	major histocompatibility complex, class I-	like sequence	major receptor for HIV-1; member of	immunoglobulin supergene family; T cell	surface glycoprotein T4	malate dehydrogenase 1, NAD (soluble)	the property of NAND(+)-dependent
·	U68018		U68019		U68019		U44378		U59913		AF035528		AF010193		D32129		U15085		M83664		M83664		J00194		M16941		AF031469			U47924	1)55654	
മ	MADH2	!	MADH3		MADH3		MADH4		MADHS		MADH6		MADH7		HLA-A		HLA-DMB		HLA-DPB1		HLA-DPB1		HLA-DRA		HLA-DRB1		HLALS			CD4	MDH1	
A	453 at	15-004	1477 38944 at		1478 1433_g_at		1479 36953 at		1480 1013 at		1481 1955 s at		1482 1857 at		1483 41237 at		1484 41609 at		1485 38096 f at		1486 38095 i at		1487 37039 at		1488 33261_at		1489 34425_at			1490 34003_at	1401 36608 at	30000 at
-	1476 1453		1477		1478		1479		1480		1481		1482		1483		1484		1485		1486		1487		1488		1489			1490	1	2

ME2 M55905 mitochondrial NaD(+)-dependent, mitochondrial NaD(P) mitochondrial NaD(P				C		ינו
ME2 M55905 malic enzyme 2, NAD(+)-dependent, ninochondrial minochondrial MKNK1 AB000409 kinase-interacting serine/threonine kinase-interacting serine/threonine kinase-interacting serine/threonine MAP/microtubule alfinity-regulating kinase MARK3 M80359 3 MAP/microtubule alfinity-regulating kinase MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, complete cds. F MAPKAPK5; PRA AF032437 Complete cds. F MAPKAPK5; PRA AF032437 Complete cds. F MAPKAPK5; PRA AF032437 Complete cds. F Sw.P04270 F F Sw.P04289 Tr.O27487 Sw.P04309 Tr.C49133 Sw.P7829 Tr.C47229 Tr.C49133 Sw.P7820 Sw.P7782 Sw.P0780 Sw.P7820 Sw.P7782 Sw.P0780 Sw.P0780 Sw.P0780 Tr.C27710 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P0780 Sw.P078		A	В	כ		cilon denondant will be to the secondary
MEZ M55905 mitochondrial MPI X76057 mannose phosphate isomerase MAP MAP kinase-interacting serine/threonine MAPK3 MAP/microtubule affinity-regulating kinase MAPK3 MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein FRK; Homo sapiens BAC clone CTB-10432 FRX; MAPK-activated protein kinase; PRK; PRX; Homo sapiens BAC clone CTB-1011 from FRX; MAPK-activated protein kinase; PRK; PRX; Homo sapiens BAC clone CTB-1011 from PRX;					-	mitochondriai IVAU(r)+ -dependent manc
MPI X76057 mannose phosphate isomerase P MKNK1 AB000409 kinase 1 MAP/microtubule affinity-regulating kinase AB000409 MAP/microtubule affinity-regulating kinase BMAP/microtubule affinity-regulating kinase F MARK3 M80359 3 MAPK-activated protein kinase; PRK; PK MAPKAPK5; PRA AF032437 Complete cds. Complete cds. F MAPKAPK5; PRA AF032437 Complete cds. F MAPKAPK5; PRA AF032437 Complete cds. F MAPKAPK5; PRA AF032437 Sw.P04040 Sw.P0432 Sw.P04304 Sw.P17336 Tr.O77229 Tr.Q49133 Sw.P44390 Tr.CA49133 Sw.P44390 Tr.Q49133 Sw.P03825 Sw.P17872 Tr.Q49133 Sw.P44390 Tr.CA59602 Tr.P77924 Sw.C059170 Sw.P1502 Sw.D9825 Sw.P1389 Sw.P1502 Tr.C59263 Sw.P1389 Sw.P1502 Tr.C59263 Sw.P1389 AR AL035079 Match ESTs. W94164 N28621 Match ESTs. W94164 N28621 MUGSC.H. RG04/AC005053 TrQ21112; H. RG04/D111; Homo sapiners BAC clone CTB-4D11 from Sapiners BAC clone CTB-4D11 from Tq21, complete sequence.	1493	36599 at	ME2	M55905		enzyme
MARNK1 AB000409 kinase-interacting serine/threonine MAP kinase-1	1494	36673 at		X76057		phosphomannose isomerase
MKNK1 AB000409 kinase 1 MAPKNK1 AB000409 MAP/microtubule affinity-regulating kinase 3 3 MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, romplete cds. Homo sapiens mitogen activated protein kinase gene, romplete cds. Homo sapiens mitogen activated protein kinase gene, romplete cds. Fig. 272437 Complete cds. Fig. 272437 Complete cds. Fig. 272487 Sw.P24270 Tr.O62839 Sw.P040432 Sw.P24270 Tr.O62839 Sw.P04322 Sw.P14338 Tr.O18193 Tr.O77229 Tr.O49133 Sw.P26901 Sw.P55306 Sw.P14390 Tr.O49133 Sw.P56901 Sw.P55306 Sw.P07820 Sw.P07820 Sw.P07820 Sw.P14390 Tr.O27710 Sw.O9265 Sw.P1389 Sw.P07820 Tr.O38613 Sw.P14500 Tr.O38613 Sw.P1464 N28621 (NID:316521), A4032221 (NID:316521), A4032221 (NID:316521), A4032221 (NID:3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from Traces (Sw.T1012); HEAD (Sw.T10111); Head Traces (Sw.T10111); Head Traces (Sw.T1012); Head (Sw.T10111); Head Traces (Sw.T1012); Head (Sw.T10111); Head Traces (Sw.T10111); Head Traces (Sw.T1012); Head (Sw.T101111); Head Traces (Sw.T101111); Head Traces (Sw.T1012); Head Traces (Sw.T1012); Head Traces (Sw.T101111); Head Traces (Sw.T101111); Head Traces (Sw.T1011111); Head Traces (Sw.T1011111); Head Traces		200				
MARK3 M80359 3	1495	35299 at	MKNK1	AB000409	$\overline{}$	MNK1
MARK3 M80359 3 MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, romplete cds. Homo sapiens mitogen activated protein kinase gene, romplete cds. Complete complete cds. Complete comp					_	
MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, richiase gene, ge	1496	40826 at	MARK3	M80359		protein p78
Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, complete cds. MAPKAPK5; PRA AF032437 complete cds. match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P04322 Sw:P17336 Tr:P9682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:O95228 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P138 Sw:P15202 Tr:O59635 Sw:D71138 Sw:O92405 Sw:O59296 Tr:O33613 Sw:O92405 Sw:O59296 Tr:O33613 Sw:O92405 Sw:O392405 Sw:O33613 Sw:O92405 Sw:O3363 Sw:O92405 Sw:O33613 Sw:O92405 Sw:O93635 Sw					MAPK-activated protein kinase; PRK;	
MAPKAPK5; PRA AF032437 complete cds. range activated protein kinase gene, range ra						
MAPKAPK5; PRA AF032437 complete cds. match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P040432 Sw:P47736 Tr:O62839 Sw:P040432 Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:O59170 Sw:P15202 Tr:P77924 Sw:O59170 Sw:P15202 Tr:C59296 Tr:O33613 Sw:O92405 Sw:O59635 Sw:P81138 Tr:Q59602 Tr:P77924 Sw:O59170 Sw:P15202 Tr:C59296 Tr:O33613 Sw:O92405 Sw:O59296 Tr:O33613 Sw:O92405 Sw:O59295 Tr:O9361138 Tr:O92405 Sw:O92405 Sw:O59295 Tr:O9361138 Tr:O92405 Sw:O92405 Sw:O59295 Tr:O9361138 Tr:O92405 Sw:O92405 Sw:O92621138 Tr:O92405 Sw:O92405 Sw:O92621138 Tr:O92405 53 Sw:O92621138 Tr:O92405 Sw:O92621138 Tr:O9	_					mitogen activated protein kinase activated
match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59235 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g3165213), and Al167942 (NID:g31652183), and Al167942 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	1497	41506_at	MAPKAPK5; PRA	AF032437		protein kinase
match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P5306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P15202 Tr:O59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:316521), AA032221 (NID:3165218), and A1167942 (NID:3165218), and A1167942 (NID:33701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.						
Sw.P24270 Tr:O62839 Sw:P00432 Sw.P17336 Tr:P90682 Tr:O27487 Sw.O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P4390 Tr:Q27710 Sw:C96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:33165221), AA032221 (NID:33165221), AB041011.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from 7021, complete sequence.					match proteins: Sw:P04040 Sw:P04762	
Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P30263 Tr:P7924 Sw:O59170 Tr:Q5902 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59235 Sw:P81138 match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g3165213), and Al167942 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:P24270 Tr:O62839 Sw:P00432	
Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P30265 Sw:P7782 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g3165213), and Al167942 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:P17336 Tr:P90682 Tr:Q27487	
Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P07820 Tr:Q5969 Tr:O33613 Sw:Q92405 Sw:Q59296 Tr:O33613 Sw:Q92405 Sw:P7872 Sw:Q92405 Sw:P7872 Sw:Q92405 Sw:P7872 Sw:Q92405 Sw:P7872 Sw:Q92406 Sw:Q92406 Sw:P7872 Sw:Q92406 Sw					Sw:O61235 Tr:O18193 Tr:O77229	
Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:Q92405 Sw:Q59635 Sw:P81138 Sw:Q92405 Sw:Q59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs A4316181 (NID:g3165221), A4032221 (NID:g31652183), and Al167942 (NID:g31652183), and Al167942 (NID:g316521112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Tr:Q49133 Sw:P26901 Sw:P55306	
Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:C39296 Tr:C33613 Sw:Q92405 Sw:Q59635 Sw:P81138 CAT AL035079 match to ESTs: W94164 N28621 match to ESTs: W94164 N28621 (NID:g3165211), AA032221 (NID:g31652183), and Al167942 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:P30263 Tr:P95631 Sw:P44390	
Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:G59635 Sw:P81138 Sw:Q92405 Sw:Q59635 Sw:P81138 match ESTs: W94164 N28621 match to ESTs A4316181 (NID:g316521), A4032221 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Tr:Q27710 Sw:Q96528 Sw:O13289	
CAT AL035079 Tr:Q59602 Tr:D5224 Sw:Q59170 Sw:P15202 Tr:G59635 Sw:P81138 Sw:Q92405 Sw:G59635 Sw:P81138 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P07820 Sw:P30265 Sw:P77872	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3165221), HRG041D11.1; Homo sapiens BAC clone CTB-41D11 from yq21, complete sequence.					Tr:Q59602 Tr:P77924 Sw:Q59170	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:P15202 Tr:Q59296 Tr:O33613	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:93165221), AA032221 (NID:93165221), AA032221 (NID:93701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:Q92405 Sw:Q59635 Sw:P81138	
match to ESTs AA3f6181 (NID:g3165221), AA032221 (NID:g1502183), and A167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	1498	337009 at	CAT	AL035079	match ESTs: W94164 N28621	dJ53C18.1 (Catalase)
(NID:g3165221), A4032221 (NID:g1502183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					match to ESTs AA316181	
(NID:g1502183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from WUGSC:H_RG04AC005053 7q21, complete sequence.					(NID:g3165221), AA032221	
(NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from WUGSC:H_RG04AC005053 7q21, complete sequence.					(NID:g1502183), and Al167942	
wugsc:H_RG04 AC005053 7q21, complete sequence.					(NID:g3701112); H_RG041D11.1; Homo	3
WUGSC:H_RG04AC005053 7q21, complete sequence.					sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
	149	9 40297 at	WUGSC:H_RG0	4 AC005053	7q21, complete sequence.	prostate

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				match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283	
				D38535 D38595 match: proteins Q06033	
			•	P97280 O54882 O35802 Q61704 Q14624	
				P79263 Q63416 O42141 P19823 O02668	P79263 Q63416 Q42141 P19823 Q02668 hepatocellular carcinoma associated protein;
1500	500 34860 g at	BCG1	Z98046	Q61703 P97279 Q29052	breast cancer associated gene 1
				match: cDNAs: Em:AL050345 match:	
				ESTs: Em:AA304885 Em:AA447346	
				Em:AA314213 Em:AA209368	
				Em:AA209372 Em:T84723 Em:H23039	
				Em:AA542125 Em:W41686	
1501	501 35336 at	HS508115A	AL021707	Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
1502	502 32658 at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503	1503 31545 at	dJ1033B10.1	AL031228	match: protein 015214	BING4
1504	504 36986_at	dJ886K2.1	AL031295	match: protein SPTREMBL; Q14241	UDP-galactose-4-epimerase
				match: proteins CE02000 O59733	
				CE01999; supported by FGENES and	
1505	1505 38072 at	dJ465N24.1	AL031432	GENSCAN	hypothetical protein dJ465N24.2.1
				match: proteins O15037 CE16881	
				supported by GENSCAN possibly this	
				partial gene and dJ281H8.1 are part of	dJ281H8.2 (PUTATIVE novel protein similar
1506	1506 32478 f at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)

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5073	1507 39759_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3′ part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebratish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 2))
508	1508 39760_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse OKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKO-1 (Quaking proteins) and cebrafish ZKO-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 2))
609	1509 32573_at	COX6A	AL021546	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 cytochrome c oxidase subunit Vla P13182 O13085 O13082 polypeptide 1	cytochrome c oxidase subunit Vla polypeptide 1



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			938533 Q03933 P38530 P38529 P38531 Q63717	boot chook transcription factor 9
	HSF2	299129	P38532 Q99472	neat snock transcription factor z
			match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA	
_			sequence from clone 512B11 on chromosome 6p24-25. Contains the	
			Desmoplakin I (DPI) gene, ESTs, STSs	MOON Common of the Control of the Co
,	dJ512B11.1	AL031058	and GSSs, complete sequence.	Q3512B11.1 (Desillopianii 1 (Dr.1))
			match: proteins Q14209 Q16254 U35261 000716 Q61501 Q90977 Q01094	
	E2F-2	AL021154	Q27368	E2F transcription factor 2
			match: proteins Q15774; match: protein O01968 P32019: Homo sapiens DNA	
			sequence from PAC 454M7 on	
			chromosome Xq25-26.3. Contains the	[cacacadoscoc]o
			OCRL1 gene for Lowe Oculocerebrorenal (dJ454M7.1.2 (Lowe Oculocerebrorenal Conditions and an OCRL-1) (isoform 2)	GJ454M7.1.2 (Lowe Oculocerebioleilal Syndrome protein OCRL-1) (isoform 2);
			ESTs. STSs and GSSs, complete	dJ454M7.1.1 (Lowe Oculocerebrorenal
	OCRL1	AL022162	sednence.	Syndrome protein OCRL-1) (isoform 1)
				dJ341E18.1 (Serine/Threonine Protein
			match: proteins Q62726 P20793 Q04859	Kinase (presumptive isolog of Rat protein
1514 38990 at	dJ341E18.1	AL031178	Q39423 P43294 O49669	[Q62726])

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1515	1515 34782_at	ICMOMUL		match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516	1516 37350_at	dJ889N15.1	AL031177	665 Q91664 1667 O60939 0426 P06907 1573 P10522 uence 180040 I FGENES	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517	1517 39738_at	APOL2	Z82215	match: proteins: Sw:O14791	apolipoprotein L
1518	31824 at	ME1	AL049699	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))
1519	32766 at	OTK27 SSFA1	Z 83840	match: proteins: Sw:P12956	non-histone chromosome protein 2 (S. cerevisiae)-like 1
1520	39756	XBP1	Z93930	match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.	bK292E10.1 (X-box binding protein 1 (TREB5))
	1221 22-22				

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ш		bK292E10.1 (X-box binding protein 1	(601)								dJ376D21.1 (Moesin (Membrane-organizing	Extension Spike protein))				ribosomal protein L3					Case 87 1 (ubiquitin-conjugating enzyme E2)	coopy (appearing conjugation)	(nomologous to yeast obos))		septin 3	small nuclear ribonucleoprotein polypeptide B"
L	1		1			_					ਚੋਂ	ত্র				\neg	_		_		<u>.</u>	<u> </u>	틱_		Т	
	0	match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete	sequence.	match: proteins: Sw:P26038 11:035/63 Sw:P26041 Sw:P26042 Sw:P26044	Sw:P35241 Sw:P26043 Sw:P19311 Sw:P31976 Sw:P26040 Tr:Q26520	Tr:Q24788 Tr:Q24796 Tr:Q94815; Human	DNA sequence from clone 376D21 on	chromosome Xq11.1-12 Contains the	MSN gene for mossin (memoranic	ESTs, STSs, GSSs, genomic marker	DXS8029 and a putative CpG island,	complete sequence.	match: proteins: Sw:P39023 Sw:O16797	Sw:P21531 Sw:P39872 Sw:P27659	Sw:Q92901 Sw:P49149 Sw:P22738	Sw:P35684 Sw:P17094 Wp:CE05598	match: proteins: Sw;P50550 Sw:O09181	Tr:062622 Sw:P40984 Sw:P50623	Tr:Q42551 Tr:O24240 Tr:Q42973	Sw:P52478 Sw:Q02159 Sw:P15732	SW:000102 11:076542 SW:PZ/949	SW:P4942/ 11:01/424 SW:P2366/	Sw:P52490	match: proteins: Sw:Q12772 Sw:Q60429	Sw:P36956 Sw:Q60416 1r:U15352	match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865
· ·	၁		Z93930									Z98946	i			AL022326		•					AL031714		299716	AL034428
	.		XBP1			,						MSN				RPL3							UBE21		bK250D10.3	SNRPB2
	⋖		at									1522 40771_at				1523 31722 at							1524 33136_at		1525 36607_at	1526 38399_at
			1521 39755									1522				1523							1524		1525	1526

					1
T	A	8	၁	O	n
T				match: proteins: Tr:O54791 Sw:Q90595	
				Sw:Q61827 Sw:Q90596 Tr:O54790	
				Tr:O15525 Sw:C90889 Tr:O/36/9	
					Transfer to one frame E
527	1527 36711_at	HS506A DKFZP5 AL021977	AL021977		chromosome 22 open reading manie 3
528	1528139561 at	DNAL4	AL008583		chromobox homolog 6
,				Tr.Q9QYC8 Tr.Q9WUZ9 Tr:O70214	dJ738P15.2 (CD39-like 2 (a nucleoside
1529	39876 at	dJ738P15.1	AL035252	Tr:Q9QYC9	phosphatase))
				match: proteins: Tr:094136 Sw:Q99798	
				Sw:P49609 Sw:P20004 Sw:P16276	dJ347H13.1 (aconitase 2, mitochondrial
				Tr:O75809 Tr:O74699 Wp:CE00516	(Aconitate Hydratase, EC 4.2.1.3, Citrate
1530	1530 37189 at	ACO2	AL023553	Sw:P19414 Tr:O75944 Sw:O13966	Hydrolyase))
				match: proteins: Tr:P70386 Sw:Q02527	
531	1531 41235 at	TAXREB67 TXRE	EAL022312	Sw:Q10470 Sw:Q09327	activating transcription factor 4
3					dJ117516.1 (Ras inhibitor JC265 (Ras
				match: proteins: Tr:Q00425 Sw:Q13671	association (RalGDS/AF-6) domain
1532	1532 36550 at	dJ1175l6.1	AL049538	Tr:O15010 Tr:P97680	containing protein))
				match: proteins: Tr:Q14621 Tr:Q64012	
			-	Sw:P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
1533	1533 39368 at	P542	AL031668	Sw:Q14011 Sw:P26686	isoform
				match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
1534	1534 33821 at	dJ483K16.1	AL034374	Sw:P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
1535	39029 at	G10	U11861	maternal G10 transcript	maternal G10 transcript
1536	1536 35145 at	MNT	X96401	MAX binding protein	ROX protein
3	m=0.100				MAX interacting protein 1, isoform a; MAX
1537	1537 39072 at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
					MAX interacting protein 1, isoform a; MAX
1538	1538 654 at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
				MCM2 minichromosome maintenance	
1539	539 35312 at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
				MCM3 minichromosome maintenance	
				deficient 3 (S. cerevisiae) associated	
1540	1540 40469 at	MCM3AP	AB011144	protein	KIAA0572 protein

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-	A	В	ပ	O	ט
				MCM6 minichromosome maintenance deficient 6 (MIS5 homolog. S. pombe) (S.	
77	4E44 40447 of	MCM6	D84557	cerevisiae)	HsMcm6
5	100			eloid ecotropic viral integration	
542	1542 41388 at	MEIS2	AF017418	T	homeobox protein MEISZ
				Meis1, myeloid ecotropic viral integration	
1543	1543 37486 f at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
				mel transforming oncogene (derived from	
1544	1544 35340 at	MEL	AI819948	cell line NK14)- RAB8 homolog	
				melanoma antigen, family A, 2, copy a;	
				similar to GenBank Accession Number	• • • • • • • • • • • • • • • • • • •
1545	1545 36500 at	MAGEA2A	AF027974	L18920	melanoma antigen family Aza
1546	1546 41139 at	MAGED1	W26633	metanoma antigen, family D, 1	
1547	1547 39327 at	D2S448	D86983	Melanoma associated gene	
	000E1 CI			membrane cofactor protein (CD46,	membrane cofactor protein (CD46,
				trophoblast-lymphocyte cross-reactive	trophoblast-lymphocyte cross-reactive
1548	1548 38441 s. at	MCP	X59408	antigen)	antigen)
2				membrane component, chromosome 11,	
15.40	1540 39471 at	M11S1	Z48042	surface marker 1	GPI-anchored protein p137
				membrane component, chromosome 17,	
		-		surface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
1550	1550 33444 at	M17S2	D30756	antigen CA125)	surface marker 2
	3			membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	asehilasandras allatan anathus
1551	1551 1389 at	MME	J03779	CALLA, CD10)	memorane metallo-endopephidase
	1			mesenchyme homeo box 2 (growth arrest-	
1552	1552 40399 r at	MEOX2	AI743406	specific homeo box)	
	10000			Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
				initiation codon in vitro; Homo sapiens	
			-	porin (por) mRNA, complete cds and	•
1553	1553 37697 s at	por	L08666	truncated cds.	porin
	1554 40244 c at	MPPF1	AI743654	metallo phosphoesterase	
3	170577-0-61				

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		c	(u
	A	g	3		
				metallothionein (MT)-like gene; H.sapiens	
	•		YEEROS	pseudogene for metallothionein and AG/CT repetitive element	metallothionein
1555 51975	g *	AATOA	A1547258		
1000 03001 8	8 7	MTE	V78740	anscription factor 1	metal-regulatory transcription factor
1557 38945	al	MINIT	1135113		metastasis associated protein
1558 1543_g_al	J_al	I WI I W	21.000		mataxin 9
1559 35642_at	at	MTX2	AF053551	metaxin 2	IIIelaxIII Z
- 00	1	000	V047E4	methioning-tBNA synthetase	veast methionyl-tRNA synthetase homolog
1560 39342	i di	MATO	734734	methionyl aminonentidase 1	
1561 37619_at	aí	MEIAFI	U42004	methory annihispophease	mothyl One hinding protein
1562 41828	at	MBD1	Y10746	methyl-CpG binding domain protein I	mennyl-cha binding protein
1563 33905	_at	MBD2	AF072242	methyl-CpG binding domain protein 2	methyl-CpG binding protein MBD2
1564 34386_at	at	MBD4	AF072250	methyl-CpG binding domain protein 4	methyl-CpG binding protein MBD4
					Construction of Colonial Control Control
				methylene tetrahydrofolate	methylene tetranydroloiate denydrogenase
		-		dehydrogenase (NAD+ dependent),	(NAD+ dependent), methenyitetranydrofolate
1565 40074 at	at	MTHFD2	X16396	methenyltetrahydrofolate cyclohydrolase	cyclohydrolase, precursor
				methylenetetrahydrofolate dehydrogenase	
				(NADP+ dependent),	(NADP+ dependent),
				methenvitetrahydrofolate cyclohydrolase.	methenyltetrahydrofolate cyclohydrolase,
1566 674 a at	ŧ	MTHED1	J04031	formyltetrahydrofolate synthetase	formyltetrahydrofolate synthetase
1567 40105 at	100	MUT	M65131	methylmalonyl Coenzyme A mutase	methylmalonyl-CoA mutase
				MHC class I chain-rélated gene B; cDNA	
				sequence deposited under GenBank	
				Accession Number X91625; Human MHC	
				class I molecule (MICB) gene, complete	
1568 35937_at	Ť	MICB	U65416	cds.	MHC class I molecule
1569 36535 at	i	MEAP1	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
2201	3			microphthalmia-associated transcription	A-type microphthalmia associated
1570 38228 g at	† 5	MITE	AB006909	factor	transcription factor
1571 R20 at		MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
1572 38704	70	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
1573 35917	, a	MAP1A	W26631	microtubule-associated protein 1A	
1574 33850	i a	MAP4	W28892	microtubule-associated protein 4	
1000011	,-ai	F 12/01			

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	¥	В	ပ	O	נו
Ì	20450	*4ADDE:1	1124166	microtubule-associated protein, RP/EB	EB1
200	15/5 3345b_at		001430	microtubule-associated proteins 1A/1B	
1576	1576 39370 at	MAP1A/1BLC3	W28807		
1577		MID1	AF041210	midline 1 (Opitz/BBB syndrome)	midline 1 fetal kidney isoform 3
1578	1578 34403 at	MFGE8	U58516		BA46
				mitochondrial ATP synthase regulatory	
1579	1579 40027 at	ATPW	W52999		
1580	37174 at	MRPL19	D14660	6	mitochondrial ribosomal protein L19
1581	1581 37726 at	MRPL3	X06323		mitochondrial ribosomal protein L3
1582	1582 39717 g at	MRPL33	AI597616		
1583	1583 32221 at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	584 38899 s at	MFN1	U95822		putative transmembrane G I Pase
2,5	1585 34369 at	MEN2	D86987	mitofusin 2	KIAA0214 protein
1586	1586 36577 at	MIGS	224725	lucible 2	mitogen inducible gene mig-2
1587	1587 37733 at	MAPK14	L35263	4	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692	mitogen-activated protein kinase 6	p97mapk
1580	1589 38431 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1500	1500 1238 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
3	,				
1591	1591 1130 at	MAP2K1	L11284	-	mitogen-activated protein kinase kinase 1
				mitogen-activated protein kinase kinase	
1592	1592 1327 s at	MAP3K5	U67156	kinase 5	mitogen-activated kinase kinase xinase 5
				mitogen-activated protein kinase kinase	
1593	1593 36905 at	MAP3K7	AB009356	kinase 7	TGF-beta activated kinase 1a
				mitogen-activated protein kinase kinase	
1594	1594 38980 at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	
1595	1595 35694 at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179 at	MAPKAPK2	U12779	protein kinase 2	MAP kinase activated protein kinase 2
				mitogen-activated protein kinase-activated	
1597	1597 1637 at	MAPKAPK3	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220 at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1590	1599 38437 at	MLN51	X80199	MLN51 protein	MLN51 protein

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+-				MMS19-liké (MET18 homolog, S.	
	1600 35273 at	MMS19L	AF007151		MMS19 (ME I 18 S. cerevisiae)-like
+=	1601 34767 at	MAP-1	AI670788	modulator of apoptosis 1	
ᆣ	"	MAOA	AA420624	monoamine oxidase A	
∴l			M68840	monoamine oxidase A	monoamine oxidase A
;+≟	41770 at	MAOA	AA420624		
+	1605 37628 at	MAOB			monoamine oxidase B
+	2010			age differentiation-	monocyte to macrophage differentiation-
- ;;	1606 37565 at	MMD	X85750		associated, precursor
ıκ	1607 40861 at	MRGX		MORF-related gene X	MORF-related gene X
	11			ein 10 (U3 small	
- 60	1608 33797 at	MPHOSPH10	X98494		M phase phosphoprotein 10
16	1609 34306 at	MBNL	AB007888		muscleblind (Drosophila)-like
to	1610 35992 at	MSC	AF087036	musculin (activated B-cell factor-1)	musculin
1=	1611 31884 at	MLH3	L40399	mutL homolog 3 (E. coli)	mutL homolog 3
1				mutS homolog 2, colon cancer,	
~	1612 860 at	MSH2	U03911	nonpolyposis type 1 (E. coli)	mutS homolog 2
l e	1613 2003 s at	MSH6	U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
14		MPZI 1	AF087020	myelin protein zero-like 1	protein zero related protein
-	200.00			equence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
ľ	1615 33146 at	MCI 1	L08246	related)	related)
эΤ	100			myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
C	1616 277 at	MCI 1	L08246	related)	related)
7	11			myeloid/lymphoid or mixed-lineage	myeloid/lymphoid or mixed-lineage leukemia
				leukemia (trithorax homolog, Drosophila);	(trithorax homolog, Drosophila); translocated
7	1617 39037 at	MLLT2	L13773	translocated to, 2	to, 2
: ∞		MYLE	AF108145	MYLE protein	DEXI
15	Ш	MY01B	AJ001381	myosin IB	myh-1c
112		MY01D	AB018270	myosin ID	KIAA0727 protein
:15		MY01E	U14391	myosin IE	myosin-IC
:12		MLC1SA	A1127424	myosin light chain 1 slow a	
ll S	1623 41187 at	MLC-B	U26162	myosin regulatory light chain	myosin regulatory light chain
12	1624 35362 at	MYO10	AB018342	myosin X	_
1 3		0	XE4304	myosin, light polypeptide, regulatory, non-	myosin, light polypeptide, regulatory, non- sarcomeric (20kD)
N.	1625 3344/ at	MLCB	A34304	Salcollicity (Edito)	myotubularin related protein 3
ស្ត	1626 35739_at	MIMHS	ABOUZSOS	III) or a property of the second of the seco	

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	٧	В	ပ		1
1627	39707_at	MTMR4	AB014547		KIAA0647 protein
1628	1628 38035 at	MTMR6	AF072928		myotubularin related protein 6
1629 39607	39607 at	MTMR8	AL080178		hypothetical protein
1630	10	MTMR8	AF052099	myotubularin related protein 8	
				ein kinase C	
1631	1631 32434_at	MARCKS	D10522	substrate	80K-L protein
1632	1632 39267 at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
				N-acylsphingosine amidohydrolase (acid	
1633	1633 36938_at	ASAH	U70063	ceramidase)	acid ceramidase
				N-acylsphingosine amidohydrolase (acid	
1634 461	461_at	ASAH	U70063	ceramidase)	acid ceramidase
				NADH dehydrogenase (ubiquinone) 1	
1635	1635 36169_at	NDUFA1	N47307	alpha subcomplex, 1 (7.5KD, MWPE)	
		1	1	NADH dehydrogenase (ubiquinone) 1	NAUH-ubiquinone oxidoreduciase suburiit Cit
1636	1636 40546_s_at	NDUFAZ	AF04/185	alpha subcomplex, ∠ (okD, bo)	000
				NADH dehydrogenase (ubiquinone) 1	NADPH:ubiquinone oxidoreductase subunit
1637	1637 38462_at	NDUFAS	U64028	alpha subcomplex, 5 (13kD, B13)	B13
				NADH dehydrogenase (ubiquinone) 1	
1638	1638 32752_at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	38605_at	NDUFB1	Al345944	subcomplex, 1 (7kD, MNLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981_at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 betal NADH-ubiquinone oxidoreductase subunit Cl
1641	1641 32232_at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGDH
				NADH dehydrogenase (ubiquinone) 1 beta	
1642	1642 32774_at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
1643	38485 at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NADH dehydrogenase
1644	1644 38395 at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
	, 	(protein 4 (18kU) (NAUH-coenzyme Q	
1645	1645 38695_at	NDUFS4	AA203303	(reductase)	

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	4	В	ပ	O	ш
				NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q	
1646	1646 38060_at	NDUFS6	AI541336	reductase)	
1647	1647[34893 at	NDUEV?	A1557064	NADH dehydrogenase (ubiquinone)	
	5			natriuretic peptide receptor C/guanylate	
				tor	
1648	1648 34519_at	NPR3	M59305		atrial natriuretic peptide clearance receptor
1649	1649 34234 f at	NKTR	AI688640	natural killer-tumor recognition sequence	
1650	1650 41795 at	NCK1	X17576	NCK adaptor protein 1	NCK adaptor protein 1
1651	1651 33357_at	NCKAP1	AB011159	in 1	KIAA0587 protein
1652	1652 36073_at	NON	U35139·	necdin homolog (mouse)	NECDIN related protein
1653	1653 34202 at	DKFZP566B0846	AL050071	nectin 3	hypothetical protein
1654	1654 34264_at	NESCA	AB026894	nesca protein	NESCA
1655	1655 38719 at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
				neural precursor cell expressed,	
1656	1656 39356_at	NEDD4L	AB007899	developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
				neural precursor cell expressed,	neural precursor cell expressed,
1657	1657 40281_at	NEDDS	D63878	15	developmentally down-regulated 5
1658	1658 1695_at	NEDD8	D23662	developmentally down-regulated 8	ubiquitin-like protein
				neuroblastoma, suppression of	neuroblastoma, suppression of
1659	1659 37005 at	NBL1	D28124		tumorigenicity 1
1660	1660 31896 at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
1661	1661 37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
1662	1662 37673_at	NSMAF	X96586	activation associated factor	FAN protein
				NGFI-A binding protein 1 (EGR1 binding	
1663	1663 38692_at	NAB1	AF045451	protein 1)	transcriptional regulatory protein p54
1664	1664 34835_at	NCSTN	D87442	nicastrin	
1665	1665 37032_at	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
1666	1666 41722 at	L Z	U40490	nicotinamide nucleotide transhydrogenase	nicotinamide nucleotide transhydrogenase nicotinamide nucleotide transhydrogenase
166	1667 35366 at	QIN	M30269	nidogen (enactin)	nidogen
166	1668 753 at	NID2	D86425	nidogen 2	osteonidogen

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-	A	В	0	Q	W
1669 37047	1 1	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670 980_at	80_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671 3	1671 39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
1672 3	1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673 3	1673 36047_at	NEK1	AL050385	kinase 1	
1674 3	1674 35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675 4	0866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
16763	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
16773	1677 39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
16783	1678 36472_at	WN	U32849	N-myc (and STAT) interactor	Nai
16793	1679 36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
16804	1680 41656 at	NMT2	AF043325	N-myristoyltransferase 2	N-myristoyltransferase 2
				non-canonical ubquitin conjugating	
1681	39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
16823	1682 39039_s_at	NCUBE1	AI557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683	1683 1521_at	NME1	X17620	expressed in	Nm23 protein
		-		non-metastatic cells 2, protein (NM23B)	
16843	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685 1980	980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
1686	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687 3	38750_at	NOTCH3	G9260	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	10122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	1690 33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
				N-sulfoglucosamine sulfohydrolase	
1691	1691 35626_at	SGSH	U30894	(sulfamidase)	N-sulphoglucosamine sulphohydrolase
1692	37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	1694 40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1695	1695 32789 at	NCBP2	AA149428	nuclear cap binding protein subunit 2, 20kD	
		1			

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1	*	۵		1	niclost distribution gene C (A nidulans)
000	000		A DO 10 40 8	nuclear distribution gene o nomotog (A.	Hacreal distribution gene O (A.modrans)
080	1696 33636 at	2	3		
1697	1697 39782_at		X95592	nuclear UNA-binding protein	CID protein
1698	1698 40063_at	NDP52	U22897	nuclear domain 10 protein	NDP52
					C T
1699	1699 853_at	NFEZLZ	3/401/	flucted factor (elythlold-defined 2)-line 2	CCAAT/enhancer hinding profein (C/ERP)
1	1700 20254 24	CEBPB: LAP: CB	DIXESEO		beta
3	00004_at			lls,	nuclear factor of activated T-cells,
1701	1701 40822 at	NFATC3	L41067	13	cytoplasmic, calcineurin-dependent 3
				qe	
1702	1702 38438_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
				nuclear factor of kappa light polypeptide	
1703	1703 1377_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
				nuclear factor of kappa light polypeptide	nuclear factor of kappa light polypeptide
1704	1704 1461 at	NEKBIA	M69043	gene enhancer in B-cells inhibitor, alpha	gene enhancer in B-cells inhibitor, alpha
1705	1705 37544 at	NFIL3	X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
1706	1706 38648 at	CIZ	U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
				nuclear phosphoprotein similar to S.	
1707	1707 40816_at	PWP1	L07758	cerevisiae PWP1	IEF SSP 9502
1708	1708 34312_at	NCOA2	AI040324	nuclear receptor coactivator 2	
1709	1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Amplified in Breast Cancer
1710	1710 39174 at	NCOA4	X77548	nuclear receptor coactivator 4	Ret fused gene
1711	1711 40088_at	NRIP1	X84373	nuclear receptor interacting protein 1	nuclear factor RIP140
				nuclear receptor subfamily 2, group F,	
1712	39397_at	NR2F2	M64497	member 2	apolipoprotein Al regulatory protein-1
				nuclear receptor subfamily 3, group C,	nuclear receptor subfamily 3, group C,
1713	1713 36690 at	NR3C1	M10901	member 1	member 1
1714	1714 35302 at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715	37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
				nuclear transcription factor, X-box binding	
1716	1716 34667_at	NFX1	U15306	1	NFX1
				nuclear; Homo sapiens tyrosine	
171,	1717 33413_at	PRL-1	AF051160	phosphatase (PRL-1) gene, complete cds. lyrosine phosphatase	tyrosine phosphatase

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АВВС	0		\mathbf{H}^{2}	D Directors constitute alement binding protein	ш
1718 32340 s at NSEP1 M85234 1	M85234		nucie 1		nuclease sensitive element binding protein-1
NUCB2 X76732	X76732		nucle	nucleobindin 2	NEFA protein
1720 36597 at NOLC1 D21262 nucle	D21262		nucle	nucleolar and coiled-body phosphprotein 1 ORF	JRF
HSA6591 AJ006591	91 AJ006591		nucle	nucleolar cysteine-rich protein	cysteine-rich protein
HUMAUANTIG L05425	L05425		nucle		nucleolar GTPase
NUP133 AF052123	AF052123	23	nuclec		
NUP153 Z25535	Z25535		nucle		nuclear pore complex protein hnup 153
NUP98 AF042357	AF042357		nuclec		
NAP1L1 M86667	M86667		nuclec		nucleosome assembly protein 1-like 1
NAP1L3 D50370	D50370		uncled		nucleosome assembly protein
NAP1L4 U77456	U77456		nuclec	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
U18919	U18919		nucled	nucleotide binding protein	nucleotide binding protein
		xipnu	nudix	nudix (nucleoside diphosphate linked	diphosphoinositol polyphosphate
1730 41584 at NUDT3 AF062529 moiety	AF062529		moiety	moiety X)-type motif 3	phosphohydrolase
L40393	L40393		qunu	numb homolog (Drosophila)	numb homolog
		ob15e	ob15e	ob15e02.s1 NCI_CGAP_Kid3 Homo	
sapien	sapien	sapien	sapien	sapiens cDNA clone IMAGE:1323770 3'	
simila	simila	simila	simila	similar to SW:ROA3_HUMAN P51991	
HETE	HETE	HETE	HETE	HETEROGENEOUS NUCLEAR	
RIBC	RIBC	RIBC	RIBC	RIBONUCLEOPROTEIN A3:, mRNA	
1732 35916_s_at INHBC AA877215 sequ	AA877215		sedn	sequence.	
OCRL U57627	U57627		ocnk	oculocerebrorenal syndrome of Lowe	ocrl1
		olfact	olfact	olfactory receptor; Human olfactory	
1734 31921 at OLF3 U56421 recep	U56421		recep	receptor (OLF3) gene, complete cds.	HsOLF3
		O-link	O-link	O-linked N-acetylglucosamine (GlcNAc)	
transf	transf	transf	transf	transferase (UDP-N-	
acety	acety	acety	acety	acetylglucosamine:polypeptide-N-	
AL050366	AL050366		acetyl	acetylglucosaminyl transferase)	hypothetical protein
OGFR AF109134	AF109134		pioido	opioid growth factor receptor	09-InC
OPA1 AB011139	AB011139		optic	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
OPTN AF070533	AF070533		optin	eurin	optineurin
			OR1	OR11-3; offactory receptor; Homo sapiens	
			OR7	OR7E12P pseudogene, complete	
1739 34539_at OR7E12P AF065854 sequ	AF065854		88	sednence.	

Fig.21

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	A	a	٥		7 9 diamino polarionic acid
140	AFEV BioCo of		104423	OBF 1	aminotransferase
<u> </u>	1/40 AFFA-DIOC-3_at DIOA				7,8-diamino-pelargonic acid
1241	1741 AFEX. Rio B. M athio A		J04423	ORF 1	aminotransferase
	ייין מייין אייין אייין				7,8-diamino-pelargonic acid
1742	1742 AFFX-BioDn-5 abioA		J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFEX-BioDn-3 abioA	-	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5 at bioA	bioA	J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	A Sicional Composition
1745	1745 32412_at	RPS14	M13934	S14 gene, complete cds.	unknown protein; ribosofinal protein 314
				ORF1; ORF 2; no start codon; Human	
				mRNA for ornithine decarboxylase	
1746	1746 1315_at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme i
				reference V bionites assembly of 100 to 100	
	,		00000	ORF-Z; ORF-S; nullal reliable A receptor	retinoid X recentor alpha
1747	1747 32800_at	HXHA; NHZB1	00000	alpha Ilinika, 3 OTn, palitai sequence.	criain recognition complex subunit 5
,	1	000	1100538	origin recognition complex, subunit 5-like	
1/48	1/48/38135_at	חטטרט		Oznithino eminotransferase (rovate	
		ŀ	1110007	of milling an importance and (9) and	ornithine aminotransferase
1749	1749 36636_at	CAI	M1220/	allopiny	
1750	1750 1959 at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
1751	1751 33367_s_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor antizyme inhibitor	antizyme innibitor
				ornithine decarboxylase; Human ornithine	
1752	1752 1081_at	000	M33764	decarboxylase gene, complete cds.	ornithine decarboxylase i
				orphan G protein-coupled receptor; Homo	
7	24	2002	AE027957	sapiens o protein-coupled receptor (GPR35) gene, complete cds.	G protein-coupled receptor
ć -	1/33 31 / UU_at	Gruss	A1 021 331		
1754	1754 1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like) osteoblast specific factor 2	osteoblast specific factor 2
,	177.00	OK A 1	Yangas	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like
í E	1/55/39//4_at	OVAIL	CEOCOV	מאוממים (כלוסמווים ווים כל מספרים)	

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	A	8	ပ	O	'n
756	756 39136 at		AB017642	oxidative-stress responsive 1	oxidative-stress responsive 1
757	757 41438 at	870			oxysterol-binding protein-like protein 8
758	758 34329 at			e 2	
759					P311 HUM
760			15	protein	Pig11
192	761 40441 g at	3P1		PAI-1 mRNA-binding protein	hypothetical protein
1762				PAI-1 mRNA-binding protein	hypothetical protein
763	1762 22001 e at			paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
3	35001_3_at				paired box gene 8, isoform PAX8A; paired
	-				box gene 8, isoform PAX8B; paired box
	-				gene 8, isoform PAX8C; paired box gene 8,
					isoform PAX8D; paired box gene 8, isoform
1764 121	121 at	PAX8	66969X	paired box gene 8	PAX8E
1765	765 40127 at		M95929	paired mesoderm homeo box 1	homeobox protein
1766	766 41191 at	992	AB023209	palladin	KIAA0992 protein
1767	767 40504 at		AF001601	paraoxonase 2	paraoxonase
				partially supported by FGENES and	
1768	1768 36032 at	dJ167A19.1	AL031427	GENSCAN	hypothetical protein
1769	769 39243 s at		U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	1770 41665 at		AB020631	PCF11p homolog	KIAA0824 protein
1771	1771 38758 at	PDAP1	R98910	PDGFA associated protein 1	
1772	772 36937 s at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	32026 s at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745 at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF; Human pigment epithelium-derived	_
1775	1775 40856 at	SERPINF1; PEDF U29953	U29953	factor gene, complete cds.	pigment epithelium-derived tactor
	•			pentaxin-related gene, rapidly induced by	•
1776	1776 1491 at	PTX3	M31166	IL-1 beta	tumor necrosis factor
				peptidylglycine alpha-amidating	peptidylglycine alpha-amidating
1777	1777 38465_at	PAM	M37721	monooxygenase	monooxygenase
1778	1778 35803 at	alda	M63573	peptidylprolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein
	133023 at	2	2.22		



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1779	779 37422 at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C
1780	1780 37385_at	PPIG	U40763	/clophilin G)	CARS-Cyp
1781	781 36829 at	PER1	AF022991		Rigui
1782	1782 35835 at	PDL-108	AB019409	periodontal ligament fibroblast protein	
				peripheral benzodiazepine receptor;	peripheral benzodiazapine receptor;
				Human peripheral benzodiazepine	peripheral benzodiazapine receptor short
1783	1783 32806 at	BZRP; MBR; PBR	R M36035	receptor (hpbs) mRNA, complete cds.	form
1784	784 38653 at	PMP22	D11428	peripheral myelin protein 22	PMP-22(PAS-II/SR13/Gas-3)
1785	785 41213 at	PRDX1	X67951	peroxiredoxin 1	peroxiredoxin 1
					Aop1_Human, MER5(Aop1_Mouse)-like
1786	1786 36631 at	PRDX3	D49396	peroxiredoxin 3	protein
1787			U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788		_	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789	1789 36864 at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
				peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790	1790 36625 at	ZAP128	L40401	thioesterase	thioesterase
				peroxisomal membrane protein 3 (35kD,	
1791	1791 33265_at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792		PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793		PHF3	D87685	PHD finger protein 3	PHD finger protein 3
					PHD zinc finger protein XAP135, isoform a:
1794	1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	PHD zinc finger protein XAP135, isoform b
1705	1705 1434 at	PTEN	U92436	prospriates and tensin nomology (mutated in multiple advanced cancers 1)	MMAC1
3	101				type-2 phosphatidic acid phosphatase alpha-
1796	1796 34797 at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	
1707	40 0000	DDAD2B	AE017786	nhoenhatidic acid nhosnhatasa type 28	phosphatidic acid phosphohydrolase
	33005 at	27 17 1		phosphatidylinositol 4-kinase, catalytic.	
1798	1798 40783 s at	PIK4CA	L36151	alpha polypeptide	phosphatidylinositol 4-kinase
	L	7	1145076	phosphatidylinositol binding clathrin	= N
36/1	1/99 3/685_at	IFICALIVI	043370	descently protein	

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	A	В	ن	O	
		0		phosphatidylinositol glycan, class A	PIG. A protein
1800);	1800 39993_at			(8)	
1801	1801 314_at	PIGB	D42138	phosphatidylinositol glycan, class B	PIG-B
2	754 24	0010	D85418	chasenhatidylinositol alycan class C	phosphatidylinositol-glycan-class C (PIG-C)
700	/ɔɪ_aɪ	201			
1803 776	776_at	PIGF	D13435		1-512
1804	1804 40629 at	PIGH	L19783	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
				phosphatidylinositol transfer protein,	homologue of Drosphila retinal degeneration
1805	1805 38297 at	MNdTId	X98654		B gene
	1			phosphatidylinositol-4-phosphate 5-	phosphatidylinositol-4-phosphate 5-kinase
1806	1806 35741 at	PIP5K2B	U85245		type II beta
1807	1807 37320 at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
				phosphodiesterase 4B, cAMP-specific	
				(phosphodiesterase E4 dunce homolog,	
1808	1808 33705 at	PDE4B	L20971	Drosophila)	phosphodiesterase
				phosphodiesterase 4D interacting protein	
1809	1809 39422 at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
1810	1810 37676 at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
				phosphoenolpyruvate carboxykinase 2	
1811	1811 37188 at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812	812 39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813	1813 32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814	1814 36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815	37677 at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816	41221 at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 2
1817	1817 35665 at	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
				phosphoinositide-3-kinase, regulatory	
1818	1818 1269 at	PIK3R1	M61906	subunit, polypeptide 1 (p85 alpha)	
				phosphoinositide-3-kinase, regulatory	
1819	1819 37961 at	PIK3R3	1090907	subunit, polypeptide 3 (p55, gamma)	
1820	1820 32775 r at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
0	10000	DEA16	YBEBOO	nhosenhonrotein enriched in astrocytes 15	
1001	32200_al	3	20000	phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase
1822	1822 36489 at	PRPS1	D00860	prospriorizesyr pyropriospriate symmetrical	prospinosyr pyropriospriate syrinotation prospinosyr pyropriospriate syrinotation (

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R22 37338_at PRPSAP1 D61391 associated protein 1 mideace prosphoribosylaminoimidazole prosphoribosylaminoimidazo						
PRPSAP1 D61391 associated protein 1 PRPSAP1 D61391 associated protein 1 PAICS X53793 carboxylase, PHKB X84908 phosphoribosylaminoimidazole PAICS X63793 succinocarboxamide synthetase PHKB X84908 phosphorylase kinase, beta PHKB U47025 phosphorylase kinase, beta PHKB AF023462 disease) PTG1IP Z50022 protein PTG1IP Z50022 protein PDGFRA M21574 apha subunit (45kD) PDGFRA M21574 apha polypeptide PDGFRA M21574 apha polypeptide PSCD1 M85169 plestin homology, Sec7 and coiled/coil PRCD1 M85169 pleckstrin homology, Sec7 and coiled/coil PARG AF030339 plexin C1 PARG AF030339 plexin C1 PARG AF030339 plexin C1 PARG AF030339 plexin C1 PARDC1 V00345 poly(IC) binding protein 2 PARDC1 V00345 poly(IC) binding protein 2 PARDC1 X78136 poly(IC) binding protein 2 PCRP2 X78136 poly(IC) binding protein 3 Tal PCBP3 PCBP3 poly(IC) binding protein 3 Tal PCBP3 PCBP3 POly(IC) binding protein 3 Tal PCBP3 PCBP3 POly(IC) binding protein 3			8	ပ	O	n ,
PRPSAP1 D61391 associated protein 1	T				phosphoribosyl pyrophosphate synthetase-	phosphoribosypyrophosphate synthetase-
phosphoribosylaminolimidazole carboxylase, phosphoribosylaminolimidazole carboxylase, phosphoribosylaminolimidazole pAICS X53793 succinocarboxamide synthetase phosphorylase, beta phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase) (Resum phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase) (Resum phytanoyl-CoA hydroxylase) (Resum phytanoyl-CoA hydroxylase) (Refsum phytanoyl-CoA) (Refsum phytanoylase) (Refsum phetal-derived growth factor receptor, placefstrin homology, Sec7 and coiled/coil domains 1 (Cytohesin-1) (Refsum phetal-derived growth factor receptor, pleckstrin homology, Sec7 and coiled/coil domains 2 (Cytohesin-2) (Refsum phetal-derived growth factor receptor, pleckstrin homology, Sec7 and coiled/coil domains 2 (Cytohesin-2) (Refsum phetal-derived growth factor receptor, alpha polytohesin-2) (Refsum phetal-derived growth factor receptor, alpha phetal-derived growth factor receptor, alp	823	37338 at	PRPSAP1	D61391		associated protein 39
PAICS X53793 succinocarboxamide synthetase phosphorylase, phosphorylase, beta phosphorylase kinase, beta phosphorylase kinase, beta phosphorylase kinase, beta phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase) phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase) photein at PAEAH1B1 L13385 polycom by alpha subunit (45kD) plactelet-activating factor acetylhydrolase, plackstrin homology, Sec7 and coiled/coil domains 1 (cydohesin 1) plackstrin homology, Sec7 and coiled/coil domains 2 (cydohesin 1) plackstrin homology, Sec7 and coiled/coil domains 2 (cydohesin 2) plackin C1 at PABPC1 AR030339 plexin C4 adactivity and poly(C) binding protein C4 adactivity and poly(C) binding protein C4 at AD030334 poly(C) binding protein C4 at AD030334 poly(C) binding protein C4 at						absenborbowyaminojmidazoje carboxvlase.
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PAICS X53793 Structucocana Comming PAICS X63793 Structucocana Comming PAICS X64908 Phosphorylase glycogen; brain			(000	Œ	succinocarboxamide synthetase
PHKB X84908 phosphorylase Minase, Deal phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Refsum disease)	824	39056_at	PAICS	X53/93		phoenhorviase kinase
PYGB U47025 phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase (Refsum U77718 pinin, desmosome associated protein (45kD) plastin 3 (T isoform) PAFAH1B1	825	37392 at	PHKB	X84908	phosphorylase Kinase, peta	Thought Thompson B
PHYH AF023462 disease disease Depty	826	36667 at	PYGB	U47025	phosphorylase, glycogen; brain	glycogen prospriory as a spha-
at PHYH AF023462 disease) at PNN U77718 pinin, desmosome associated protein at PTG1IP Z50022 protein at PLS3 M22299 plastin 3 (T isoform) platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD) platelet-derived growth factor receptor, alpha polypeptide pDGFRA M21574 alpha polypeptide plackstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1) pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1) pSCD1 M85169 domains 2 (cytohesin 1) pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1) pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin 2) at PLXNB2 AB002313 pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin 2) at PLXNB2 AB002313 plexin B2 at PARG AF030339 plexin B2 at PABPC1 V00345 poly(Ab binding protein, cytoplasmic 1 pABPC1 Y00345 poly(Ab binding protein, cytoplasmic 1 at PCBP2 X78136 poly(C) binding protein 2		i			phytanoyl-CoA hydroxylase (Hetsum	peroxisolitai priyrantoyroon arprix
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PTTG1IP Z50022 protein	828	33543 s at	PNN	U77718	pinin, desmosome associated protein	Dinin
at PTTG1IP Z50022 protein at PLS3 M22299 plastin 3 (T isoform) p PAFAH1B1 L13385 isoform lb, alpha subunit (45kD) p PDGFRA M21574 alpha polypeptide p PDGFRA M21574 alpha polypeptide p PCD1 M85169 domains 1(cytohesin 1) p PSCD2 U70728 domains 2 (cytohesin 1) at PLXNB2 AB002313 pleickstrin homology, Sec7 and coiled/coil p PSCD2 U70728 domains 2 (cytohesin 1) at PLXNB2 AB002313 pleickstrin homology, Sec7 and coiled/coil p PSCD2 U70728 domains 2 (cytohesin 1) at PLXNB2 AB002313 pleickstrin homology, Sec7 and coiled/coil p PSCD2 U70728 domains 2 (cytohesin 2) at PARGC1 AB002313 pleickstrin homology, Sec7 and coiled/coil p PSCD2 U70728 pleickstrin homology, Sec7 and coiled/coil p PSCD2		-			pituitary tumor-transforming 1 interacting	diological and a second
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PAFAH1B1 L13385 isoform lb, alpha subunit (45kD) platelet-derived growth factor receptor, alpha polypeptide plackstrin homology, Sec7 and coiled/coil pleckstrin homology, Sec7 and coiled/coil					platelet-activating factor acetylhydrolase,	
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at PDGFRA M21574 alpha polypeptide 6_at PSCD1 M85169 domains 1(cytohesin 1) 1_at PSCD2 U70728 domains 2 (cytohesin 1) 1_at PSCD2 U70728 domains 2 (cytohesin 1) 10_at PLAGL1 U81992 pleiomorphic adenorma gene-like 1 10_at PLXNB2 AB002313 plexin B2 10_at PLXNC1 AF030339 plexin C1 10_at PARG AF005043 poly (ADP-ribose) glycohydrolase 15_sat PABPC1 AF005043 poly (ADP-ribose) glycohydrolase 15_at PABPC1 AF005043 poly (ADP-ribose) glycohydrolase 15_at PABPC1 Y00345 poly (A) binding protein, cytoplasmic 1 15_at PABPC1 Y00345 poly (A)-specific ribonuclease 13_at PCBP1 Z29505 poly (C) binding protein 1 25_5at PCBP2 X78136 poly (C) binding protein 2 45_tat PCBP2 AL046394 poly (C) binding protein 3	3	32303_aii			platelet-derived growth factor receptor,	platelet-derived growth factor receptor A
6_at PSCD1 M85169 domains 1(cytohesin 1) 1_at PSCD2 U70728 domains 2 (cytohesin 1) 1_at PLAGL1 U81992 pleckstrin homology, Sec7 and coiled/coil 1_at PLAGL1 U81992 pleckstrin homology, Sec7 and coiled/coiled 1_at PLAGL1 U81992 pleckstrin homology, Sec7 and coiled/coi	1822		PDGFRA	M21574	ľ	chain
PSCD1 M85169 domains 1(cytohesin 1)	200				pleckstrin homology, Sec7 and coiled/coil	
PSCD2 U70728 domains 2 (cytohesin-2)	1833	38666 at	PSCD1	M85169	domains 1(cytohesin 1)	
at PSCD2 U70728 domains 2 (cytohesin-2) at PLAGL1 U81992 pleiomorphic adenoma gene-like 1 PLXNB2 AB002313 plexin B2 PLXNC1 AF030339 plexin C1 PARG AF005043 poly (ADP-ribose) glycohydrolase PABPC1 Z48501 poly (ADP-ribose) glycohydrolase PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Y00345 poly(A)-specific ribonuclease PARN AJ005698 (deadenylation nuclease) R PCBP1 Z29505 poly(C) binding protein 1 at PCBP2 X78136 poly(C) binding protein 2 at PCBP2 X78136 poly(C) binding protein 2 at PCBP2 POly(BP34 poly(C) binding protein 3	3	1			pleckstrin homology, Sec7 and coiled/coil	
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at PARG AF005043 poly (ADP-ribose) glycohydrolase at PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Y00345 poly(A) binding protein, cytoplasmic 1 PABPC1 Y00345 poly(A)-specific ribonuclease PARN AJ005698 (deadenylation nuclease) PCBP1 Z29505 poly(C) binding protein 1 at PCBP2 X78136 poly(C) binding protein 2 at PCBP2 X78136 poly(C) binding protein 2 t PCBP2 AL046394 poly(C) binding protein 3	2 2	732193 at	PLXNC1	AF030339	plexin C1	VESPH - (* DB : 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1
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PARN AJ005698 (deadenylation nuclease) PCBP1 Z29505 poly(rC) binding protein 1 at PCBP2 X78136 poly(rC) binding protein 2 at PCBP2 X78136 poly(rC) binding protein 2 at PCBP2 AZ78136 poly(rC) binding protein 3 t PCBP3 AL046394 poly(rC) binding protein 3			PARPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytopiasitiic i
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PCBP2 X78136 poly(rC) binding protein 2 PCBP2 X78136 poly(rC) binding protein 2 PCBP3 AL046394 poly(rC) binding protein 3	188	2 34305 at	PCBP1	Z29505	poly(rC) binding protein 1	Subz.3
PCBP2 X78136 poly(rC) binding protein 2 PCBP3 AL046394 poly(rC) binding protein 3	184	335746 r at	PCBP2	X78136	poly(rC) binding protein 2	
PCBP3 AL046394	18	4 35745 f at	PCBP2	X78136	poly(rC) binding protein 2	ווושוואריבג
	184	5 39868_at	PCBP3	AL046394	poly(rC) binding protein 3	

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	¥	B	٥	lemosotile (cases)	
Γ		`	0000	polycystic Kidney disease 2 (autosoniai	polycystin 2
846				ONA directed) sigma	LAK-1
847	1847 33380_at F	POLS	AB005/54	6	polymerase (DNA directed), epsilon 3 (p17
			A E070640	polymerase (DIVA directed), epsilori o (n17 subunit)	subunit)
848	1848 38702_at	POLES	ALO(1040	BNA) II (DNA directed)	
		V C 0 10 0	X63564	polynterase (1.177) (2.100)	RNA polymerase II largest subunit
843	1849 40791 at			polymerase (RNA) II (DNA directed)	
1850	1850 39746 at	POLR2B	X63563	polypeptide B (140kD)	RNA polymerase II 140 kDa subunit
3				polymerase (RNA) II (DNA directed)	
1851	1851 36027_at	POLR2F	AA418779	polypeptide r	
2		POI R2H	U37689	polymerase (HNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
7001			COCTO	polymerase (RNA) II (DNA directed)	BNA polymerase II subunit
1853	1853 1248_at	POLRZH	03/689	polypepide i i	
1	1000	log log	0692611	polymerase (HNA) II (DNA directed) polypeptide L (7.6kD)	RNA polymerase II subunit
1834	503 at	רטבוובר		polymerase (RNA) II (DNA directed)	
1855	1855 35841_at	POLR2L	N24355	polypeptide L (7.6kU)	
1856	34320 at	PTRF	AL050224	polymerase I and transcript release factor	Debending in recentor
1857	1857 34005 at	PIGR	X73079	polymeric immunoglobulin receptor	Polyment mindinglobam coopie
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein I	Inclear Hoolingtochiocan
1050	33600 c at	PMS211	D38435	postmeiotic segregation increased 2-like 1	
<u> </u>	31000_s_a			pot. ORF1 (aa 1-73); ORF2, put. cre	
,	# 3 You'V FIRM		X03453	gene for recombinase protein.	
ğ _	שביים אים ואים ואים ואים ואים ואים ואים וא			pot. ORF1 (aa 1-73); ORF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
186	1861 AFFX-CreX-3_at	-	X03453	gene for recombinase protein.	
186	1862 315_at	PRDM2	D45132	PR domain containing 2, with ZNF domain zinc-finger DNA-binding protein	zinc-finger DNA-binding protein
186	1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3 homeobox protein	homeobox protein

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╁				precursor; Human prolyl 4-hydroxylase	
		-		beta-subunit and disulfide isomerase	
				lene, exon 11, clones 66-	
364 3	1864 36666 at	P4HB	M22806		prolyl 4-hydroxylase beta-subunit
365 3	1865 34321 i at	GS3786	D87120	predicted osteoblast protein	GS3786
866 4		PFDN4	U41816	prefoldin 4	C-1
867	1867 38698 at	PREI3	AL080070	preimplantation protein 3	hypothetical protein
868	1868 40269_at	PRP18	U51990	ctor 18	hPrp18
				ephalin	
869	1869 38291 at	PENK	J00123		proenkephalin
8706	1870 641 at	PSEN1	L76517	sease 3)	presenilin 1
871	1871 40621 at	PAWR	U63809	٦	prostate apoptosis response protein par-4
8724	1872 41773 at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
873	1873 31609 s at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
Γ					
874	1874 34795 at	PLOD2	U84573		lysyl hydroxylase isoform 2
	1			procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
875	1875 36184 at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876/37037 at	P4HA1	M24486	alpha polypeptide l	polypeptide I
				procollagen-proline, 2-oxoglutarate 4-	!
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390 at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
				-	
		•		procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase), beta	
				polypeptide (protein disulfide isomerase;	polypeptide (protein disulfide isomerase;
1878	1878 691 g at	P4HB	J02783	thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1879	1879 38840 s at	PFN2	L10678	profilin 2	profilin II
1880	1880 38839 at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	
1881	1881 38802 at	PGRMC1	Y12711	component 1	putative progesterone binding protein
				progesterone receptor membrane	nio joya paipaid ouosetassas
1882	1882 38821_at	PGRMC2	AJ002030	component 2	progresserone binding protein

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8833		500	AF006010		progestin induced protein
8843	at		AF006010	progestin induced protein	progestin induced protein
38.		D10	AF022385	0	TFAR15
8863	1886 37569 at	PDCD6	AF035606		calcium binding protein
				ell death 8 (apoptosis-	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
1887 3	32212_at	PDCD8 .	AL049703	actor)	hypothetical protein
1888	36592_at	PHB	S85655		pronibilin
1889 1884	1884 s at	PCNA	M15796		proliferating cell nuclear antigen
8904	1890 41600 at	PA2G4	U59435	П	cell cycle protein p38-2G4 homolog
	1			proline-rich Gla (G-carboxyglutamic acid)	
1891	1891 35978 at	PRRG1	AF009242		proline-rich Gla protein 1
1892	1892 36023 at	PRH1	AI864120		
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing memorane
1893	1893 40803 at	PORIMIN	AL050161	injury gene	injury gene
				propionyl Coenzyme A carboxylase, alpha	propionyl Coenzyme A carboxylase, alpha Propionyl-Coenzyme A carboxylase, alpha
1894	1894 1348 s at	PCCA	S79219	polypeptide	polypeptide precursor
				propionyl Coenzyme A carboxylase, beta	
1895	1895 36561 at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
				proprotein convertase subtilisin/kexin type	•
1896	1896 41032_at	PCSK5	U56387	5	protease PC6 isoform A
				prosaposin (variant Gaucher disease and	prosaposin (variant Gaucher disease and
1897	1897 36795 at	PSAP	703077	variant metachromatic leukodystrophy)	variant metachromatic leukodystrophy)
1808	1898 38406 f at	PTGDS	A1207842	prostaglandin D2 synthase (21kD, brain)	
3				prostaglandin E receptor 2 (subtype EP2),	
1899	1899 828_at	PTGER2	U19487	53kD	prostaglandin E2 receptor
1900	1900 1890 at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
1901	1901 32611 at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902	11	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1903		PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1904	1904 33368 at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
1905	1905 40078 at	SPUVE	AF015287	protease, serine, 23	serine protease
1906	1906 39845 at	PRSS25	AF020760	protease, serine, 25	serine protease
1007	1007 688 at	PSMC1	1.02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit
	000 al	LOMO	L02720		

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				proteasonie (prosonie, macropani) 203	MSC1 protein
908	1908 35353_at	PSMC2	D11094		MISS I DIGICILI
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 26S
606	1909 592 at	PSMC3	M34079	subunit, ATPase, 3	subunit, ATPase, 3
				proteasome (prosome, macropain) 26S	
1910	1910 37766_s_at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	,
1911	1911 949_s_at	PSMC6	D78275	subunit, ATPase, 6	proteasome subunit p42
				proteasome (prosome, macropain) 26S	:
1912	1912 1314_at	PSMD1	D44466	subunit, non-ATPase, 1	proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192 at	PSMD12	AB003103	subunit, non-ATPase, 12	26S proteasome subunit p55
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 26S
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
				268 (medorane macronal 268	
1015	1915 945 at	PSMD7	D50063	subunit. non-ATPase, 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
	5-21-2				
				proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
				proteasome (prosome, macropain) 26S	
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	AI347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	1919 41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1920	1920 1184_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1921	36974_at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
1922	1922 38371_at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
		-		proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1923	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
300	1440	DEMAA	000762	proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1324	1924 1448 at	PSIMAS	וחחחת	Subuliit, aipila type, o	apria type, o



A B C C Professome (prosone, macropain) A B C Professome (prosone, macropain) subunit, alpha type, 4 A Subunit, alpha type, 4 A A A B A B B C B B B B B B B						
pSMA4 D00763 subunit, alpha type, 4 proteasome (prosome, macropain) proteasome (prosome, macro		A	8	၁		Ψ.
PSMA4 D00763 Subunit, alpha Vpe, 4						oroteasome (prosome, macropain) subunit,
PSMA4 D00763 Subunit, alpha type, 4	1925	1450 g at	PSMA4	D00763		alpha type, 4
PSMA4 D00763 Subunit, alpha type, 4						proteasome (prosome, macropain) subunit,
PSMA5 Al246726 subunit, alpha type, 5 proteasome (prosome, macropain) PSMA6 X59417 subunit, alpha type, 6 proteasome (prosome, macropain) PSMB1 D00761 subunit, beta type, 1 proteasome (prosome, macropain) proteasome (proso	1926	1449 at	PSMA4	D00763		alpha type, 4
PSMA5 Al246726 Subunit, alpha type, 5					proteasome (prosome, macropain)	
PSMA6 X59417 Subunit, alpha type, 6	1927	37046 at	PSMA5	AI246726	subunit, alpha type, 5	
PSMA6 X59417 Subunit, alpha type, 6						
PSMB1 D00761 Subunit, beta type, 1	1928	36122 at	PSMA6	X59417		prosomal P27K protein
at PSMB1 D00761 subunit, beta type, 1 It at PSMB2 D26599 subunit, beta type, 2 4_at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 6 b_at PSMB5 D29011 subunit, beta type, 6 c_at PSMB5 D29012 subunit, beta type, 6 at PSMB6 D29012 subunit, beta type, 6 at PSMB7 D38048 subunit, beta type, 7 at PSMB7 D38048 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7 subunit, beta type, 7						proteasome (prosome, macropain) subunit,
at PSMB2 D26599 subunit, beta type, 2 4_at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) proteasome (prosome, macropain) at PSMB5 D29011 subunit, beta type, 5 board proteasome (prosome, macropain) proteasome (prosome, macropain) board proteasome (prosome, macropain) proteasome (prosome, macropain) board proteasome (prosome, macropain) proteasome (prosome, macropain) cat PSMB7 D38048 subunit, beta type, 6 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain)	1929	1447 at	PSMB1	D00761		beta type, 1
at PSMB2 D26599 subunit, beta type, 2 proteasome (prosome, macropain) protea						
at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 4 at PSMB4 D26600 subunit, beta type, 4 at PSMB5 D29011 subunit, beta type, 6 at PSMB5 D29011 subunit, beta type, 6 profeasome (prosome, macropain) profeasome (prosome, macropain) pat profeasome (pr	1930		PSMB2	D26599		proteasome subunit HsC7-I
at PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) proteasome (prosome, macropain) at PSMB4 D26600 subunit, beta type, 4 Image: 4 macropain macropain macropain) at PSMB5 D29011 subunit, beta type, 5 macropain macropain) Image: 4 macropain macropain macropain) at PSMB6 D29012 subunit, beta type, 6 macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 macropain) at PSMB7 D38048 subunit, beta type, 7 macropain) at PSMB7 D38048 subunit, beta type, 7 macropain) at PSMB7 D38048 subunit, beta type, 9 (large multifunctional macropain) proteasome (prosome, macropain) subunit, beta type, 7 noteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) pat proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain)						
PSMB4 D26600 Subunit, beta type, 4	1931		PSMB4	D26600		proteasome subunit HsN3
PSMB4 D26600 Subunit, beta type, 4 PSMB4 D2600 Proteasome (prosome, macropain)		11				
at PSMB5 D29011 subunit, beta type, 5 proteasome (prosome, macropain) at PSMB6 D29012 subunit, beta type, 6 proteasome (prosome, macropain) at PSMB7 D38048 proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional protease 2) at protein inhibitor of activated STAT3 at PRKCBP1 M22296 protein kinase (cAMP-dependent, catalytic) inhibitor gamma at PRKCI L33881 protein kinase C binding protein 1 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C-like 2	1932		PSMB4	D26600		proteasome subunit HsN3
at PSMB5 D29011 subunit, beta type, 5 proteasome (prosome, macropain) proteasome (prosome, macropain) at PSMB7 D38048 proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) at PSMB9 AA808961 proteasome (prosome, macropain) at PSMB9 protein type, 7 nultifunctional at PSMB9 protein disulfide isomerase-related protein at PRKCB AB01851 protein kinase (cAMP-dependent, at PRKCBP1 W22296 protein kinase C binding protein 1 at PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota at PRKCL2 U33052 protein kinase C-like 2						
PSMB6 D29012 subunit, beta type, 6 PSMB7 D38048 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) protein disultide isomerase-related protein protein kinase (cAMP-dependent, catalytic) inhibitor of activated STAT3 protein kinase C binding protein 1 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota	1933		PSMB5	D29011		proteasome subunit X
PSMB6 D29012 subunit, beta type, 6 PSMB7 D38048 subunit, beta type, 7 PSMB7 D38048 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) protein disultide isomerase-related protein protein kinase (cAMP-dependent, multifunctional protein to protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota					proteasome (prosome, macropain)	
PSMB7 D38048 Subunit, beta type, 7	1934	941_at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
PSMB7 D38048 subunit, beta type, 7 PSMB7 D38048 subunit, beta type, 7 PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 (large multifunctional proteasome (prosome, macropain) (large multifunctional protean disultide isomerase-related protein (large multifunctional protein kinase (cAMP-dependent, macropain) (large multifunctional protein kinase (cAMP-dependent, macropain) (large multifunctional protein kinase (colora (large multifunctional					proteasome (prosome, macropain)	:
at PSMB7 D38048 proteasome (prosome, macropain) 7_at PSMB7 D49489 proteasome (prosome, macropain) 2_at PSMB9 AA808961 protease 2) I 8_at PIAS3 AB021868 protein disulfide isomerase-related protein 6_at PKIG AB019517 catalytic) inhibitor of activated STAT3 7_at PRKCBP1 W22296 protein kinase (cAMP-dependent, catalytic) inhibitor gamma at PRKCI L33881 protein kinase C binding protein 1 g_at PRKCI L33881 protein kinase C, iota g_at PRKCL2 D33052 protein kinase C-like 2	1935	39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) 2 at PSMB9 AA808961 protease 2) . 2 at PAS3 AB021868 protein disulfide isomerase-related protein 6 at PKIG AB019517 catalytic) inhibitor of activated STAT3 7 at PRKCBP1 W22296 protein kinase (cAMP-dependent, catalytic) inhibitor gamma at PRKCI L33881 protein kinase C binding protein 1 g at PRKCI L33881 protein kinase C, iota g at PRKCL2 U33052 protein kinase C-like 2					proteasome (prosome, macropain)	:
T_at PSMB9 AA808961 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) 2_at PSMB9 protein disulfide isomerase-related protein and protein inhibitor of activated STAT3 8_at PIAS3 AB021868 protein inhibitor of activated STAT3 6_at PKIG AB019517 catalytic) inhibitor gamma 7_at PRKCBP1 W22296 protein kinase C binding protein 1 at PRKCI L33881 protein kinase C, iota g_at PRKCI L33881 protein kinase C, iota g_at PRKCL2 U33052 protein kinase C-like 2	1936	1313 at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
PSMB9 AA808961 protease 2) . PSMB9 AA808961 protease 2) . PS D49489 protein disulfide isomerase-related protein PIAS3 AB021868 protein inhibitor of activated STAT3 PRIG AB019517 catalytic) inhibitor gamma t PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota t PRKCI L33881 protein kinase C, iota t PRKCL U33052 protein kinase C-like 2		1			proteasome (prosome, macropain)	
PSMB9 AA808961 protease 2) . P5 D49489 protein disulfide isomerase-related protein protein inhibitor of activated STAT3 R PIAS3 AB021868 protein inhibitor of activated STAT3 R AB019517 catalytic) inhibitor gamma R PRKCBP1 W22296 protein kinase C binding protein 1 R PRKCI L33881 protein kinase C, iota R PRKCI L33881 protein kinase C, iota R PRKCI L33881 protein kinase C, iota R PRKCL U33052 protein kinase C-like 2					subunit, beta type, 9 (large multifunctional	
P5 D49489 protein disulfide isomerase-related protein pliAS3 AB021868 protein inhibitor of activated STAT3 PIAS3 AB021868 protein inhibitor of activated STAT3 PRIC AB019517 catalytic) inhibitor gamma t PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota	1937	38287_at	PSMB9	AA808961	protease 2)	
PIAS3 AB021868 protein inhibitor of activated STAT3	1038	141750 at	55	D49489	protein disulfide isomerase-related protein	human P5
PKIG AB019517 catalytic) inhibitor gamma	5 5	132558 at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
PKIG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota II PRKCI L33881 protein kinase C, iota PRKCL U33052 protein kinase C-like 2		100000			protein kinase (cAMP-dependent,	
PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota AI PRKCI L33881 protein kinase C, iota PRKCL2 U33052 protein kinase C-like 2	1940	34376 at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
PRKCI L33881 protein kinase C, iota 11 PRKCI L33881 protein kinase C, iota PRKCL2 U33052 protein kinase C-like 2	194	1 36957 at	PRKCBP1	W22296	protein kinase C binding protein 1	
at PRKCI L33881 protein kinase C, iota It PRKCL2 U33052 protein kinase C-like 2	194	2 1602 at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
at PRKCL2 U33052 protein kinase C-like 2	194	3 1603 q at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
	194		PRKCL2	U33052	protein kinase C-like 2	PRK2

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T	C)			
945	1945 41768 at	PRKAR1A	M33336	regulatory, type I, alpha (tissue specific certinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
					AMP-denendent protein kinase twe I-alpha
946	1946 227 g at	PRKAR1A	M33336	acilic	subunit
	-6-				
- 1	•	× × × × × × × × × × × × × × × × × × ×	M22226	regulatory, type I, alpha (tissue specific ordinarisher 1)	cAMP-dependent protein kinase type I-alpha subunit
747	1947 220_ai				
	1			protein kinase, interferon-inducible double protein activator of tile litter erot-induced	protein activator of the interferor-induced
1948	1948 32205_at	PHKHA	AFU/2800	bunit	serine /threonine specific protein
10/0	10/0 37725 at	PPP1CC	X74008		phosphatase
3	m-03110			protein phosphatase 1, regulatory	
1950	1950 40438 at	PPP1R12A	D87930		myosin phosphatase target subunit 1
				protein phosphatase 1, regulatory	
1951	1951 39366 at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540 at	PPP1R7	Z50749	7	yeast sds22 homolog
				protein phosphatase 1A (formerly 2C),	
1953	1953 857 at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1A (formerly 2C),	
1954	1954 36501 at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305	dependent, delta isoform	Wip1
				protein phosphatase 2 (formerly 2A),	
1956	924 s at	PPP2CB	J03805	catalytic subunit, beta isoform	
				protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PR 52), alpha	
1957	1957 41167 at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
				protein phosphatase 2 (formerly 2A),	
1050	10501383 24	DDD0B0A	M64929	isoform	protein phosphatase-2A subunit-alpha
	10001			protein phosphatase 2, regulatory subunit	
1956	1959 32734_at	PPP2R5E	L76703	B (B56), epsilon isoform	protein phosphatase B56-epsilon



 	A	В	ပ	\neg	E Eliphat redulatory
			030501	protein phosphatase 2, regulatory subunit B (BSS) namma isoform	subunit
980	960 40786_at	PPPZHSC		equiatory subunit	protein phosphatase 2A B'alpha1 regulatory
126 04	76.04	PPP2R5C	U37352	_	subunit
<u>-</u>	10 al	2017		se 2A, regulatory	
962	1962 39127 f at	PPP2R4	X73478		phosphotyrosyl phosphalase activator
3	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			protein phosphatase 3 (formerly 2B),	protein phosphatase 3 (101111e1ly 20),
				eurin	catalytic subunit, beta Isoloffii (calcineum A
1963 38277	38277 at	PPP3CB	M29550	A beta)	Dora)
				protein phosphatase 3 (formerly 2b),	
				catalytic subunit, gamma isoform	6 to 1 to
1964 32541	32541 at	PPP3CC	S46622	(calcineurin A gamma)	calcineurin A catalytic suburil
	11			protein phosphatase 4, regulatory subunit	
1965	34371_at	PPP4R1	U79267		
000	37581 21	Cada	X92972	protein phosphatase 6, catalytic subunit	protein phosphatase 6
000	ة ¢	DD001	M15036	protein S (alpha)	protein S (alpha)
202	196/32/32_s_dl	20010	A A D B 2 1 2 0	protein transfocation complex beta	
1968	1968 32564_at	SECOID	1,0000	arotoin turocine kinase 9	protein tyrosine kinase
1969	1969 1064_at	PTK9	002680	protein tylosing wingso 5	
		DTD444	1148206	protein tylosine priospriatase type in the member 1	protein tyrosine phosphatase PTPCAAX1
1970	1970 843_at	7174A1	040230	Washer the NA	
	1	D-TO-A-D	1114603	protein tyrosine priospriatase type 175.	protein-tyrosine phosphatase
19/1	19/1 38415_at	r i r 4M2	2001	protein tyrosine phosphatase type IVA.	
7	7	DTDAAO	1114603	member 2	protein-tyrosine phosphatase
7/61	1241 at	307		protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
1072	40137 at	PTPN1	M31724	receptor type 1	type 1
2/2	5 0			protein tyrosine phosphatase, non-	-
1074	1077 1463 at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
	5			protein tyrosine phosphatase, non-	
				receptor type 13 (APO-1/CD95 (Fas)-	
1075	24400 04	DTDN13	1112128	associated phosphatase)	protein tyrosine phosphatase 1E
2/2	34130		31.1.		protein tyrosine phosphatase, receptor type,
			•		A, isoform 1 precursor; protein tyrosine
				protein tyrosine phosphatase, receptor	phosphatase, receptor type, A, isoform 2
1976	1976 1496 at	PTPRA	M34668	type, A	precursor

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1	ζ			protein tyrosine phosphatase, receptor	
1977	1977 36204 at	PTPRF	Y00815		put. LAR preprotein (AA -16 to 1881)
T				protein tyrosine phosphatase, receptor	
	,			type, f polypeptide (PTPRF), interacting	
1978	1978 41780_at	PPFIA1	U22816	protein (liprin), aipna 1	LAR-interacting protein 1b
				tyrosine phosphatase, receptor	
1979	1979 1488_at	PTPRK	L77886	type, K	protein tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1980	995_g_at	PTPRM	X58288		protein-tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1981	31892 at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
				protein-kinase, interferon-inducible double	
		_			
1982	1982 41141 at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
*				protein-L-isoaspartate (D-aspartate) O-	
1983	1983 37737 at	PCMT1	D25547	methyltransferase	PIMT isozyme I
Γ		-		protein-L-isoaspartate (D-aspartate) O-	
1984	1984 37736 at	PCMT1	D13892	methyltransferase	carboxyl methyltransferase
1985	1985 32227_at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986	1986 38590 r at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987	 	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988	37936_at	HPRP4P	Al184802 ·	PRP4/STK/WD splicing factor	
				pseudoferritin H protein; Human ferritin H	
1989	1989 31697_s_at	FTHP1	J04755	processed pseudogene, complete cds.	
1990	1990 36117_at	PTK2	L13616	PTK2 protein tyrosine/kinase 2	focal adhesion kinase
1991	1991 40048_at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992	1992 35359_at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993	1993 35221_at	PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-	
				340), numan iivel iiiniva joi peta-subumi	
				signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
1994	1994 33341_at	GNB1	X04526	(g).	indust
1995	1995 33720_at	LOC56902	L48692	putatative 28 kDa protein	
1996	1996 39363 at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	BC-2 protein
		1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			

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1997	1997 39884 n at	HSA9761	AF091078	\neg	putative dimethyladenosine transferase
	5-6-, 5555			<u>.</u>	putative glialblastoma cell differentiation-
1998	1998 38841 at	GDBR1	AF068195		related protein
1999	1999 41188 at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984 at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
2002	2002 35286 r at	RY1	X76302	putative nucleic acid binding protein RY-1 nucleic acid binding protein	nucleic acid binding protein
				Putative prostate cancer tumor	
2003	2003 36852_at	N33	U42349	suppressor	
				ein similar to nessy	
2004	2004 33710_at	SF	U72515		Car
2005	40203 at	SUIT	AJ012375	or	putative translation initiation factor
2006	2006 37678 at	NMA	U23070	_	putative transmembrane protein
				putative transmembrane protein; homolog	
		· · · · · ·		of yeast Golgi membrane protein Yif1p	
2007	2007 35326 at	54TM	AF004876	(Yip1p-interacting factor)	54TMp
				putative; Homo sapiens PTS gene,	
2008	2008 35697 at	PTS	L76259	complete cds.	6-pyruvoyttetrahydropterin synthase
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2006	2009 40887 g at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
201	2010 40886 at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
201	2011 33219 at	VDU1	AB029020		KIAA1097 protein
	1			Pyruvate dehydrogenase complex, lipoyl-	-
				containing component X; E3-binding	pyruvate dehydrogenase complex protein X
201	2012 36164_at	PDX1	U82328	protein	subunit precursor
201	2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate Kinase, muscie
201	2014 260_at	adda	M16447	quinoid dihydropteridine reductase	quinoid dinydropterialine reductase

Fig. 2

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†				R3H domain (binds single-stranded	•
2015	2015 36610 at	R3HDM	D21852		KIAA0029 protein
19	2016 39030 at	RABAC1	AJ133534		renylated hab acceptor () ()
2		0000	100000	Rab geranylgeranyltransferase, beta	rab geranylgeranyl transferase
2017	2017 37703_at	HABGGIB	10001	in toolor	quanine nucleotide exchange factor mss4
2018	2018 38264_at	RABIF	U74324	HAB Interacting factor	
2010	2010 3660 at	BAB11A	AF000231		rab11a
	30000 at	DAB14	AF052113	RAB14, member RAS oncogene family	
2020	2020 35325 at	44040	AI OSOSER		hypothetical protein
2021	2021 34393_r_at	HABIA	ALCOCKO	Γ	hypothetical protein
2022	2022 34392_s_at	HABIA	ALUSU200	Γ	RAB21, member RAS oncogene family
2023	2023 33326_at	RAB21	D4208/	Τ	
7007	2024 809 at	BAB27A	U57094	RAB27A, member RAS oncogene family	Rab27a
2000	2024 003 at	BAB31	U59877	RAB31, member RAS oncogene family	low-Mr G P-binding protein Habs I
2028	2025 3337 1_s_at	RABSA	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
	21.00			rabe GTPase activating protein (GAP and	Accorded to the state of the st
2027	2027 35289 at	GAPCENA	AJ011679	centrosome-associated)	Rabe G i Pase activating protein, GALCEIN
202	2027 35304 at	RABGA	AF052130	RAB6A, member RAS oncogene family	
	2020 2020 at	RARGA	AI671547	RAB9A, member RAS oncogene family	
	2029 33020 at	BC3	AB020663	rabconnectin-3	KIAA0856 protein
3	10.71	2		Rac/Cdc42 guanine nucleotide exchange	
203	2021 37543 at	ARHGEF6	D25304	factor (GEF) 6	
	0 00057 at	PAD:	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
3 8	2032 30037 _at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
ξ	20014				XP-C repair complementing protein
203	2034 1874 at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	(p58/HHK23B)
8	77700	BAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
3	33 32/31_al	5		RAGE-4 ORF2; one of 2 possible coding	
				regions; RAGE-4 ORF3; one of 2 possible	
				coding regions; Human renal cell	
				carcinoma antigen HAGE-4 mHNA,	
203	2036 1524_at		U46194	complete putative cds.	Bi IP76 profein
233	2037 36628_at	RALBP1	L42542	raly binding protein 1	KIAA0959 profein
203	2038 37539_at	RGL	AB023176	Hald DS-like gene	

Fig. 2

r	A	В	0	0	Ξ
2039	2039 41342 at	RANBP1	D38076	RAN binding protein 1	Ran-BP1(Ran-binding protein 1)
2040	2040 40824 at	RANBP16	AB018288	9	KIAA0745 protein
20414	2041 41174 at	RANBP2L1	AF012086	RAN binding protein 2-like 1	Ran binding protein 2
2042	2042 35255_at	RANBP7	AF098799		RanBP7/importin 7
2043	2043 32602 at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1 smg GDS	smg GDS
2044	2044 1848 at	RAP1A	M22995	RAP1A, member of RAS oncogene family ras-related protein	ras-related protein
2045	2045 40146 at	RAP1B	AL080212	RAP1B, member of RAS oncogene family hypothetical protein	hypothetical protein
		i d	L	Ras association (RalGDS/AF-6) domain	nietwa voseanne remit evitation
2046;	2046 39601_at	RASSF1	AF061836	lamily 1	putative turnor suppressor protein
2047	2047 37598 at	RASSF2	D79990	Has association (HalGDS/AF-b) domain family 2	has association (halobovar-o) domain family 2
2048 1659	1659 s at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049		ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	2050 1394 at	ARHA	L25080	ras hornolog gene family, member A	GTP-binding protein
2051	2051 35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
				RAS p21 protein activator (GTPase	
2052	2052 36935_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675 at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793_at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 botulinum toxin substrate 1	
i c	40004	0 0	N25274	(rho family, small GTP binding protein	
200	2030 +0004 _at	2	חבסבו ז	ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	
2056	2056 2050 s at	RAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316 at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	2058 33234 at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	2060 34684 at	RECOL	L36140	RecQ protein-like (DNA helicase Q1-like)	DNA helicase
	15 - 10 C				

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1	4	g	2	D	1
2061	2061 34685 at	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
				regulated at the translational level;	
				contains I-mfa domain; untilizes unique	
				protein isoform p40 and HIC protein	HIC protein isoform p40; HIC protein isoform
2062	2062 37842 at	일	AF054589		p32
				regulator of G-protein signalling 19	
2063	2063 35756_at	RGS19IP1	AF089816		RGS-GAIP interacting protein GIPC
2064	2064 37701_at	RGS2	L13463	24kD	helix-loop-helix phosphoprotein
2065	2065 35722_at	RENT2	AL080198	regulator of nonsense transcripts 2	hypothetical protein
				related RAS viral (r-ras) oncogene	
2066	2066 32827_at	RRAS2	Al365215	homolog 2	
				remainder of gene in clone 549K18	
2067	2067 34845_at	dJ796117.4	AL035398	(AL023654)	CGI-51 protein
	1	i L			soulination factor C 37 kDs culturit
2068	2068 1055_g_at	KFC4	M8/339	(OV/C) + (1)	ובטוולמוסוו ומכוסו כי סי -חסמ שמשמוווו
2069	2069 38481_at	RPA1	M63488	replication protein A1 (70kD)	replication protein A, 70-kDa subunit
2070	2070 652 g_at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071	2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
				restin (Reed-Steinberg cell-expressed	
2072	2072 34350_at	HSN	X64838	intermediate filament-associated protein)	restin
2073	2073 31851_at	RFP2	AJ224819	ret finger protein 2	tumor suppressor
				reticulocalbin 1, EF-hand calcium binding	
2074	2074 40556_at	RCN1	D42073	domain	reticulocalbin
				reticulocalbin 2, EF-hand calcium binding	,
2075	2075 37727_i_at	RCN2	X78669	domain	EF-hand protein
				reticulocalbin 2, EF-hand calcium binding	
2076	2076 37728_r_at	RCN2	X78669	domain	EF-hand protein
2077	2077 31536_at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078	2078 39964 at	ЯРЭ	A,1007590	retinitis pigmentosa 2 (X-linked recessive) XRP2 protein	XRP2 protein
2079		RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
				retinoblastoma 1 (including	
2080	2080 2044_s_at	RB1	M15400	osteosarcoma)	retinoblastoma 1 (including osteosarcoma)

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f				O	т.
	A	n		Catinoblactoma hinding protein 8	CtBP interacting protein CtIP
2081 3	35227_at		072056	009	KIAA0462 protein
0823	2082 33860_at	300	AB00/931		130K protein
0833	12597 at	RBL2	X76061	(20)	
	2004 25040 24	NA117	AL049432	retinoic acid induced 17	
ğ	33040 at			retropseudogene; Human	
				DNA, complete	
- 10	1 01010	DEMC1D. MSSP1	D82351	-	MSSK-1
8	2085 316/2_g_ai	- 1		unit of DNA	1.00
- 2	\$0.000 c	ופראשו	AL096744		hypothetical protein
ģ	2000 30300_3_at			reversion-inducing-cysteine-rich protein	
-	20000	BECK	AA099265	with kazal motifs	
	2067 33230_9_ai	111111111111111111111111111111111111111		reversion-inducing-cysteine-rich protein	
	10 30030	BECK	AA099265	with kazal motifs	
8	2000 33233 at			ig-cysteine-rich protein	
oacc	2000 35234 at	RECK	D50406		HECK protein precuisor
	2003 3253 a at	ARHGAP1	U02570		CUC42 G1 Fase-activating process
200	200 G	A DHICA D1	A1961929	Rho GTPase activating protein 1	
1807	2031 39700 at			Rho guanine nucleotide exchange factor	10 rotach appropriate this section 10
000	1000	A D H G F F 10	AB002292	(GEF) 10	Rho guanine nucleolide excitatige factor 10
2032	2032 34 180 at	2 12		Rho guanine nucleotide exchange factor	
000	40000 of	ARHGFF7	D63476	(GEF) 7	PAK-interacting excitating lactor beta
3	40020_at			rho/rac guanine nucleotide exchange	
200	40100	ABHGFF2	U72206	factor (GEF) 2	guanine nucleotide regulatory ractor
2034	2034 40 100 at			Rho-specific guanine nucleotide exchange	
2006	2000 at 2000	P114-RHO-GEF	AB011093	factor p114	_
	44040	пррзв	U77664	ribonuclease P (38kD)	Rivaser protein roo
	2030 4 1040 at	RNASF4	D37931	ribonuclease, RNase A family, 4	HNase 4
	32001 at	HNG	X13973	ribonuclease/angiogenin inhibitor	ribonuciease/arigiogerini irinibilor
<u> </u>	2098 3618/_at			apituamion tM contained the	M1 subunit of ribonucleotide reductase
2606	9 34314 at	RRM1	X59543	ribonucieotide reduciase ini polypopiase	Wilm's tumor-related protein
100	2100 2016 s at	RPL10	M64241	ribosomal protein L10	ribosomal protein 11
9 6	2101 41178 at	RPL11	X79234	ribosomal protein L11	
100	2102 33668 at	RPL12	AF037643	ribosomal protein L12	ihocomal protein 113
10	2103 31509 at	RPL13	X64707	ribosomal protein L13	10030 Illumination Protein
	2104 35119 at	RPL13A	X56932	ribosomal protein L13a	shoomal protein 14
	2105 31907 at	RPL14	D87735	ribosomal protein L14	IIDOSOIII DIOCCIII
1	20125				

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∀	8	O	D	4
2106 32432_f_at	at RPL15	L25899	ribosomal protein L15	ribosomal protein L10
32440	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108 31546 at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109 33614_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110 32435 at	RPL19	X63527	ribosomal protein L19	ribosomal protein L19
2111 32337_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
33451_s	at	AI526079	ribosomal protein L22	
-	at	X55954	ribosomal protein L23	HL23 ribosomal protein
ဟ	at RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
-	at RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
2116 33677 at		M94314	ribosomal protein L24	ribosomal protein L30
2117 32444 at	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118 39830 at	RPL27	AA044823	ribosomal protein L27	
2119 32436 at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120 31708 at	RPL30	105095	ribosomal protein L30	ribosomal protein L30
2121 33676_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122 32276 at	I RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123 33657_at		L38941	ribosomal protein L34	ribosomal protein L34
2124 41765_at		AI541285	ribosomal protein L35	
2125 41152 f	at	T89651	ribosomal protein L36a	
2126 33656_at		D23661	ribosomal protein L37	ribosomal protein L37
2127 31962 at	t RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128 34085 at	t RPL38	Z26876	ribosomal protein L38	ribosomal protein
2129 33485 at	t RPL4	D23660	ribosomal protein L4	ribosomal protein
				human homologue to yeast ribosomal
2130 32466_at	It RPL41	Z12962	ribosomal protein L41 ,	protein YL41
2131 33660 at	It RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132 31952_at		X69391	ribosomal protein L6	ribosomal protein L6
2133 36333 at	It RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134 31505 at		Z28407	ribosomal protein L8	ribosomal protein L8
2135 31568 at		U14972	ribosomal protein S10	ribosomal protein S10
2136 32330_at		X06617	ribosomal protein S11	ribosomal protein S11
2137 33116_f	f_at RPS12	AA977163	ribosomal protein S12	
2138 33619_at		L01124	ribosomal protein S13	ribosomal protein S13
2139 34317_g	at	W52024	ribosomal protein S15a	ribosomal protein S15a
2140 38061_at	at RPS16	Al541256	ribosomal protein S16	

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		(metallopanstimulin a X-linked Ye, PO	ribosomal protein S17 ribosomal protein S17 S19 ribosomal protein S2 ribosomal protein S2 ribosomal protein S20 ribosomal protein S24 ribosomal protein S24 ribosomal protein S24 ribosomal protein S3 v-fos transformation effector protein ribosomal protein S3 ribosomal protein S3 ribosomal protein S3 ribosomal protein S5 ribosomal protein S5
g_att RPS17 M13932 at RPS17 M13932 at RPS19 M81757 at RPS20 L06498 at RPS20 L06498 at RPS24 M31520 at RPS24 M31520 at RPS27 A1557852 at RPS27 A14970 at RPS34 M58458 at RPS3 U14970 at RPLP1 M17886 at RPLP1 M17886 at RPLP1 M17886 at RPLP1 M17886 at RRBP1 A5000346 at RNF1 AF037204		(metallopanstimulin a X-linked Ye, Po	ossomal protein S17 Je ribosomal protein S17 Je ribosomal protein S2 ossomal protein S20 ossomal protein S24 ossomal protein bosomal protein bosomal protein S3 fos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S5 bosomal protein S5 bosomal protein S5
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at RPS2 X17206 at RPS20 L06498 at RPS24 M31520 at RPS24 M31520 at RPS24 M64716 at RPS27 A1557852 at RPS27 S79522 at RPS28 R87876 at RPS3A M84711 at RPS3A M14970 at RPS5 U14970 at RPS9 U14971 at RPLP1 M17886 r_at RPLP1 M17886 at RNF6 AJ010346 at RNF6 AJ010346 at RNF11 U69559 at RNF13 AR037263		(metallopanstimulin a A Linked Y-linked Je, PO	ossomal protein S2 ossomal protein S20 ossomal protein S24 oosomal protein biquitin carboxyl extension protein fos transformation effector protein bosomal protein S3 bosomal protein S4X isoform bosomal protein S5 bosomal protein S5 bosomal protein S5
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at RPS23 D14530 at RPS24 M31520 at RPS24 M64716 at RPS27 A1557852 at RPS27A S79522 at RPS28 R87876 at RPS3 X55715 at RPS3A M84711 at RPS3A M84711 at RPS3 U14970 at RPS9 U14971 at RPLP1 M17886 c AFDP0 M17886 at RPLP1 M17886 at RPLP1 M17886 at RPLP1 M17885 at RPLP1 M17886 at RNF0 M17886 at RNF6 AJ010346 at RNF1 U69559 at RNF13 AF037204	25	(metallopanstimulin a	ossomal protein Sosomal protein S24 Sosomal protein biquitin carboxyl extension protein Flos transformation effector protein Bosomal protein S4X isoform Bosomal protein S5 Bosomal protein S5 Bosomal protein S5
at RPS24 M31520 at RPS25 M64716 at RPS27 A1557852 at RPS27A S79522 at RPS28 R87876 at RPS3A X55715 at RPS3A M84711 at RPS3A M84711 at RPS3A M14970 at RPS9 U14971 at RPLP1 M17886 c I at RPLP1 M17886 at RNF6 AJ010346 at RNF6 AJ010346 at RNF11 U69559 at RNF13 AR032683	22	(metallopanstimulin a X-linked Je, PO	ossomal protein S24 bosomal protein biquitin carboxyl extension protein flos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S5 bosomal protein S5
at RPS25 M64716 at RPS27 A1557852 at RPS28 R87876 at RPS3 X55715 at RPS3A M84711 at RPS4X M58458 at RPS9 U14970 at RPLP1 M17885 at RPLP1 M17886 at RPLP1 AF006751 at RNF6 AJ010346 at RNF1 U69559 at RNF13 AR02263	2	(metallopanstimulin a	biquitin carboxyl extension protein bosomal protein S3 bosomal protein S4X isoform bosomal protein S5 bosomal protein S5 bosomal protein S5 bosomal protein S5
at RPS27 AI557852 at RPS27A S79522 at RPS28 R87876 at RPS3 X55715 at RPS3 M84711 at RPS5 U14970 at RPS9 U14971 at RPLP1 M17886 r_at RPLP1 M17886 at RRBP1 AF006751 at RNF6 AJ010346 at RNF1 U69559 at RNF13 AF037264	25		biquitin carboxyl extension protein bosomal protein S3 -fos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S9
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RPS28		X-linked Je, P0	bosomal protein S3 fos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S9
RPS3 X55715		X-linked Je, P0	bosomal protein S3 -fos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S9
RPS3A M84711		X-linked Je, PO	fos transformation effector protein bosomal protein S4X isoform bosomal protein S5 bosomal protein S9
RPS4X M58458 RPS5			bosomal protein S4X isoform bosomal protein S5 bosomal protein S9
RPS5 U14970 RPS9 U14971 RPS9 U14971 RPLP1 M17886 A17886		ge, Po	bosomal protein S5 bosomal protein S9
at RPLP1 M17885 at RPLP1 M17886 at RPLP1 M17886 at RRBP1 AF006751 at RNF AJ010346 bridge AJ010346 t RNF AM010346 t RNF AM010346 t RNF AM010346	10 (0) (0	ge, P0	bosomal protein S9
at RPLP1 M17885 at RPLP1 M17886 at RPLP1 M17886 at RRBP1 AF006751 t RNF AJ010346 t RNF1 U69559 t RNF13 AF037204		ge, Po	
at RPLP1 M17886 at RPLP1 M17886 at RRBP1 AF006751 RIT Y07566 R RNF6 AJ010346 R RNF1 U69559 t RNF13 AF037204			ribosomal protein P0
at RNF6 AJ010346 at RNF6 AJ010346 at RNF1 U69559 at RNF13 AF037204 at RNF13 AF037204			ribosomal protein P1
33213 g_at RRBP1 AF006751 38331_at RIT Y07566 35656_at RNF6 AJ010346 39150_at RNF11 U69559 35811_at RNF13 AF037204	ribosome bindir		ribosomal protein P1
33213_g_at RRBP1 AF006751 38331_at RIT Y07566 35656_at RNF6 AJ010346 39150_at RNF11 U69559 35811_at RNF13 AF037204		homolog	
38331_at RIT Y07566 35656_at RNF6 AJ010346 39150_at RNF11 U69559 35811_at RNF13 AF037204			ES/130
RNF6 AJ010346 RNF11 U69559 RNF13 AF037204		Ric-like, expressed in many tissues	:
RNF6 AJ010346 RNF11 U69559 RNF13 AF037204			Ric-like, expressed in many tissues
RNF11 U69559 RNF13 AF037204 DNE14 AR022663		3H2C3 type) 6	RING-H2
RNF13 AF037204			
DNE14			RING zinc finger protein
20072000	AB022663 ring finger protein 14		ring finger protein 14
RNF2 Y10571			ring finger protein 2
RNF3 W25793		in 3	
35777 at RNF4 AB000468			zinc finger protein
	ring zinc-finger	ring zinc-finger protein; escapes X	
chromosome ir	chromosome ii	chromosome inactivation; Human ring zinc	
finger protein (finger protein (127-Xp) gene and 5'	
7-Xp U41315	U41315		ZNF127-Xp
2170 37732_at RYBP AL049940 RING1 and YY		RING1 and YY1 binding protein	

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	A	В	0	Q	ш
2171 38073		RNMT	AB007858	RNA (guanine-7-) methyltransferase	RNA (guanine-7-) methyltransferase
21724	2172 41460 at	RBM14	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
2173 41741	11741_at	RBM3	U28686		RNPL
2174 35351	15351_at	RBM4	U89505		Hlark
21753	2175 32804_at	RBM5	AF091263		RNA binding motif protein 5
21764	2176 40870_g_at	RBM6	AF069517		RNA binding protein DEF-3
21774	2177 40260_g_at	RBM9	AL009266	RNA binding motif protein 9	hypothetical protein
21783	2178 39731 at	RBMX	223064	RNA binding motif protein, X chromosome hnRNP G protein	hnRNP G protein
				RNA binding motif, single stranded	RNA binding motif, single stranded
21793	2179 33867_s_at	RBMS1	X77494		interacting protein 1, isoform a
				iding protein S1, serine-rich	
2180	2180 36186_at	HNPS1	L37368	domain	RNA-binding protein
				RNA guanylyltransferase and 5'-	
2181	2181 35202_at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
2182	2182 33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	2184 38762 at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
				RNA-binding protein gene with multiple	
2185	2185 38049 g_at	RBPMS	D84110	splicing	RBP-MS/type 4
				RNA-binding protein gene with multiple	
2186	2186 38047_at	RBPMS	D84109	splicing	RBP-MS/type 3
2187	2187 38974 at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
				RNA-binding region (RNP1, RRM)	
2188	2188 39725_at	RNPC2	L10910	containing 2	splicing factor
2189	2189 38011_at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
2190	2190 35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
				runt-related transcription factor 1 (acute	
2191	2191 943 at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML1b protein
					erythrocyte cytosolic protein of 54 kDa, ECP-
2192	2192 40124 at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	54
2193	2193 35758 at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
				S100 calcium binding protein A10	
2194	2194 39338 at	S100A10	AI201310	polypeptide (p11))	

Fig. 21

T	A	В	၁	D	ш
I				ntaining inositol	
195	2195 36089_at	SAC2	AB023183		KIAA0966 protein
				ntaining inositol	
2196	2196 41101_at	SAC3	D87464	-	KIAA0274 gene product
				uppressor of actin mutations 1-like	
197	2197 36511_at	SACM1L	AB020658	(yeast)	KIAA0851 protein
2198	2198 34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1 hypothetical protein	hypothetical protein
2199		AHCYL1	R59606	S-adenosylhomocysteine hydrolase-like 1	
Š	2200 36685 at	AMD1	W63793		
500		AMD1	M21154		S-adenosylmethionine decarboxylase 1 precursor
2002	2202 1202 gar	SGCE	AJ000534		epsilon-sarcoglycan
2203	2203 36083 at	SAS	U01160	sarcoma amplified sequence	SAS
2204	at l	SCHIP1	AF070614	otein 1	schwannomin interacting protein 1
2205	at	SEC13L1	AF052155		SEC13 (S. cerevisiae)-like 1
2206		SEC13L1	AF052155		SEC13 (S. cerevisiae)-like 1
2207		SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208		SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
				SEC24 related gene family, member A (S.	
2209	2209 34199 at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
				SEC24 related gene family, member B (S.	
2210	2210 35845 at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
				SEC24 related gene family, member D (S.	
2211	2211 32770 at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
2212	34349 at	SECESL	AJ011779	SEC63 protein	SEC63 protein
2213	2213 32521 at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
				secreted phosphoprotein 1 (osteopontin,	
				bone sialoprotein I, early T-lymphocyle	,
2214	2214 34342 s at	SPP1	AF052124	activation 1)	osteopontin
				secreted protein, acidic, cysteine-rich	secreted protein, acidic, cysteine-rich
2215	2215 671_at	SPARC	J03040	(osteonectin)	(osteonectin)
2	240EF 04	S GNE1	V00757	secretory granule, neuroendocrine protein	secretory granule, neuroendocrine protein 1 (7B2 protein)
3 6	2210 34203 at	SEI ENRP1	1129091	selenium binding protein 1	selenium-binding protein
77	01+02_all	מברבוזהו	25000		

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	A	В	S	O	IJ
2218	39078_at		U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
2219	2219 34363_at		211793	selenoprotein P, plasma, 1	selenoprotein P
				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2220 377	377_g_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2221	2221 376_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	
2222	2222 35666_at	SEMA3F	U38276	(semaphorin) 3F	semaphorin III family homolog
2223	2223 38826_at	2-Sep	2-Sep D50918	septin 6	septin 2
					phosphotyrosine independent ligand for the
2224	2224 40898_at	SQSTM1	U46751	sequestosome 1	Lck SH2 domain p62
				serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
				clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125_at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor,	
				clade H (heat shock protein 47), member	
2227	2227 39167_r_at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyltransferase, long chain	
2228	2228 38818_at	SPTLC1	Y08685	base subunit 1	serine palmitoytransferase, subunit l
				serine threonine kinase 39 (STE20/SPS1	
2229	2229 40966_at	STK39	AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737 at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	2231 36019_at	STK19	L26260	serine/threonine kinase 19	RP protein
				serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424 .	homolog, yeast)	MST2
2234	2234 32784 at	PRP4	AB011108	serine/threonine-protein kinase PRP4 homolog	KIAA0536 protein
5501	02101_dt		2011	60.000	



serum response factor (c-fos serum response element-binding transcription factor) Jo3161 factor) serum response factor (c-fos serum response element-binding transcription response element-binding transcription factor) AF059617 serum-inducible kinase serum-is serum-is serum-inducible kinase seryl-tRNA synthetase SET translocation (myeloid leukemia- seryl-tR SET translocation (myeloid leukemia- associated) U76247 seven in absentia homolog 1 (Drosophila) hSIAH1
V76248 seven in absentia homolog 2 (Urosopri Seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7)
Al337192 protein SH3 domain binding glutamic acid-rich AF042081 protein like
AB007960 SH3-domain Ghbz-line encopularity SHC (Src homology 2 domain containing) transforming protein 1
, and a
U51920 signal recognition particle 3700

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	∢	8	C		ı
2255 33837	33837_at	SRP72	AF069765	0	signal recognition particle 72
2256	at	SRP9	AF070649	signal recognition particle 9kD	
-				ptor	signal recognition particle receptor ('docking
2257	2257 36679_at	SRPR	X06272		protein')
				signal transducer and activator of	
2258	2258 AFFX-HUMISGF STAT1	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2259	2259 32860 g at	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2260	2260 32859_at	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2261	2261 33338_at	STAT1	M97936	transcription 1, 91kD	
				signal transducer and activator of	
				transcription 3 (acute-phase response	
2262	2262 39708 at	STAT3	L29277	factor)	DNA-binding protein
				signal transducing adaptor molecule (SH3	
2263	2263 160_at	STAM	U43899	domain and ITAM motif) 1	STAM
				similar to Drosophila ash2 gene; Homo	
				sapiens ASH2L gene, complete cds,	
2264	2264 35804_at	ASH2L	AB022785	similar to Drosophila ash2 gene.	
2265	2265 41552 g_at	RER1	AW044624	similar to S. cerevisiae RER1	
2266	2266 41551 at	RER1	AW044624	similar to S. cerevisiae RER1	
2267	2267 33632 q at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
				similar to SW:GOLI_DROME Q06003	
2268	2268 35083_at	G1L	AL031670	GOLIATH PROTEIN	ring tinger protein 24
2269	2269 37178_at	na	M74089	similar to TB1	
				similar to Wiskott-Aldrich syndrome	
2270	2270 40787_at	WIRE	U90911	protein interacting protein	
2271	2271 34705_at	BET3	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	2272 39131_at	UPF3A	N36842	similar to yeast Upf3, variant A	
2273	2273 41277_at	SAP18	AW021542	sin3-associated polypeptide, 18kD	
2274	2274 33859_at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2275	2275 40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
		7,710		sine oculis homeobox homolog 1	sine oculis homeobox (Drosophila) homolog
2276	2276 40004_at	SIX1	1791868	(Urosopnila)	

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-	Α	8	ပ	O.	11
Γ				fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057		actin bundling protein
2278	2278 39086 g at		AA768912		
2279	11 1		AL080076	2	hypothetical protein
					400,000
2280	2280 35294_at	SSA2	M25077	ę	6UKU Ho/SSA autoantigen
2281	2281 35295_g_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
				Sjogren syndrome antigen B (autoantigen	
2282	2282 38450_at	SSB	X69804		
2283	2283 37715 at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389 at	IMAGE145052	Al346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	
2287	2287 37337_at	SNRPG	A1803447	polypeptide G	
				small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
				small nuclear RNA activating complex,	
2289	2289 35247_at	SNAPC5	AI557062	polypeptide 5, 19kD	
				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	
2291	32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	
				SMT3 suppressor of mif two 3 homolog 1	
2292	38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185_f_at	SMT3H2	AI971724	(yeast)	
2294	2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
L				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2296	2296 40928 at	WSB1	W26496	SOCS box-containing WD protein SWiP-1	
	יושרקים מיינים	100:1	22:02:1		

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卜	A	В	O	Vinite daid falls to the standard	
- 5	**	SI C183	D26443	solute carrier tarniny i (gilar riigit arriilit) quitamate transporter), member 3	glutamate transporter
29/3	2297 36609_at				
		0110	AR004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 NRAMP2	NRAMP2
2983	2298 35320_at		2000		
				carboxylic	
299	2299 33143_s_at	SLC16A3	U81800	acid transporters), member 3	monocarboxylate transporter
			,	solute carrier family 16 (monocarboxylic	solute carrier family 16 (monocarboxylic acid transporters), member 4
8	2300 39260_at	SLC16A4	008100	ted glucose	solute carrier family 2 (facilitated glucose
2004	0201126070 of	SI C2A3	M20681	transporter), member 3	transporter), member 3
	20313_at			solute carrier family 22 (organic cation	organic cation transmorter OCTN2
2302	2302 32084 at	SLC22A5	AF057164	transporter), member 5	Organic canon nambers
			1	solute carrier family 23 (nucleobase	
2303	2303 38122_at	SLC23A1	D87075	transponers), member i	solute carrier family 25 (mitochondrial
				carrier adenine nucleotide translocator),	carrier; adenine nucleotide translocator),
		7 200	102066	member 4	member 4
2304	2304 32822_at	SLUZDA4	202200	solute carrier family 25 (mitochondrial	solute carrier family 25 (mitochondrial
				carrier; adenine nucleotide translocator),	carrier; adenine nucleotide translocator),
1000	10 - 07240	CI C25A5	,102683	member 5	member 5
2002	2303 37 740_1_at			solute carrier family 25 (mitochondrial	
				carrier; adenine nucleotide translocator),	
2306	230E 40436 u at	SLC25A6	J03592	member 6	
300	18-00t0t			solute carrier family 25 (mitochondrial	
				carrier; adenine nucleotide translocator),	
7000	40.40k	SIC25A6	303592	member 6	
250	40433_a(OLC COLO		solute carrier family 25 (mitochondrial	
0000	0000 27575 at	SI C25A3	X60036	carrier; phosphate carrier), member 3	phosphate carrier protein
3	3/0/5 at	2010		solute carrier family 29 (nucleoside	
2300	2300 33901 at	St C29A1	U81375	transporters), member 1	equilibrative nucleoside transporter i
3	5-1000			solute carrier family 31 (copper	
2310	2310 40364 at	SLC31A1	U83460	transporters), member 1	Ingn-arrinity copper uptake protein



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33.11	2311 34749 at	SI C31A2	U83461	solute carrier family 31 (copper transporters), member 2	putative copper uptake protein
3	5			CMP-sialic acid	
2312	2312 37895 at	SLC35A1	D87969		CMP-sialic acid transporter
				solute carrier family 35 (UDP-N-	
				<u>্</u>	
2313	2313 38208 at	SLC35A3	AB021981		UDP-N-acetylglucosamine transporter
				solute carrier family 4, sodium bicarbonate	
2314	2314 34936_at	SLC4A7	AB012130		sodium bicarbonate cotransporter2
				mitter	
2315	2315 34166_at	SLC6A7	S80071	transporter, L-proline), member 7	brain-specific L-proline transporter
				solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid
2316	2316 32186_at	SLC7A5	M80244	transporter, y+ system), member 5	transporter, y+ system), member 5
	m_00130				
				solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid
2317	2317 39533_at	SLC7A6	D87432	transporter, y+ system), member 6	transporter, y+ system), member 6
				solute carrier family 9 (sodium/hydrogen	
,	70000	0000	C68616	exchanger), Isolorii I (aliuportei, Matzirit, amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
22 18	2318 32681_al	OLC3A!	010000	allicities occionites)	
		<u> </u>		solute carrier family 9 (sodium/hydrogen	
2319	2319 36542_at	SLC9A6	AF030409	exchanger), isoform 6	sodium-hydrogen exchanger 6
2320	2320 39097_at	SON	X63753	SON DNA binding prótein	SON DNA-binding protein
2321	9391 39857 at	8082	L13858	son of sevenless homolog 2 (Drosophila)	guanine nucleotide exchange factor
232	2322 41462 at	SNX2	AF065482	sorting nexin 2	sorting nexin 2
2323		SNX3	AF034546	sorting nexin 3	sorting nexin 3
2324		SNX4	AA524345	sorting nexin 4	
2325	2325 37808 at	SNX7	AL049989	sorting nexin 7	hypothetical protein
				Source: H.sapiens genes for histones	
2326	2326 33352_at	H2A	X57985	H2B.1 and H2A.	histone H2A
2327	736112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	2328 36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2



_			Source: Homo sapiens chromosome 10	
	-	HG172-HT3924	SEQUENCE, 8 unordered pieces.	
			Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete	·
	44M2.1	AC004381	sednence.	hypothetical protein FLJ20274
Γ			Source: Homo sapiens clk2 kinase	
			(CLK2), propin1, cote1,	
			glucocerebrosidase (GBA), and metaxin	·
			genes, complete cds; metaxin	
			pseudogene and glucocerebrosidase	
			pseudogene; and thrombospondin3	
	COTE1	AF023268	(THBS3) gene, partial cds.	chromosome 1 open reading frame 2
			Source: Homo sapiens hJTB gene,	
	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
			Source: Homo sapiens hJTB gene,	
	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
			Source: Homo sapiens mRNA for	
	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
			Source: Homo sapiens mRNA for	
	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
			Source: Human CCAAT-box-binding	
	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
			Source: Human CCAAT-box-binding	
	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
			Source: Human Chromosome 16 BAC	
			clone CIT987SK-A-101F10, complete	
	101F10.3	AC002550	sequence.	hypothetical protein
			Source: Human Chromosome 16 BAC	-
			clone CIT987SK-A-211C6, complete	
	A-211C6.1	AC002394	sequence.	hypothetical protein A-211C6.1
			Source: Human Chromosome 16 BAC	
	A 2000 A	106740	codie of sor of A condition	hypothetical protein A-362G6 1

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Π				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-61E3, complete	
2341	2341 41733 at	61E3.1	AC003007		Unknown gene product (partial)
				Source: Human DNA sequence from	
2345	2342 36894 at		AL031846	complete sequence.	
	in -			Source: Human mRNA for HLA class I	
2343	2343 37383 f at	HLA class I - locus X58536	X58536		HLA class I heavy chain
				Source: Human N-	
				acetyiglucosaminyltransferase I (GlcNAc-	acetyiglucosaminyitransferase I (GlcNAc- mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
2344	2344 39778_at	GLYT1 GLCNAC-	- M55621	TI) mRNA, complete cds.	N-acetylglucosaminyltransferase
2345	2345 41573 at	SP3	X68560	Sp3 transcription factor	
				spastic ataxia of Charlevoix-Saguenay	
2346	2346 32102_at	SACS	AB018273	_	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
2347	2347 35171 at	SPG4	AB029006	spastin)	KIAA 1083 protein
2348	2348 39423 f at	SPOP	AJ000644		SPOP
2349	2349 38924 s at	SSH3BP1	AF001628		interactor protein AbIBP4
2350	2350 33886 at	SSH3BP1	AF006516		e3B1
2351	2351 39556 at	SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
2352	2352 34304_s_at	SAT	AL050290 ·	spermidine/spermine N1-acetyltransferase	
				sphingomyelin phosphodiesterase 1, acid	
2353	2353 32574_at	SMPD1	X59960	lysosomal (acid sphirtgomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
225.4	22E4 2E142 at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
3	20142			spinocerebellar ataxia 2	
	- · · -	-		(olivopontocerebellar ataxia 2, autosomal	
2355	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
				splicing factor 30, survival of motor neuron	
2356	2356 38040_at	SPF30	AF107463	related	splicing factor
235	7 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145KU	spliceosome associated protein



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				splicing factor proline/glutamine rich	
2358	2358 36224 q at	SFPQ	AI827895	(polypyrimidine tract binding protein associated)	
				splicing factor proline/glutamine rich	•
- 0		0	710077	(polypyrimidine tract binding protein	OTO proposition of the propositi
2359	2359 40638 at	SFFC	X/0944	associated)	r i p-associated splicifig factor
				splicing factor, arginine/serine-rich 1	splicing factor, arginine/serine-rich 1 (splicing
2360	2360 36098_at	SFRS1	M72709	(splicing factor 2, alternate splicing factor) factor 2, alternate splicing factor)	factor 2, alternate splicing factor)
				0	
2361	2361 140_s_at	SFRS10	U68063		transformer-2 beta
2362	2362 32183_at	SFRS11	M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
				splicing factor, arginine/serine-rich 2,	
2363	2363 35258_f_at	SFRS2IP	AF030234	interacting protein	splicing factor Sip1
2364	2364 40457_at	SFRS3	AF038250	splicing factor, arginine/serine-rich 3	
2365	2365 36991_at	SFRS4	L14076		pre-mRNA splicing factor
2366	2366 40453_s_at	SFRS5	U30826	splicing factor, arginine/serine-rich 5	SRp40-1
2367	2367 40262 at	SBP46	AE031166	Solicing factor arginine/serine-rich 46kD	SBp46 splicing factor
2366	2269 26830 04	שוכט	D78130	sauplane enoxidase	schalene epoxidase
3	- COCC		200	saliamons cell carcinoma antiden	
2360	2369 39047 at	SARTS	ABOZOBBO	recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370	2370 41784 at	964	B0769 AL080186	SR rich protein	hypothetical protein
2371	2371 36091 at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	2372 41354 at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	2376 41823 at	STAU	AJ132258	staufen. RNA binding protein (Drosophila)	staufen protein
2377	2377 38669 at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
L				stem cell growth factor; lymphocyte	
2378	2378 37147_at	SCGF	AF020044	secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2375	36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
000	2000	o Lo	Miceog	steroid sulfatase (microsomal),	steroid sulfatase (microsomal), arylsulfatase
238	2380 38034_BI	515	INI FOSOS	aryisullatase O, ISOZYIIIE O	0, 1302)1110 0

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				$\overline{}$	steroid-5-alpha-reductase, alpha polypeptide
				polypeptide 1 (3-oxo-5 alpha-steroid delta	1 (3-oxo-5 alpha-steroid delta 4-
2381 589 at	389 at	SRD5A1	M32313	4-dehydrogenase alpha 1)	dehydrogenase alpha 1)
2382	2382 33369 at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
				sterol-C5-desaturase (ERG3 delta-5-	
2383	33421_s_at	SCSDL	AB016247	desaturase homolog, fungal)-like	sterol-C5-desaturase
2384 4	t0419 at	EPB72	X85116	stomatin; H.sapiens epb72 gene exon 1	band 7 integral membrane protein
2385	2385 33322 i at	SFN	X57348		stratifin
				stress-associated endoplasmic reticulum	
238G	2386 27035 at	SERP1	A1557272	protein 4	
3					stromal cell derived factor receptor 1 isoform
					b; stromal cell derived factor receptor 1
2387	2387 35747 at	SDFR1	AF035287	stromal cell derived factor receptor 1	isoform a
2388	2388 32666_at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389		SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390	2390 41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
				succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
2391	2391 34826 at	SDHA	L21936	subunit A, flavoprotein (Fp)	subunit
				succinate dehydrogenase complex,	
				subunit C, integral membrane protein,	
2392	2392 34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
				succinate dehydrogenase complex,	:
2393	2393 40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
				succinate-CoA ligase, ADP-forming, beta	ATP-specific succinyl-CoA synthetase beta
2394	2394 40893_at	SUCLAZ	AF058953	subunit	subunit
2395	2395 35832 at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
2396	2396 33712 at	SULT4A1	N63574	sultotransferase family 4A, member 1	
2397	2397 34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
	1			superkiller viralicidic activity 2-like (S.	
2398	37998 at	SKIV2L	U09877	cerevisiae)	helicase-like protein
				superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
2399	2399 36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
2400	2400 40069 at	SVIL	AF051850	supervillin	supervillin
2401	2401 36676 at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

Fig. a

	٩	B	0	O	ង
2402	2402 33297_at	CBF-B HAP2 NF.	AL031778	supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform 1
2403	2403 34825 34	ТТВАР	AI 031775	Separation of the production o	TBAE and TNE recentor-associated protein
3	04050_all	3	20011	nicity 13 (colon	
2404	2404 1640 at	ST13	U17714		putative tumor suppressor ST13
2405	2405 37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
2406	2406 37805_at	SRPUL	AF060567		sushi-repeat protein
		0	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	sushi-repeat-containing protein, X	
240/	2407 31855_at	SHPX	U613/4		
2408	2408 31869_at	KIAA0640	AB014540	\rightarrow	KIAA0640 protein
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2409	2409 40213_at	SMARCA1	M88163	subfamily a, member 1	transcription activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2410	2410 40961_at	SMARCA2	X72889	subfamily a, member 2	HBRM
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2411	2411 32579_at	SMARCA4	U29175	subfamily a, member 4	transcriptional activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2412	39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
2413	2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414	2414 41692_at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
2415	2415 38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416	2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
					synaptosome associated protein of 23
2417	2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kD	kilodaltons, isoform A
				syndecan 2 (heparan sulfate proteoglycan	· (
2418	2418 39757_at	SDC2	J04621	1, cell surface-associated, fibroglycan)	
2419	2419 32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420	2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421	1 1	STX12	AL035306	syntaxin 12	hypothetical protein
2422	2422 38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3



			ű		U
	A	20	3	D	
2423	2423 38774_at	STX7	U77942	syntaxin 7	syntaxin /
2424	2424 37510 at	STX8	AF036715	syntaxin 8	syntaxin 8
2425	at	STXBP1		inding protein 1	hUNC18b
2426	at	STXBP3	De3506		unc-18homologue
				Synthetic construct chimeric DNA-binding	
2427	2427 33315 at		M29204		chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				g protein (TBP)-associated factor,	
2428	2428 192 at	TAF7	U18062		TFIID subunit TAFII55
				TAF9 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2429	2429 193 at	TAF9	U21858	32 kD	TAFII32 precursor
				TAFII20; contains homology to histone	-
				H2B; TFIID subunit; TAFII15; contains	
		-		homology to histone H2B; TFIID subunit;	
			-	Human TFIID subunits TAF20 and TAF15	
2430	2430 37620_at	TAF12; TAF2J; T/	TAU57693	mRNA, complete cds.	TAF20; TAF15
2431	32166_at	TLN1	AB028950	talin 1	KIAA1027 protein
2432	2432 39765 at	TLN2	AB002318	talin 2	
2433	2433 41168 at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	2434 39779 at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	TAR RNA loop binding protein
2435	2435 32241 at	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	2436 39416 at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
	l			Tax1 (human T-cell leukemia virus type I)	
2437	2437 498_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	
2438	2438 35279_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	36702 at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196_at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	34791 at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	t-complex-associated-testis-expressed 1-like
				t-complex-associated-testis-expressed 1-	t-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	

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ш		TGFb inducible early protein; early growth response protein alpha		telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1	hypothetical protein	testis ennanced gene transcript (555 inhibitor 1)	tetracycline transporter-like protein		tetratricopeptide repeat protein	TPRO	zinc finger transcription factor		TGIF protein						growth factor-binding protein-3 precuisor						growth factor-binding protein-5 precursor
	TOP COLORS	TEIG; EGHa; Homo sapiens, 1 or binducible early protein and early growth response protein alpha genes, complete		telomeric repeat binding factor (NIMA- interacting) 1	us)	Testis enhanced gene transcript (BAX	totrocucline transporter-like protein	tellacycinic transporter into pro-	tetraspan o	tetratricopeptide repeat domain 3	Tetratricopeptide repeat dolliam 3	TGFB inducible early growin response	GFB-induced factor (ALE family homoohov)	O e0004/	I he AAs encoded by bases 57 co-57 co-67 and 5917-5926 may be ASN-linked	glycosylation sites; insulin-like precursor;	Homo sapiens growth factor-binding	protein-3 precursor (IGFBP3) gene,	complete cds.	The AAs encoded by bases 5728-5736	and 5917-5926 may be ASN-linked	glycosylation sites; insulin-like precursor;	Homo sapiens growth factor-binding	protein-3 precursor (IGFBP3) gene,	complete cds.
Ů	ပ	D 4 CO 601 10	AFUSULIO	U40705	AL050162		X/5861	600117	M69023	U46570	D83077	S81439		06/68X					M35878						M35878
	В	7	TIEG; EGHA; KLP	TERF1	TES		TEGI	TETHAN	TSPAN-3	TTC1	TTC3	TIEG		TGIF					IGERP3	5					IGFBP3
	A		2444 38374_at	2445 32255_i_at	0446 30134 at	10.120 10.120	2447 33988_at	2448 32080_at	2449 38612_at	2450 37321_at	39065_s_at	2452 224 at		2453 38805_at					4 07040 pt	2424 37319 at					2455 1586 at
			444	445	1446		2447	2448	2449	2450	2451	2452		2450					1	543					245

Fig. 21

	A	В	၁	O	ш
				The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And	
				the second ATG codon is potential	
	·			initiation point for translation of NPPase.; Human mRNA for nucleotide	
2456	2456 342_at	ENPP1; M6S1; NF	NFD12485	pyrophosphatase, complete cds.	NPPase
2457	2457 36992_at		AI653621	thioredoxin	
2458	2458 34768_at	TXNDC	AL080080	thioredoxin domain-containing	hypothetical protein
2459	2459 31508 at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460	2460 39425_at	TXNRD1	X91247	thioredoxin reductase 1	thioredoxin reductase (NADPH)
2461	2461 32214_at	TXNL	AF003938	thioredoxin-like, 32kD	thioredoxin-like protein
2462	2462 38473_at	TARS	M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463	2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464	2464 658_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
					G/T mismatch-specific thymine DNA
2465	2465 40865_at	TDG	U51166	thymine-DNA glycosylase	glycosylase
2466	2466 31557_at	TMSB4X	M17733	thymosin, beta 4, X chromosome	thymosin, beta 4
				thyroid hormone receptor coactivating	
2467	2467 32654_g_at	SMAP	AW020536	protein	
2468	2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469	2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470	2470 39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471	37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
	1- 30077	TDADOAO	A DO11165	thyroid hormone receptor-associated	KIAA0593 protein
2472	2472 41023 at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
) = 0.10.0			TIA1 cytotoxic granule-associated RNA	TIA1 protein, isoform 1; TIA1 protein,
2474	33852_at	TIA1	M77142	binding protein	isoform 2
				TIA1 cytotoxic granule-associated RNA	:
2475	2475 41763_g_at	TIAL1	D64015	binding protein-like 1	T-cluster binding protein
2476	36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801_at	TJ6	AF112972	TJ6 protein	TJ6

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\vdash	A	8	ပ		
47813	2478 35238 at	TRAF5	AB000509	ated factor 5	I HARD
4703		GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
	2480 40310 at	TI R2		toll-like receptor 2	Toll/interleukin-1 receptor-like protein 4
481	-	T0P1			DNA topoisomerase I
		TOP2R		II beta (180kD)	DNA topoisomerase II
100	1 4	TORIB	AF007872		torsinB
	2483 32233_at	TI K1	D50927		KIAA0137 protein
	2485 35321 at	TI K2	AB004884		PKU-alpha
	2005			TRAF family member-associated NFKB	
486	2486 39742 at	TANK	U59863	╗	LTRAF
487	2487 40051 at	KIAA0057	D31762		TRAM-like protein
488	2488 1073 at	TCEA1	M81601		transcription elongation factor Sil
				transcription elongation factor A (SII)-like	►
489	2489 38317 at	TCEAL1	M99701		transcription elongation factor A (Sit)-like i
				transcription elongation factor B (SIII),	RNA polymerase II elongation factor 5III, n15 subjinit
8	2490 1399_at	ICEBI	L3458/	polybeblide (1985, elongin 9)	RNA notymerase II elongation factor-like
-	44750 24	TCER1	747087	polypeptide 1-like	protein
	60/1			transcription elongation regulator 1	
2402	2402 30426 at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
3	m-031.00			transcription factor 12 (HTF4, helix-loop-	:
2493	2493 33348 at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
	1			transcription factor 3 (E2A immunoglobulin	
2494	2404 1373 at	TCF3	M31523	enhancer binding factors E12/E47)	
1	5-0.01			transcription factor 8 (represses	
2495	2495 33440 at	TCF8	U19969	interleukin 2 expression)	ZEB
	100			transcription factor AP-4 (activating	
2496	2496 39638 at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497	2497 37757 at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription lactor
2498	2498 32578 at	TCFL4	AW005997	transcription factor-like 4	
				transcription factor-like 5 (basic helix-loop	$\overline{}$
2499	2499 35614_at	TCFL5	AB012124	helix)	ADA Illo motolin
2500	2500 35749_at	TADA3L	AF069733	transcriptional adaptor 3-like	ADAG-like protein



	A	89	၁	Q	E
					KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein
2501	35297_at	GGA2 VEAR	AC002400		2
203	2502 33876 of	TA7	AI 050107	transcriptional co-activator with PDZ- hinding motif (TAZ)	hypothetical protein
3	20070_81	2	2000	priessor: Himan	
				clencing mediator of retinoid and thyroid	
				Ф	silencing mediator of retinoid and thyroid
2503	2503 39358 at	SMRT	U37146		hormone action
				transcriptional regulator interacting with	
2504	2504 37312_at	TRIP-Br2	D50917	the PHS-bromodomain 2	KIAA0127 gene product
2505 40631	40631 at	T081	D38305	transducer of ERBB2, 1	Tob
2506		TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	2507 37324 at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	2508 39344 at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
				transforming growth factor beta-stimulated	
2509	2509 39032_at	TSC22	AJ222700	protein TSC-22	TSC-22
				transforming growth factor, beta 1	transforming growth factor, beta 1 (Camurati-
2510	2510 41445_at	TGFB1	X02812	(Camurati-Engelmann disease)	Engelmann disease)
				transforming growth factor, beta receptor	
2511	2511 1815_g_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta receptor	
2512	2512 1814_at	TGFBR2	D50683	II (70-80KD)	TGF-betallR alpha
				transforming growth factor, beta-induced,	
2513 1385	1385_at	TGFBI	M77349	68kD	transforming growth factor induced protein
				transforming, acidic coiled-coil containing	
2514	2514 40841_at	TACC1	AF049910	protein 1	TACC1
				transforming, acidic coiled-coil containing	
2515	2515 38816_at	TACC2	AF095791	protein 2	TACC2 protein
2516	2516 36931_at	TAGLN	M95787	transgelin	smooth muscle protein
2517	36678 at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	2518 31829 r at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
				transient receptor potential cation channel,	
2519	2519 39124_r_at	TRPC1	X89066	subfamily C, member 1	TRPC1 protein
2520	2520 39123 c at	TBPC1	Хвалев	transient receptor potential cation channel, subfamily C. member 1	TRPC1 protein
222	33123_3_at	5	COCCA		

13.2

-	A	8	ပ	Q	Ш
				RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP): Human homolog of splodingsitTERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirllS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (214044) murine valosin-containing protein; 99% identical to hypothetical protein; 90% identical to hypothetical protein; Most similar to hypothetical protein (AL021766) (Schizosaccharomyces pombe) producing hypothetical protein (AL021766) (Saccharomyces cerevisiae) (Saccharomyces (Z73136) ORF YLL031C (SZ7412.9 (Gaenorhabditis elegans): (Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical moteins; PiDle276130 (Z81072) F30A10.5 TERA_HUMAN; XRCC9; P1.11659_3;	TERA_HUMAN; XRCC9; P1.11659_3;
521	2521 34380_at	XRCC9	AC004472	72655IYB28	P1.11659_4; P1.11659_5
522	2522 33351_at	GC20	AF064607	6	GC20 protein
523	2523 40537_at	IF2	AB018284	translation initiation factor IF2	KIAA0741 protein
524	2524 32173_at	UK114	X95384	translational inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5
1					

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	A	В	.	O	
2525	2525 41051_at	TSNAX	X95073	translin-associated factor X	I ranslin associated protein A
1		TINANATA	A A 453183	translocase of inner mitochondrial membrane 17 homolog A (veast)	
9707	2256 32631 at	Z / IMIMI	20100	translocase of outer mitochondrial	
2527	2527 36198 at	TOMM20-PENDIND13641	D13641		mitochondrial outer membrane protein 19
	1			translocase of outer mitochondrial	
2528	2528 37050 r at	TOMM34	AI130910	membrane 34	
				translocase of outer mitochondrial	
2529	2529 32853_at	TOMM70A	AB018262	membrane 70 homolog A (yeast)	KIAA0719 protein
				translocating chain-associating membrane	
2530	2530 34796_at	TRAM	X63679	protein	TRAM protein
2531	2531 38100 at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531 at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362 r at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
				transmembrane 7 superfamily member 1	
2535	2535 32083_at	TM7SF1	AF027826	(upregulated in kidney)	putative seven pass transmembrane protein
2536	2536 38835 at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
					01
2537	2537 34307_at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p/b
2538	2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37445_at	TMEM5	AB015633	transmembrane protein 5	type II membrane protein
2540	2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982 at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382 at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825 at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537 at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545	2545 32635 at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547	2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548	2548 36791_g_at	TPM1	M19267		tropomyosin 1 (alpha)
2548	2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	rropomyosin i (alpha)

Ris-al

TPM1						
TPM1		∢	മ	ပ	O .	T)
TPM2 M12125 tropomyosin 2 (beta) t WABB Y12478 tryptophan rich basic protein 0 WARS X59892 tryptophan/tRNA synthetase 1 TULP3 AI028290 tubby like protein 3 1 TULP3 AI028290 tubby like protein 3 1 TULP3 AI028290 tubby like protein 3 1 TULB3 AF035316 tubulin, beta polypeptide 1 TUBB X79538 tubulin, beta polypeptide 1 TUBB AF035316 tubulin, beta polypeptide 1 TUBB X79538 tubulin, apma polypeptide 1 TUBB X79534 tubulin, apma polypeptide 1 TUBC U61234 tubulin, specific chaperone c 1 TBCC U61234 tubulin, specific chaperone c 1 TBCC U61232 tubulin, specific chaperone c 1 TBCC U61232 tubulin, specific chaperone c 1 TBCC U61232 tubulin, specific chaperone c 1	25503	16792 at	TPM1	224727	tropomyosin 1 (alpha)	tropomyosin isoform
WRB Y12478 tryptophan rich basic protein WARS X59892 tryptophanyl-IRNA synthetase TUEM S75463 Tu translation elongation factor, TULP3 Al028290 tubbulin, alpha, ubiquitous TULP3 Al028290 tubbulin, beta polypeptide TUBB AF035316 tubulin, beta polypeptide TUBB AF035316 tubulin, beta polypeptide TUBB X79535 tubulin, peta polypeptide TUBB X79535 tubulin, peta polypeptide TUBC U61232 tubuli	25513	12313 at	TPM2	:	tropomyosin 2 (beta)	tropomyosin 2 (beta)
WARS X59892 tryptophamy4-IRNA synthetase TUEN S75463 Tu translation elongation factor, mitochondrial TULPA S75463 tubby like protein 3 TULPA AI028290 tubby like protein 3 TUBB AF035316 tubbulin, alpha, ubiquitous f TUBB A79535 tubulin, alpha, ubiquitous f TUBG1 M61764 tubulin, beta polypeptide f TUBG1 M61733 tubulin, peta polypeptide f TBCC U61232 tubulin-specific chaperone c f TDE1 U49188 tumor necrosis factor receptor g TDE2 U49188 tumor necrosis factor receptor g TNFRSF10B AF016266 superfamily, member 12 (translocating chain-association membrane protein) f TNFRSF11 U83598 chain-association membrane protein) f TNFRSF5 X60592 superfamily, member 14 f TNFRSF6 X63717 superfamily, member 5 f TNFAIP2 M92357 protein 1 f	25523	12777 at	WRB		tryptophan rich basic protein	congenital heart disease 5 protein
TUEM S75463 Tutanslation elongation factor, TULPM S75463 Tubulin, bela polypeptide TULPB A1028290 Tubulin, palpa, ubiquitous TUBB A7028316 Tubulin, palpa polypeptide TUBB A779535 Tubulin, palpa polypeptide TUBGT U61234 Tubulin, palpa polypeptide TUBCC U61234 Tubulin, palpa polypeptide TUBCC U61234 Tubulin, palpa polypeptide TUBCC U61232 Tubulin, palpa polypeptide TUBCC U61232 Tubulin, palpa polypeptide TUBCC U61234 Tubulin, palpa polypeptide TUBCC U61232 TUBCC	25533	38121_at			tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
TUFM S75463 mitochondrial TULP3 Al028290 tubby like protein 3 TULP3 Al028290 tubby like protein 3 TUBB AF035316 tubulin, beta polypeptide TUBB AF03535 tubulin, beta polypeptide TUBB AF0344 tubulin, peta polypeptide TUBB AF0344 tubulin, gamma l TUBB AF0348 tubulin, specific chaperone c TUBB Lumor necrosis factor receptor TURESE LOB AF016266 superfamily, member 12 (translocating TUMPASE1 U83598 chain-association membrane protein) AK0526 superfamily, member 13 (translocating TUMOR NECROSIS factor receptor tumor necrosis factor receptor TURAINESE X60592 superfamily, member 6 TUMOR NECROSIS factor receptor tumor necrosis factor receptor </td <td></td> <td></td> <td></td> <td></td> <td>Tu translation elongation factor,</td> <td></td>					Tu translation elongation factor,	
TULP3 Al028290 tubby like protein 3 K-ALPHA-1 K00558 tubulin, alpha, ubiquitous 1 TUBB X78535 tubulin, beta polypeptide 1 TUBB X78535 tubulin, beta polypeptide 1 TUBB X78535 tubulin, gamma 1 1 TBCC U61232 tubulin-specific chaperone c 0 TBCE U61232 tubulin-specific chaperone c 0 TDE1 U49188 tumor necrosis factor receptor 0 TNFRSF10B AF016266 superfamily, member 12 (translocating 0 TNFRSF1A M58286 superfamily, member 12 (translocating 0 TNFRSF5 X60592 superfamily, member 5 0 TNFAIP M80783 0 0	2554 3	19867_at	TUFM	S75463	mitochondrial	P43
K-ALPHA-1 K00558 tubulin, alpha, ubiquitous tubulin, beta polypeptide TUBB X79535 tubulin, beta polypeptide TUBB X79535 tubulin, beta polypeptide TUBB X79535 tubulin, beta polypeptide TBC U61234 tubulin-specific chaperone e TBCC U61232 tubulin-specific chaperone e TBC U64232 tubulin-specific chaperone e TBC U64232 tubulin-specific chaperone e TNFRSF10B AF016266 superfamily, member 10b tumor necrosis factor receptor superfamily, member 12 (translocating tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced <td>25553</td> <td>31944_at</td> <td>TULP3</td> <td></td> <td>tubby like protein 3</td> <td></td>	25553	31944_at	TULP3		tubby like protein 3	
TUBB AF035316 tubulin, beta polypeptide at TUBB X79535 tubulin, beta polypeptide TUBG1 M61764 tubulin, peta polypeptide 1 TBCC U61234 tubulin-specific chaperone c 1 TBCE U61232 tubulin-specific chaperone c 1 TBCE U61232 tubulin-specific chaperone c 1 TDE1 U49188 tumor differentially expressed 1 1 TDE1 U49188 tumor differentially expressed 1 1 TDE1 U49188 tumor necrosis factor receptor 1 TNFRSF10B AF016266 superfamily, member 12 (translocating protein) 1 TNFRSF12 U83598 chain-association membrane protein) 1 TNFRSF1A M58286 superfamily, member 12 (translocating protein) 1 TNFRSF5 X60592 superfamily, member 5 1 TNFRSF6 X63717 superfamily, member 6 1 TNFAIP1 M80783 protein 1 1 TNFAIP2 M59465 prot	25563	32272_at	K-ALPHA-1		tubulin, alpha, ubiquitous	tubulin, atpha, ubiquitous
TÜBB X79535 tubulin, beta polypeptide TÜBG1 M61764 tubulin-specific chaperone c TBCC U61234 tubulin-specific chaperone c TBCC U61232 tubulin-specific chaperone e TBCE U61232 tubulin-specific chaperone e TDE1 U49188 tumor necrosis factor receptor TNFRSF10B AF016266 superfamily, member 10b TNFRSF12 U83598 chain-association membrane protein) TNFRSF13 M58286 superfamily, member 12 (translocating tumor necrosis factor receptor TNFRSF3 X60592 superfamily, member 5 TNFRSF6 X63717 superfamily, member 6 TNFAIP1 M80783 tumor necrosis factor receptor TNFAIP2 M60783 protein 1 (endothelial) TNFAIP2 M92357 protein 1 (endothelial) TNFAIP3 M59465 protein 2 TNFAIP3 M59465 protein 2 TPD52L2 tumor protein D52-like 2 TPD53BP2 tumor protein D52-like 2 TPS3BP1 tumor protein p53 binding prote	2557 3	39332_at	TUBB	AF035316	tubulin, beta polypeptide	
TUBG1 M61764 tubulin, gamma 1 TBCC U61234 tubulin-specific chaperone c TBCE U61232 tubulin-specific chaperone e TDE1 U49188 tumor differentially expressed 1 TNFR tumor necrosis factor receptor TNFRSF10B AF016266 superfamily, member 10b TNFRSF12 U83598 chain-association membrane protein) TNFRSF14 M58286 superfamily, member 12 (translocating superfamily, member 14 TNFRSF5 X60592 superfamily, member 1A TNFRSF6 X63717 superfamily, member 5 TWMOT necrosis factor receptor tumor necrosis factor receptor TNFAIP1 M80783 tumor necrosis factor alpha-induced TNFAIP2 M92357 protein 1 (endothelial) TNFAIP3 M59465 protein 2 TNFAIP3 M59465 protein 2 TPD52L2 AF004430 tumor protein D52-like 2 TP53BP2 U58334 tumor protein D53 binding protein, 1 TP53BP1 tumor protein D53-binding protein, 2	25583	39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
TBCC U61234 tubulin-specific chaperone c TBCE U61232 tubulin-specific chaperone e TDE1 U49188 tumor differentially expressed 1 TDE1 U49188 tumor necrosis factor receptor TNFRSF10B AF016266 superfamily, member 10b TNFRSF12 U83598 chain-association membrane protein) TNFRSF14 M58286 superfamily, member 12 (translocating chain-association membrane protein) TNFRSF1A M58286 superfamily, member 14 TNFRSF5 X60592 superfamily, member 14 TNFRSF6 X63717 superfamily, member 5 TNFAIP1 M80783 tumor necrosis factor aceptor TNFAIP2 M92357 tumor necrosis factor, alpha-induced TNFAIP2 M59465 tumor necrosis factor, alpha-induced TNFAIP3 M59465 tumor necrosis factor, alpha-induced TNFAIP3 M59465 tumor necrosis factor, alpha-induced TNF3BP1 tumor protein 2 tumor protein 3 TNF3BP2 tumor protein D52-like 2 TNF3BP1 tumor protein p53 binding prot	2559 3	33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
TBCE U61232 tubulin-specific chaperone e TDE1 U49188 tumor differentially expressed 1 TDE1 U49188 tumor necrosis factor receptor TNFRSF10B AF016266 superfamily, member 10b tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) tumor necrosis factor receptor t TNFRSF1A M58286 superfamily, member 1A t tumor necrosis factor receptor tumor necrosis factor receptor t TNFRSF5 X60592 superfamily, member 5 t tumor necrosis factor alpha-induced t tumor necrosis factor, alpha-induced t tumor protein D52-like 2 t </td <td>25603</td> <td>36176 at</td> <td>TBCC</td> <td>U61234</td> <td>tubulin-specific chaperone c</td> <td>cofactor C</td>	25603	36176 at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
TDE1 U49188 tumor differentially expressed 1 TNFRSF10B AF016266 superfamily, member 10b TNFRSF10B AF016266 superfamily, member 10b TNFRSF12 U83598 chain-association membrane protein) TNFRSF1A M58286 superfamily, member 12 (translocating chain-association membrane protein) TNFRSF1A M58286 superfamily, member 1A TNFRSF5 X60592 superfamily, member 5 TNFRSF6 X63717 superfamily, member 6 TNFAIP1 M80783 tumor necrosis factor receptor TNFAIP2 M92357 tumor necrosis factor, alpha-induced TNFAIP2 M92357 protein 1 (endothelial) TNFAIP3 M59465 protein 2 TNFAIP3 M59465 protein 2 TNFAIP3 M59465 protein 3 TNFAIR91 U09477 tumor protein D52-like 2 TP53BP1 U08477 tumor protein p53 binding protein, 1 TP53BP1 U08233 tumor protein p53 binding protein, 2 TP53BP1 U082939 tumor protein p53-binding protein, 2 <td>2561</td> <td>35159_at</td> <td>TBCE</td> <td>U61232</td> <td>tubulin-specific chaperone e</td> <td>cofactor E</td>	2561	35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
TNFRSF10B AF016266 tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) TNFRSF12 U83598 chain-association membrane protein) TNFRSF14 M58286 superfamily, member 12 (translocating chain-association membrane protein) TNFRSF5 X60592 superfamily, member 5 (tumor necrosis factor receptor superfamily, member 6 (tumor necrosis factor alpha-induced protein 1 (endothelial) TNFAIP1 M80783 protein 1 (endothelial) TNFAIP2 M92357 protein 2 (tumor necrosis factor, alpha-induced protein 2 (tumor necrosis factor, alpha-induced protein 3 (tumor protein 53 binding protein, 1 (tumor protein 53 binding protein, 1 (tumor protein p53 binding protein, 2 (tumor protein p53 binding protein, 2 (tumor protein p53-binding protein) 2 (tumor	2562	37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
TNFRSF10B AF016266 Superfamily, member 10b					tumor necrosis factor receptor	
tumor necrosis factor receptor superfamily, member 12 (translocating superfamily, member 12 (translocating chain-association membrane protein) tumor necrosis factor receptor superfamily, member 14 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor alpha-induced protein 1 (endothelial) tumor necrosis factor, alpha-induced protein 2 tumor necrosis factor, alpha-induced protein 2 tumor necrosis factor, alpha-induced protein 2 tumor necrosis factor, alpha-induced protein 3 tumor protein p53 binding protein, 1 tumor protein p53 binding protein, 1 tumor protein p53 binding protein, 2 tumor protein p53-binding protein, 2 tumor p53-binding protein, 2 tumor p54-binding protein, 2 tumor p54-binding pr	2563	34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
1190_at TNFRSF12 U83598 chain-association membrane protein) 1563_s_at TNFRSF1A M58286 tumor necrosis factor receptor 35150_at TNFRSF5 X60592 superfamily, member 5 37643_at TNFRSF6 X63717 superfamily, member 5 38631_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP538P1 U09477 tumor protein p53 binding protein, 1 34822_at TP538P2 tumor protein p53 binding protein, 2 40076_at TP538P1 tumor protein p53 binding protein, 2 40076_at TP538P2 tumor protein p53 binding protein, 2 48822_at TP538P2 tumor protein p53-binding protein, 2 40076_at TP538P2 tumor protein p53-binding protein, 2					tumor necrosis factor receptor	
11190_at TNFRSF12 U83598 chain-association membrane protein) 1563_s_at TNFRSF1A M58286 superfamily, member 1A 35150_at TNFRSF5 X60592 superfamily, member 5 37643_at TNFRSF6 X63717 superfamily, member 5 38631_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 2 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP1 U08433 tumor protein p53 binding protein, 2 40076_at TP53BP1 tumor protein p53 binding protein, 2 40076_at TP53BP1 tumor protein p53 binding protein, 2 40076_at TP53BP1 tumor protein p53-binding protein, 2					superfamily, member 12 (translocating	
1563_s_at TNFRSF1A M58286 superfamily, member 1A	2564	41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
1563_s_at TNFRSF1A M58286 superfamily, member 1A 35150_at TNFRSF5 X60592 superfamily, member 5 37643_at TNFRSF6 X63717 superfamily, member 5 36988_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP1 U084334 tumor protein p53 binding protein, 2 4868 at TP53BP1 U08239 tumor protein p53-binding protein, 2					tumor necrosis factor receptor	
35150_at TNFRSF5 X60592 superfamily, member 5 37643_at TNFRSF6 X63717 superfamily, member 5 36988_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP1 U08239 tumor protein p53-binding protein, 2 40076_at TP53BP1 U09477 tumor protein p53 binding protein, 2 40076_at TP53BP1 tumor protein p53-binding protein, 2	2565	1563_s_at	TNFRSF1A	M58286	superfamily, member 1A	tumor necrosis factor receptor
35150_at TNFRSF5 X60592 superfamily, member 5 37643_at TNFRSF6 X63717 superfamily, member 6 36988_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP1 U82334 tumor protein p53 binding protein, 2 1753BP1 U82939 tumor protein p53-binding protein, 2					tumor necrosis factor receptor	
37643_at TNFRSF6 X63717 tumor necrosis factor receptor 36988_at TNFAIP1 M80783 tumor necrosis factor, alpha-induced 36988_at TNFAIP2 M92357 protein 1 (endothelial) 38631_at TNFAIP2 M92357 protein 2 40076_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2 1753BP1 U82939 tumor protein p53-binding protein, 2	2566	35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
37643_at TNFRSF6 X63717 superfamily, member 6 36988_at TNFAIP1 M80783 tumor necrosis factor, alpha-induced 38631_at TNFAIP2 M92357 protein 1 (endothelial) 595_at TNFAIP2 M92357 protein 2 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP1 U82939 tumor protein p53-binding protein, 2 38568_at TP53BP1 U82939 tumor protein p53-binding protein, 2					tumor necrosis factor receptor	:
36988_at TNFAIP1 M80783 tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced protein 2 38631_at TNFAIP2 M92357 protein 2 tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced protein 3 595_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BPL U82939 tumor protein p53-binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein	2567	37643	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
36988_at TNFAIP1 M80783 protein 1 (endothelial) 38631_at TNFAIP2 M92357 tumor necrosis factor, alpha-induced 595_at TNFAIP3 M59465 protein 2 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BPL U82939 tumor protein p53-binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein					tumor necrosis factor, alpha-induced	
38631_at TNFAIP2 M92357 protein 2 595_at TNFAIP3 M59465 protein 2 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BPL U82939 tumor protein p53-binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein	2568	36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
38631_at TNFAIP2 M92357 protein 2 595_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BPL U82939 tumor protein p53-binding protein					turnor necrosis factor, alpha-induced	
595_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BPL U82939 tumor protein p53-binding protein 38568_at TP53BPL U82939 tumor protein p53-binding protein	2569		TNFAIP2	M92357	protein 2	B94 protein
595_at TNFAIP3 M59465 protein 3 40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP538P1 U09477 tumor protein p53 binding protein, 1 34822_at TP538P2 U58334 tumor protein p53 binding protein, 2 38568 at TP538PL U82939 tumor protein p53-binding protein					tumor necrosis factor, alpha-induced	
40076_at TPD52L2 AF004430 tumor protein D52-like 2 1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein	2570	595_at	TNFAIP3	M59465	protein 3	A20
1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein	2571	40076_at	TPD52L2	AF004430	tumor protein D52-like 2	hD54+ins2 isoform
34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2 38568_at TP53BPL U82939 tumor protein p53-binding protein	2572	1711	TP538P1	U09477	tumor protein p53 binding protein, 1	p53-binding protein
TP53BPL U82939 tumor protein p53-binding protein	2573	34822_at	TP538P2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
	2574	38568_at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

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F 75 3	2575 31584 at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
2	201				į
5763	2576 31888 s at	TSSC3	AF001294		IPL
2577 147_at	47_at	TSG101	U82130	tumor susceptibility gene 101	turnor susceptibility protein
_				twist homolog (acrocephalosyndactyly 3;	•
5784	2578 40328 at	TWIST	X99268		B-HLH DNA binding protein
5702	2579 2086 s at	TYRO3	D17517		SKY
2002		TYRO3	U18934	7	receptor tyrosine Kinase
3	05-10-dt			tophan 5-	tyrosine 3-monooxygenase/tryptopnan 5-
				monooxygenase activation protein, beta	monooxygenase activation protein, beta
25813	2581 32324 at	YWHAB	X57346	polypeptide	polypeptide
3				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2582 409 at	# 601	YWHAO	X56468	polypeptide	14.3.3 protein
3	5-02			tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	•
2020	7502 22530 at	VWHAD	X56468	polypeptide	14.3.3 protein
2027	05200_at			tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, zeta	:
PODC	0E04 1035 at	YWHA7	M86400	polypeptide	phospholipase A2
1007	2304 1233 at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sufforansierase-1
2500	2303 327 10_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfofransferase-2
25.00	2587 38077 at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tHNA synthetase
1000	n - 1 1 2 2 2			U2(RNU2) small nuclear RNA auxillary	Handra II and reference in the control of the
2588	2588 36517 at	U2AF1	M96982	factor 1	UZ SNKINP auxiliary raciol siliali subulin
25.89	2589 32858 at	UBN1	Al341565	ubinuclein 1	
2590	2590 34824 at	UBQLN2	AB015344	ubiquilin 2	ubiquiin 2
				ubiquinol-cytochrome c reductase (6.4kD)	
2591	38451 at	UQCB	T58471	subunit	
				ubiquinol-cytochrome c reductase binding	
2502	2592 39427 at	UOCRB	T79616	protein	
				ubiquinot-cytochrome c reductase core	ubiquinol-cytochrome c reductase core
2593	2593 40854 at	UQCRC2	J04973	protein II	protein II

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T)	,	ubiquinol-cytochrome c reductase hinge	
2594	2594 36104_at	UQCRH	AA526497	protein	
2595 1366	1366_i_at	NBC	M26880	ubiquitin C	ubiquitin C
2596 1367	1367_f_at	UBC	M26880		ubiquitin C
				arboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	2597 36990_at	UCHL1	X04741	(ubiquitin thiolesterase)	(ubiquitin thiolesterase)
2598	2598 811_at	UFD1L	U64444	ubiquitin fusion degradation 1-like	ubiquitin fusion-degradation 1 like protein
2599	2599 40623_at	UBE3B	AI749193	ubiquitin protein ligase	
				ubiquitin protein ligase E3A (human	
				papilloma virus E6-associated protein,	E6-associated protein E6-AP/ubiquitin-
2600	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2601	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602 37683_at	USP10	D80012	ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
				ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA 1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KIAA 1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	Т)	isopeptidase T
				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z72499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	
2611	2611 32572_at	USP9X	X98296	chromosome (fat facets-like Drosophila)	ubiquitin hydrolase
				ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	
2613	2613 36579 at	I IBEAA ·	D50916	ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
	3-	100		ubianitination factor E4D / IED3 hamalad) cacy
2614	2614 41339 at	UBE4B	AF043117	veast)	ubiquitin-fusion degradation protein 2
				7, 7,	
2615	2615 36959_at	UBE2V1	U49278	ubiquitin-conjugating enzyme E2 variant 1 UEV-1	UEV-1

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616	A	В	၁		E
218					
216 20				conjugating enzyme E2A (RAD6	ubiquitin-conjugating enzyme EZA (KADS
200	2616 890 at	UBE2A	M74524		homolog)
				ubiquitin-conjugating enzyme E2D 1	
617 37	2617 37826 at	UBE2D1	AF020761	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
618 38	2618 38705 at	UBE2D2	Al310002	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2619 832 at	32 at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
-				ubiquitin-conjugating enzyme E2D 3	
620 35	2620 39083 at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
	1			ubiquitin-conjugating enzyme E2D 3	
2621 504 at	34 at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C :
				ubiquitin-conjugating enzyme E2E 3	
2622 34	2622 34850 at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
-				ubiquitin-conjugating enzyme E2G 2	
2623 3;	2623 32236 at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
				ubiquitin-conjugating enzyme E2I (UBC9	
2624 38480	8480_s_at	UBE2I	U66867	homolog, yeast)	ubiquitin conjugating enzyme 9
-				ubiquitin-conjugating enzyme E2I (UBC9	;
2625 8	2625 838_s_at	UBE2I	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
2626 223_at	23_at	UBEZL3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627 4	2627 40505 at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
				ubiquitin-conjugating enzyme E2N	:
26283	2628 36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629 4	2629 457 s at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
2630 1	2630 155 s at	UBL1	U61397	ubiquitin-like 1 (sentrin)	ubiquitin-homology domain protein PIC1
26314	2631 40839 at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632 3	2632 37336 at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
				UDP-Gal:betaGlcNAc beta 1,4-	
2633 4	2633 40960 at	B4GALT1	D29805	galactosyftransferase, polypeptide 1	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
26343	2634 34177 at	B4GALT2	AF038660	galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
2635	2635 39445_at	B4GALT3	AF038661	galactosyltransferase, polypeptide 3	beta-1,4-galactosyltransferase
				UDP-glucose ceramide	3
2636	2636 40215 at	nece	D50840	glucosyltransferase	ceramide glucosyltransferase

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2637	2637 35214_at	ИСП	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
2638	2638 37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2	uridine diphosphoglucose pyrophosphorylase
5639	2639 38041_at	GALNT1	U41514	UDP-N-acetyl-alpha-D- galactosamine;polypeptide N- acetylgalactosaminyltransferase 1 (GalNAc-T1)	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransferase
2640	2640 36515_at	GNE	AJ238764	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	UDP-N-acetylglucosamine-2-epimerase/N-UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2641	2641 41242_at	UAP1	AB011004	UDP-N-acteylglucosamine pyrophosphorylase 1	UDP-N-acetylglucosamine pyrophosphorylase
2642	2642 34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
2643	2643 37315_f_at	BM036	A1057607	uncharacterized bone marrow protein BM036	
2644	2644 35750_at	HT010	AL049948	uncharacterized hypothalamus protein HT010	
2645	2645 41058 g at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2646	2646 41057_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2647	2647 38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	keratin 10
2648	2648 34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
2649	2649 34372 at	UREB1	AB002310	upstream regulatory element binding protein 1	upstream regulatory element binding protein
2650	2650 37686 s at	UNG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
				uridine monophosphate synthetase (orotate phosphoribosyl transferase and	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-
2651	2651 33815_at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
2652	2652 41859 at	UST	AB020316	uronyl-2-sulfotransferase	dermatan/chondroitin sulfate 2- sulfotransferase
0000		0,0	Xoonso	UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene	n63 (processed form)
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					v-abl Abelson murine leukemia viral
_					oncogene homolog 1 isoform a; v-abl
				v-abl Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654	2654 39730_at	ABL1	X16416		homolog 1 isoform b
2655 35779	at		AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
				VAMP (vesicle-associated membrane	
2656 38801	38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
					vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657	2657 583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658 1953	1953_at	VEGF	AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659	2659 36100 at	VEGF	AF022375	vascular endothelial growth factor	vascular endothelial growth factor
Γ					VEGF related factor isoform VRF186
2660	2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	precursor
		C L	07707		vascular endothelial growth factor related
2661	2661 159_at	VEGFC	043142	vascular endotnellal growin lactor C	protein
				VDAC protein: similar to mouse VDAC 3:	
				Homo sapiens voltage dependent anion	
2662	2662 36102 at	VDAC3: HD.VDAC	AE038962	channel protein mRNA complete cds.	voltage dependent anion channel protein
2663	2663 40147 at		U18009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	2664 33930 at	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
	1.			vesicle-associated membrane protein 2	
2665	2665 32254 at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VIL2	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091 s at	VIM	Z19554	vimentin	vimentin
					vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	VCL
2670	2670[39091 at	JWA	AF070523	vitamin A responsive: cytoskeleton related JWA protein	JWA protein
	ı			vitamin D (1,25- dihydroxyvitamin D3)	vitamin D (1,25- dihydroxyvitamin D3)
2671	2671 1388_g_at	VDR	J03258	receptor	receptor
				v-Ki-ras2 Kirsten rat sarcoma 2 viral	
2672	2672 1940 at	KRAS2	M54968	oncogene homolog	K-ras oncogene protein

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r	A	В	ပ	Q	ш
1 2	10 0 70 21	U V V V	AE055376	v-maf musculoaponeurotic fibrosarcoma	short form transcription factor C-MAF
200	20/3 4 1304_5_all	IMIMI	0.0000	fibrocarcoma	
- 5	100001100	27 6 7	A A 725102	villal mascalcapolical cus ocar come on concorde homolog E (avian)	
20/4	20/4 32035 at	VDAC1	1.06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	2675 42195 at	VDAC2	L06328		voltage-dependent anion channel
2677	2677 171 at	VBP1	U56833		VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743 f at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776 at	RALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2680	2680 36645 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674 at	YES1	M15990	oncogene homolog 1	homolog 1
				v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
2683	2683 1402 at	LYN	M16038	oncogene homolog	oncogene homolog
2684	2684 1058 at	WASF3	Se9790	WAS protein family, member 3	
2685	2685 38736 at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
2687	2687 36009 at	CL683	AF091092	weakly similar to glutathione peroxidase 2	weakly similar to glutathione peroxidase 2 weakly similar to glutathione peroxidase 2
2688	2688 36909_at	WEE1	X62048	WEE1+ homolog (S. pombe)	wee1 tyrosine kinase
					eukaryotic translation initiation factor 4H,
				Williams-Beuren syndrome chromosome	isoform 1; eukaryotic translation initiation
2689	2689 41212 r at	WBSCR1	D26068	region 1	factor 4H, isoform 2
2690	2690 41635 at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
				wingless-type MMTV integration site	wingless-type MMTV integration site family,
2691	2691 31862_at	WNT5A	L20861	family, member 5A	member 5A precursor

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			t		Wolf-Hirschhorn syndrome candidate 2
2692	2692 34225_at	WHSC2	AF101434	indidate 2	protein
2693	2693 33438_at	WBP2	AL049981	WW domain binding protein 2	
Γ				WW domain binding protein 4 (formin	
2694	2694 35213_at	WBP4	AF071185		formin binding protein 21
2695	2695 39995_s_at	WWOX	U13395	WW domain containing oxidoreductase	oxidoreductase
				WW domain-containing adapter with a	
2696	2696 36822_at	WAC	U51334		putative RNA binding protein RBP56
_				xeroderma pigmentosum,	
7697	2697 1307_at	XPA	D14533	complementation group A	XPAC protein
				xeroderma pigmentosum,	
2698	2698 1873_at	XPC	D21089	complementation group C	XP-C repair complementing protein (p125)
				XPA binding protein 1; putative ATP(GTP)-	
, 5692	2699 41756_at	NTPBP	AJ010842	binding protein	ATP(GTP)-binding protein
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2700	2700 38733_at	XRCC5	M30938	80KD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
		•		repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2701 585	585_at	XRCC5	M30938	80KD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2702	2702 2093_s_at	XRCC5	J04977	80kD)	ATP-dependant DNA helicase II
2703	2703 35827_at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704	2704 40988_at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705	2705 891_at	YY1	M77698	YY1 transcription factor	GLI-Krupple related protein
				zb29g04.s1	
				Soares_parathyroid_tumor_NbHPA Homo	
				sapiens cDNA clone IMAGE:305046 3',	
2706	2706 34887_at		N92548	mRNA sequence.	
2707	36308 at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	Zic protein
2708	2708 35681 r at	ZFHX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein

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5/03	34/86_at	ISGA	82	zinc tinger protein	NIMAU 42 protein
2710	39977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
		i i			
7/1/2	2/11/40140 at	ZFP103		Zinc linger protein 103 nomiolog (mouse)	Zinc imger protein 103 nomong
2712	2712 36295_at	ZNF134		zinc finger protein 134 (cione pHZ-15)	Zinc tinger protein Zinr 134
2713	32192_g_at	ZNF144		zinc finger protein 144 (Mel-18)	Mel-18 protein
2714	36928_at	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715	2715 41532_at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716	2716 32628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717	2717 41436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718	2718 40724_at	ZNF200		zinc finger protein 200	zinc finger protein
2719	2719 35368_at	ZNF207	AF046001	zinc finger protein 207	zinc finger protein 207
2720	2720 41542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721	2721 840_at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722	2722 39762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723	2723 34299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724	2724 39005_s_at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725	2725 37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
				zinc finger protein 36, C3H type, homolog	
2726	2726 40448_at	ZFP36	M92843	(mouse)	zinc finger transcriptional regulator
2727	2727 38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728	2728 36046_at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
		1	7,70000		hypothetical protein, similar to (U06944)
57.53	2729 32129_at	ZINF364	ALU/9314	Zinc linger protein 304	LUNACH [Wilds IIIInsculla]
2730	2730 41033 <u>_</u> at	ZNF84	M27878	zinc finger protein 84 (HPF2)	DNA binding protein
2731	2731 40610_at	ZFR	AI743507	zinc finger RNA binding protein	
2732	2732 39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
				zinc metalloproteinase (STE24 homolog,	
2733	2733 33912_at	ZMPSTE24	Y13834	yeast)	farnesylated-proteins converting enzyme 1
2734	2734 36521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735	2735 35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736	2736 706_at		HG4582-HT4987		
2737	2737 960_g_at		HG2463-HT2559		
2738	2738 956_at		HG1980-HT2023		
2739	2739 955_at		HG1862-HT1897		
2740	2740 324 f at		HG1515-HT1515		

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2741	2741 327 f at		HG1800-HT1823		
2742	2742 333_s_at		HG2639-HT2735		
2743	2743 1840_g_at		HG1112-HT1112		
2744	2744 1664_at		HG3543-HT3739		
2745	2745 1624_at		HG2036-HT2090		
2746	2746 1278_at		HG162-HT3165		
2747	2747 1179_at		HG2855-HT2995		
2748	2748 1180_g_at		HG2855-HT2995		
2749	2749 32243_g_at		AL038340		
2750	2750 311_s_at		HG3044-HT3742		
2751	2751 297_g_at		HG4322-HT4592		
2752	2752 296_at		HG4322-HT4592		
2753	2753 1839_at		HG1112-HT1112		
2754	2754 723 s at		HG1322-HT5143		
					guanine nucleotide binding protein (G
2755	2755 33300_at	dJ283E3.1	AL031282		protein), beta polypeptide 1
					guanine nucleotide binding protein (G
2756	2756 41249_at	dJ283E3.1	AL031282		protein), beta polypeptide 1

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